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Perfect score:
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

RESULT AAW17837

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AAW17837 standard; Protein; 419

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08-NOV-1995; 95US-0554374.	05-NOV-1996; 96WO-US17584.	15-MAY-1997.	WO9717442-A1.	/note= "(Claim 9)"			/Label= Mat_protein	Protein 21419		Peptide 120	Key Location/Qualifiers		Homo sapiens.		wound healing; tumour; therapy; antagonist; antibody.	receptor tyrosine kinase; vasculogenesis; angiogenes:	Foetal liver kinase 1 binding protein; human; flk-1bp		Human foetal liver kinase A binding protein flk-lbp.		13-JAN-1998 (first entry)		AAW17837;		

AAY30518

Human Flt4 receptor tyrosine kinase ligand VEGF-C.

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The mature flk1-bp can be secreted from host cells transformed with an expression vector including an isolated flk-lbp cDNA clone (see CAM58811). Flk-lbp can be used to isolate cells to which it binds, for use in studying the roles of such cells and of flk-lin crossion vasculogenesis. Angiogenesis inhibition or increased vascularisation may be clinically desirable (e.g. to suppress solid tumour growth or in wound healing, respectively).

The flk-lbp can be administered to treat conditions with defective or insufficient flk-1. Polypeptides may also act as carriers to deliver diagnostic/therapeutic agents to cells to which flk1-bp binds, to generate antibodies, and to identify flk-lbp antagonists of useful for treating flk-lbp mediated conditions.
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             10-NOV-1997
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This polypeptide comprises the pre-pro sequence of human VEGF-C, a novel ligand that binds specifically to human Flt4 receptor tyrosine kinase (VEGFR-3), stimulating phosphorylation of the receptor. Its sequence was deduced from a CDNA clone (AAT84276) obtd. from a PC-3 prostatic adenocarcinoma cell (ATCC CRL 1435) library. The polypeptide, or its active fragments, can be expressed in transformed or transfected host cells for use in claimed methods for detecting endothelial cells (e.g. to image lymphatic vessels, endothelial venules, Flt4 receptor in histochemical tissue) and also to modulate the growth of mammalian receptor in the state of the st
                                                                                                                                                                                                                                                                                              Flt4 receptor tyrosine kinase ligand and related nucleic acid to modulate growth of endothelial cells and for diagnosis of endothelial cell diseases  \begin{array}{c} \\ \\ \\ \\ \end{array} 
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angiogenesis; wound healing; lymph vessel; lymphangioma;
cancer; metastasis; therapy; diagnosis; antibody; inhibitor
                      endothelial
                                                                                                                                                                                                                                                         Claim 7; Page 112-113; 183pp; English.
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N-PSDB; AAT84276.
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12-JAN-1996;
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419; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 112-115; 177pp; English.
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Pred. No. 8.9e-173;
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                                                                                                                                               VEGF; VRP; vascular endothelial growth factor; VEGF-related recombinant; truncated; gene therapy; anglogenesis; cardiad coronary; collateral vessel development; cell growth; migralower limb ischaemia; stroke; peripheral vascular disease; wound healing; skin; vascular permeability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human vascular endothelial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth factor (VEGF)-C sequence
                                                                                                                                                                                                                                                                                                       h factor; VEGF-related prote angiogenesis; cardiac ischant; cell growth; migration;
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intestine; protein; ischaemia;

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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subunits - lack part of the N-terminal sequence, used to stimulate angiogenesis, e.g. for treating heart disease and ischaemia
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XX WO2
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XX WO2
  22-DEC-1998;
18-MAR-1999;
08-NOV-1999;
                                                                                                                    retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote
                                                                                                                                                                                                                                          This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGF-X; vascular endothelial growth factor; human: vulnerary; cytostatic; antirheumatic; antiarthritic; antiporiatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
                                      skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting anglogenic activity or vascularization. This sequence represents the human VEGC protein used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gordon RD,
Dhanaraj SN,
Sequence
                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 11; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-442669/38
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                                                                                                  The present sequence is the protein sequence for the human vascular endothelial growth factor C (VEGF-C). It was used to demonstrate the methods of the invention, which involve the screening of individuals to determine which vascular endothelial growth factor receptor 3 (VEGFR-3, also known as Flt4 or fms-like tyrosine kinase 4) alleles they possess and thus their likelihood of developing hereditary lymphoedema. Conditions associated with lymphoedema include Milroy-Nonne syndrome,
                                                                                                                                                                                                                                                                                                                                                                     altering the receptor-3 -
                                                                                                                                                                                                                                                                                                                                                                                        Screening a human subject for increased risk of developing a lymphatic disorder, comprises assaying a nucleic acid to determine a mutation altering the sequence of a vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vascular endothelial growth factor receptor 3; VEGF Milroy-Nonne syndrome; lymphoedema praecox; VEGF-C; vascular endothelial growth factor C.
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tor 3; VEGFR-3;
                                                                            praecox,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419;
                                                                                                                                                                                                                                                                                                                                                                          receptor tyrosine kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                              vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                eptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4 ascular endothelial growth factor receptor-3; chromosome 5q3; tumour imaging; anti-tumour therapy; treatment; diagnosis; disease; lymphoma; carcinoma; breast; squamous cell; melano alignancy; VEGF-C; vascular endothelial growth factor C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                     /note= "Has a pattern of spaced cysteine residues reminiscent of a Balbiani ring 3 protein (BR3P) sequence; clearage of signal peptide and the C-terminal peptide produces a partially processed form of VEGF-C of about 29 kD which has high affinity to Flt4 (VEGFR-3)"
                                                                                                                                                      104.
                                                                                                                                                                   VEGF-C
of 21-2
                                                                                                                                                                                                                        /label= Signal_peptide
32..103
                            113..213
                                                                                                                          228..419
                                                                                                                                                              /label= N-terminal_peptide
/note= "cleavage of this peptide from partially processed
VEGF-C produces a fully processed mature form of VEGF-C
of 21-23 kD which has high affinity to VEGFR-2"
               /note= "binds
                                                                                                               /label=
                                                                                                                                       /label= Mature_VEGF-C
                                                                                                                                                                                                                                                                  Location/Qualifiers
 position 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                          C-terminal_peptide
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Pred. No. 8.9e-173;
 is essential
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stimulates VEGF-C
s essential for VE
                                                                                                                                                                                                                                                                                                                                                                                                      growth factor C.
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               receptors; Cys
 binding
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                                                                                                                                                                                                                                                                                                                                                             kinase 4;
osome 5q35;
                                                                                                                                                                                                                                                                                                                      melanoma;
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 419; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method involves administering a compound that inhibits binding of a ligand to FIL4 thereby inhibiting FIL4 mediated proliferation of vascular endothelial cells. The compound is useful for treating neoplastic disease such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas and sarcomas. FIL4 receptor tyrosine kinase binding compounds can be used for manufacturing medicament useful for diagnostic screening, imaging and treatment of malignancies characterised by FIL4-expressing blood cells. The FIL4 gene maps to chromosomal region 535 and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in their 3' sequences and are differentially expressed in HEL and DAMI cell lines. FIL4 belongs to a subfamily of class III receptor tyrosine kinases (RTKs). It is used as a target for tumour imaging and anti-tumour therapy. The present sequence is a human prepro-vascular endothelial growth factor C (VBGF-C), a specific example of FIL4 binding compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses a method to treat neoplastic disease characterised by expression of fms-like tyrosine kinase 4 [Filt4] receptor (also referred as vascular endothelial growth factor receptor-3) in endothelial cells of blood vessels adjacent to malignant neoplasm. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating neoplastic diseases such as lymphoma, carcinomas, melanomas and sarcomas, involves administering a compound capable of inhibiting binding of ligand proteins to fms-like tyrosine kinase-4 receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 15-17;
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                                                                                 PASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKCAC
                                                                                                                                                                                                                               LSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAAN 240
                                                                                                                                                                                                                                                                                                              \verb|sidnewrktqcmprevcidvg| kefgvatntffkppcvsvyrcggccnseglqcmntstsy|
                                                                                                                                                                                                                                                                                                                                                                        SIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSY 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,
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Pred. No. 8.9
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8.9e-173;
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                 Claim 5;
                                                        Preventing stenosis and restenosis endothelial growth factor proteins
                                                                                                                                                                                                                                                        (LUDW-)
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                                                                                                                                                                                          Yla-herttuala
                                                                                                                                                                                                                                                                                                                                                                  26-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human vascular endothelial growth factor (VEGF)-C protein.
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DB; AAD00339, AAD00353
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             Page
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endothelial growth factor receptor; VEGFR; vascular trauma;
ssel; cardiovascular surgery; anti-restenosis agent; prevention;
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                 51-53;
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228..419
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137
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/note= "Cl
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131..211
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104..227
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/note= "Processed vascular /
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/note= "Cleavage results in fu
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/note= "Cleavage resul
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"Cleavage results in part:
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29 kD)"
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                                                        mammals using vascular the nucleic acids encoder
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Query Match
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 (UYPI-) UNIV
                                     26-MAR-1999;
16-AUG-1999;
                                                                                           29-SEP-1999;
                                                                                                                                                                CA2283470-A1
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                     Human; gene therapy; lymphatic disorder; hereditary lymphedoema; vascular endothelial growth factor receptor-3; VEGFR-3; VEGF-C; vascular
                                                                                                                                                                                                                                                                                                             Human VEGF-C
                                                                                                                                                                                                                                                                                                                                               27-FEB-2001
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99US-0375248.
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Pred. No. 8.9e-173;
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Best Local
                                AAW13833;
                                                                   AAW13833 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to a method for screening an increased risk of developing a lymphatic disorder
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                                                                                                                                                                       ECTESPOKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRCVPSYWKRPQMS 419
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DB; AAC68953.
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Pred. No. 8.9e-173;
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                                                                                                                                                                                                                                                              A human vascular endothelial growth factor (VEGF)-related protein (VRP) (AAW1383) has been identified that binds to, and stimulates the phosphorylation of, the receptor tyrosine kinase FI44. It is postulated to be a third member of the VEGF protein family. Its amino acid sequence was deduced from a CDNA clone (AAT59329) obtd. From a glioma GG1 library. Recombinant VRF can be produced in transformed host cells and used: to promote growth of vascular and lymph endothelial cells; to stimulate phosphorylation of the tyrosine kinase domain of a FI44 receptor; as a diagnostic; as an additive to cell cultures; to screen for (ant)agonists: and to raise monoclonal antibodies used to treat conditions associated with excessive neovascularisation or vascular permeability. VRP may make it possible to avoid coronary by-pass surgery by stimulating growth of the collateral circulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               numen protein similar to vascular endothelial growth factor to treat e.g. wounds, tumours, rheumatoid arthritis, Kaposi sarcoma etc.
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Fig 1A-D; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor-releated protein; VRP; VEGF; receptor protein tyrosine kinase; Flt4; signal transduction; wound healing; vulnerary; rheumatoid arthritis; Kaposi's sarcoma;
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MHLLGFFSVACSLLAAALLPGPREAPAAAAAFESGLDLSDAEPDAGEATAYASKDLEEQL 60
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114
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                                                                                                                                                                                 99.6%;
99.8%;
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                                                                                                                                                                    0;
                                                                                                                                                                 Score 2327; DB 18;
Pred. No. 4.4e-172;
0; Mismatches 1;
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                                                                                                                                                                                           Length 419;
                                                                                                                                                                    Indels
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiogenesis; blood pressure; blood flow; immune system disorder; immune cell; cancer; autoimmune disorder; blood protein disorder; ataxia telangiectasia; common variable immunodeficiency; Digeorge syndrome; HIV infection; HIV-BLV infection; leukocyte adhesion deficiency syndrome; lymphopenia; phagocyte bactericidal dysfunction; severe combined immunodeficien wiskott-Aldrich disorder; anemia; thrombocytopenia; hemoglobinuria allergy; asthma; allergic asthma.
         The present sequence represents vascular endothelial growth factor-2 (VEGF-2). The VEGF-2 polypeptides have activities similar to VEGF. The VEGF-2 polypeptides stimulate the growth of vascular endothelial cells, stimulate endothelial cell migration, stimulate angiogenesis, decrease blood pressure, and increase blood flow. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating a medical condition. The VEGF-2 polypeptides or polynucleotides may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. The etiology of these immune deficiency of these immune cells.
                                                                                                                                                                                                                                                                                                                                                               13-MAR-1998;
30-JUN-1998;
                                                                                                                                                                              Claim 12; Fig 1A-E; 222pp; English
                                                                                                                                                                                                           New human vascular endothelial growth factor-2, used immune disorders and cancers -
                                                                                                                                                                                                                                                                        WPI; 1999-551399/46
                                                                                                                                                                                                                                                                                                                                                                                                           10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9946364-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human vascular endothelial growth factor-2; VEGF-2; vascular endothelial cell growth; endothelial cell
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                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN
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98US-0107997
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may
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RESULT 1
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AC AAY
AC AAY
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Best Local :
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                                             24-DEC-1997;
08-MAR-1994;
06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein disorders, ataxia telangiectasia, common variable immunodeficiency, Digeorge syndrome, HTV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich disorder, anemia, thrombocytopenia, or hemoglobinuria. They can also be used to modulate emostatic or thrombolytic activity. Similarly allergic reactions and conditions such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated.
  (HUMA-) HUMAN
                                                                                                                                                24-DEC-1997;
                                                                                                                                                                                                03-AUG-1999
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                                                                                                                                                                                                                                                                                                                                              endothelial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity
417; Conserv
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  GENOME
                                             97US-0999811.
94US-0207550.
95US-0465968.
                                                                                                                                                97US-0999811.
                                                                                                                                                                                                                                                                                                                                       endothelial growth factor proliferation; tissue dam
                                                                                                                                                                                                                                                                                                                                                                                                                VEGF2 protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
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Pred. No. 5.3e-172;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                            tissue damage;
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RESULT 1
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DT 22-D
CX Vasc
XX Va
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Best Local·S
Matches 417
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                                                                     WO200045835-A1
                                                                                                                                                             age-related
                                                                                                                                                                                  treatment; injury; degeneration;
angioid streaks; retinitis; pigme
                                                                                                                                                                                                                             Vascular endothelial growth factor 2; VEGF-2; retina;
                                                                                                                                                                                                                                                                                                                          22-DEC-2000
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the treatment
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les 417; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ktcptnymwnnhicrclagedfmfssdagddstdgfhdicgpnkeldeetcqcvcraglr
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DB; AAX84837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     equence is the vascular endothelial growth factor 2 (VEGF2), invention. The isolated polypeptide is useful for stimulating enesis, by promoting the proliferation of endothelial cells, from the factor of a wound, or for the treatment of tissue or bone dam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hu
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                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 419
                                                                                                                                                        degeneration; photoreceptors; eye;
tinitis; pigmentosa; human;
degeneration; diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.5%;
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                                                                                                                                                                                                                                                                             factor-2
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Pred. No. 5.3e-172;
1; Mismatches 1;
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12-FEB-1999;
03-JUN-1999;
22-DEC-1999;
       Human VEGF-B protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Administration of vascular endothelial growth factor 2 (VEGF-2) to a patient can be used for treating injury or degeneration of photoreceptors associated with e.g. angloid streaks, retinitis pigmentosa, age-related macular degeneration, diabetic retinopathy, etc. VEGF-2 promotes anglogenessis, the formation of new blood
                           05-APR-2001
                                                                AAY97570 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating injury or degeneration of photoreceptors comprises administering to a subject vascular endothelial growth factor 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            vessels in the retina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 31; Fig la-e;
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                                                                                                              PASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKCAC
                                                                                                                                                                                                                                           LSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAAN
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                                                                                                                                                      pascgphkeldrnscqcvcknklfpsqcganrefdentcqcvckrtcprnqplnpgkcac
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                          (first entry)
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99US-0119926.
99US-0137796.
99US-0171505.
                                                                 Protein; 419
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Pred.
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No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
5.3e-172;
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Matches Query Match Best Local (

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Similarity

99.6%;

Score 2326; DB 22; Pred. No. 5.3e-172; 1; Mismatches 1;

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PIXAX
                                                                                                                   (lymph)angiogenesis. The proteins are also used to identify specific binding agents (potential therapeutic agents) and to raise antibodies. The antibodies are useful as therapeutic (ant)agonists; for detection, purification and targeting of proteins for in vivo or in vitro diagnosis (including imaging) or for therapy (including when linked to e.g. a label or cytotoxin); and for immunotyping of cells, e.g. for detecting minimal residual disease or haematopoietic progenitor/stem cells. It is also contemplated that the sequences might be useful for treating a very wide range of other discretes.
                                                                                                                                                                                                                                                                                              ameliorate disease and to detect diseases, or susceptibility, by detecting mutations or the presence or amount of anyiogenic protein expression. Particularly they are used to stimulate wound healing, growth of damaged bone and tissue, and for repair of vascular tissue, especially peripheral arterial disease, critical limb ischaemia or coronary disease. Antagonists of the sequences are used to inhibit angiogenesis in tumours and to treat inflammation (where associated with increased vascular permeability), diabetic retinopathy, rheumatoid arthritis or psoriasis. Agonists are also useful for stimulating
                                                        range of other disorders, e.g. autoimmune diseases; allergy; cancer; infectious diseases (viral, bacterial, fungal or parasitic); neurodegeneration, also as chemotactic agents or for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is vascular endothelial growth factor-B (VEGF-B), which is an angiogenic protein of the invention. The angiogenic and the DNA sequences encoding them, are used to prevent, treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; angiogenic protein; wound healing; vascular tissue repair; peripheral arterial disease; critical limb ischaemia; coronary di angiogenesis; tumour; inflammation; diabetic retinopathy; psorias rheumatoid arthritis; autoimmune disease; allergy; cancer; therap infectious disease; neurodegeneration;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             critical limb ischaemia or coronary disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding angiogenic proteins, useful e.g. for promoting healing of wounds and treating peripheral arterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA91004
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419
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                                          of the nervous system
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The vascular endothelial growth factor C (VEGF-C) polypeptides have activities affecting growth and migration of vascular endothelial cells, promoting growth of lymphatic endothelial cells and lymphatic vessels, increasing vascular permeability, and affecting myelopolesis. The products can be used for stimulating angiogenesis, for inhibiting angiogenesis, for inhibiting angiogenesis, for stimulating lymphaticappenesis, treatment or prevention of inflammation, oedema, elephantiasis, or Milroy's disease. They can also be used to modulate myelopoiesis, e.g. treating granulocytopenia. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating the growth of endothelial cells and to promote or inhibit trafficking of leucocytes between tissues and lymphatic vessels or to affect migration in and out of the thymus.
                                                                                                                                                                                                                                 Example 35; Page 143-145; 177pp; English
                                                                                                                                                                                                                                                                    New isolated vascular endothelial growth factor polypeptide(s) - used to develop products for treating, e.g. cancers, inflammation, oedema, granulocytopenia or for wound healing or tissue transplantation
                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-437470/37.
                                                                                                                                                                                                                                                                                                                                                                                           Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING
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                                                                                                                                                                                                                                                                                                                                                                                             Joukov V;
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; Sequence 8, Application US/08795430

• patent No. 6130071
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Patent No. 5194596	Sequence 2, Appli	1, 1	Sequence 20, Appl	Patent No. 5219739		Patent No. 5194596	Patent No. 5332671	Sequence 35, Appl	31,	Sequence 15, Appl	Patent No. 5219739	Patent No. 5194596	Patent No. 5219739	Patent No. 5332671	Sequence 56, Appl	•	Sequence 2, Appli

ALIGNMENTS

EL 88 84 82 81 846 556 7	Patient No. 6130071 GENERAL INFORMATION: APPLICANT: Alitalo, Kari APPLICANT: Alitalo, Vladimir TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C) TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof NUMBER OF SEQUENCES: 57 CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/795,430 FILING DATE: CLASSIFICATION: 435
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Patent No. 6221839
GENERAL INFORMATION:
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Best Local Similarity
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                                             APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: <Ubknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'To-
STREET: 6300 Sears Tower,
                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Receptor Ligand NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Alitalo, Kari
Joukov, Vladomir
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                                                                                                                                                                                                         STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                            CITY: Chicago
             NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08510133A
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Pred. No. 1.
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South Wacker
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08999811 Patent No. 5932540
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Best Local :
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                   APPLICANT: CAO, LIANG TITLE OF INVENTION: VI
                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 15
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                                                                                                                                   COUNTRY: U
ZIP: 20005
FILING DATE:
               APPLICATION NUMBER:
                                                                                                                                                                    STATE:
                                                                                                                                                                                                ADDRESSEE: STERNE, KESSLER, OSTREET: 1100 NEW YORK AVENUE
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TELEFAX: 312/474-0448
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                 us/08/999,811
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Pred. No. 1.7e-202;
; Mismatches 0;
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REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local S
Matches 417
                                                                                                                                                                                                                                            Sequence 2, Applic Patent No. 6040157
                                                                                                                                                                                                                             GENERAL INFORMATION:
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FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFONMATION:
NAME: MARKOWICZ, KAREN R.
                                                                                                                                   APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULA
NUMBER OF SEQUENCES: 35
COMPUTER READABLE FORM:
                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                   STREET: 1100 NEW CITY: WASHINGTON STATE: DC
                COUNTRY: UZIP: 20005
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nes 417; Conserv
                                                                                    ADDRESSEE: STERNE, KESSLER, OSTREET: 1100 NEW YORK AVENUE
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                                                                                                                                                         VASCULAR ENDOTHELIAL GROWTH FACTOR
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                                                                                                      KESSLER, GOLDSTEIN &
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TELEPHONE: (202)371-2600
TELEPAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: (FILING DATE: HEREWITH CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US
361 ECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRCVPSYWKRPQMS 419 361 ECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRCVPSYWQRPQMS 419
                                                                                                   301 PASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKCAC
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILK 120
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                                                                               PASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKCAC
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RESULT 5 US-09-042-105-18

Sequence 18, Application US/09042105 Patent No. 6040157

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Matches 417; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: TO B
FILING DATE: 24-DEC-1997
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APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
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APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH
NUMBER OF SEQUENCES: 35
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 419 amino acids
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                                                    LSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAAN 240
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(202)371-00: 18:
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    Mismatches

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Best Local Similarity
Matches 416; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 AMINO ACID
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN
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APPLICATION NUMBER:
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MEDIUM TYPE: 3.5 INCH DISKETTE
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361 ECTESPOKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRCVPSYWKRPQMS 419
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                                                                                         61 RSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: FERRARO, GREGORY D
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                     RSVSSYDELMTVKYPEYWKMYKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILK 120
                                                                                                                                        MHSLGFFSVACSLLAAALLPGPREAPAAAAAFESGLDLSDAEPDAGEATAYASKDLEEQL 60
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Pred. No. 4.6e-201;
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                                                                                                                                                                                                                                                Length 419;
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RESULT 7
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                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-FEB-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
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                                           TELEPHONE: 312/4/4-0348
TELEFAX: 312/474-0448
TELEX: 25-3856
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                                                                                                                                         NAME: Gass, David A. REGISTRATION NUMBER: 38,153
                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 14-NO
                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/50 FILING DATE: 12-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/
FILING DATE: 01-AUG-1996
                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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   LENGTH:
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o. 6130071
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00 Sears Tower, 233
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South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6221839
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 33,
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Best Local Similarity
                  TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
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                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: <Unknown>
SEQUENCE CHARACTERISTICS
                                                                                          REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Receptor Ligand NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alitalo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIDNEWRKTOCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSY 180
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                                                                                                                                                                                                                                                                                                                                                         STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                    TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                NAME: Gass, David A. REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
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Pred. No. 1.4e-176;
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US-08-585-895-33
; Sequence 33, Application US/08585895
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Best Local Similarity
Matches 350; Conserv
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               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                       REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
                                                                                                             CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: GASS, David A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 35
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                                                                                                                                                                                         APPLICATION NUMBER:
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South Wacker Drive
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301 LLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRCVPSYWKRPQMS
                      370 LLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRCVPSYWKRPQMS 419
                                                                      181 NNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKE
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US-08-999-811-4
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                                                                        APPLICATION NUMBER: US/08/999,811
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTORNEY/ACENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                   REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 1488.1000004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 20005
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ROSEN, CRAIG A.
(202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
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                                                                                                                                                                                                                                                                                                                               Version
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TELEFAX: (202)371-254 INFORMATION FOR SEQ ID NO:

(202)371-2540

4 :

SEQUENCE CHARACTERISTICS: LENGTH: 350 amino acids

LENGTH:

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; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-824-996-2
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Best Local Simi
Matches 349;
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                                                                                                                      Matches
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: 08/207,550
EARLIER FILING DATE: 1994-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hu, Jing-Sl
APPLICANT: Rosen, Cra
APPLICANT: Cao, Liang
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                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 9 SOFTWARE: PatentIn Ver.
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                                              TYPE: amino acid
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                 QCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEIT 189
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349;
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Rosen, Craig A.
                                                                                                                    Conservative
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Pred. No. 6.7e-172;
1: Mismatches 0;
                                                                                                                  Score 1995; DB 2;
Pred. No. 6.7e-172;
1; Mismatches 0;
                                                                                                                                                 Length 350;
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; MOLECULE TYPE: protein US-09-042-105-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL
                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HU, JING-SHAN APPLICANT: ROSEN, CRAIG & APPLICANT: CAO, LIANG TITLE OF INVENTION: VASCU
                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: | |
FILING DATE: 8-MAR-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 01 FILING DATE: 06-JUN-1995
                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                 I: 350 amino acids amino acid
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(202)371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/F196/00427
APPLICATION NUMBER: PCT/F196/00427
EILING DATE: 01-AUG-1996
PRIOR APPLICATION NUMBER: 08/671,573
FILING DATE: 28-UN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
EILING DATE: 14-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular
TITLE OF INVENTION: Protein
              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                         PRIOR APPLICATION DATA:
                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
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STATE: 1
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250
                                           APPLICATION NUMBER: 08/510,133 FILING DATE: 01-AUG-1995
                                                                                     APPLICATION NUMBER: 08/5 FILING DATE: 12-JAN-1996
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRCVPSYWKRPQMS 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKE 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRCVPSYWQRPQMS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMW 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEIT 120
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                                                                                                                                                                                                                                                                                                                                                                                                           60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Illinois
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6300 Sears Tower,
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    14 - NOV - 1994
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99.7%;
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               08/340,011
                                                                                                     08/585,895
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fower, 233
                                                                                                                                                                                                                                                                                                   US/08/795,430
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South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutants
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                                                                                                                                                                                         APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILL
APPLICANT: Steven A. STAC
APPLICANT: Karl ALITALO
APPLICANT: Karl ALITALO
TITLE OF INVENTION: GROWN
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                 NUMBER OF SEQUENCES: 11
                                                                         COUNTRY:
ZIP: 200
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                                                                                                     STATE:
                                                                                                                 CITY: Washington
                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                          20005
                                                                                                     DC
                                                                                                                               E: Evenson, McI
1200 G Street,
                                                                                                                                                                                                                         Andrew F. WILKS
Steven A. STACKER
                                                                                    United States
PatentIn Release #1.0,
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ACHEN

419

298

299 239 240 179

McKeown, Edwa et, NW, Suite

Edwards Suite 700

& Lenahan

of

Version

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; MOLECULE TYPE: protein US-08-795-430-13
Sequence 3, Application US/08915795
Patent No. 6235713
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acid
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                                                                                                                                   359 CECTESPNKCFLKGKRFHHQTCSCYRPPCTVRTKRCDAGFLLAEEVCRCVRTSWKRPLMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MHLLGFFSVACSLLAAALLPGPREAPAAAAAFESGLDLSDAEPDAGEATAYASKDLEEQL 60
                                                                                                                                                        CECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRCVPSYWKRPQMS
                                                                                                                                                                                                                                                                                      RSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILK 120
                                                                                                                                                                                                                                    RPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSY 180
                                                                                                                                                                                                              RPISCGPHKELDRASCQCMCKNKLLPSSCGPNKEFDEEKCQCVCKKTCPKHHPLNPAKCI 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSVSSVDELMTVLYPEYWKMFKCQLRKGGWQHNREHSSSDTRSDDSLKFAAAHYNAEILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHLLEMLSLGCCLAAGAVLLGPRQ-PPVAAAYESGHGYYEEEPGAGEPKAHASKDLEEQL
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75.78;
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Pred. No. 1.2e-154;
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Gaps

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RESULT 15
US-08-915-795-5

; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
US-08-915-795-3

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APPLICANT: Marc G.
APPLICANT: Andrew
APPLICANT: Steven
APPLICANT: Kari AL
                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08915795 Patent No. 6235713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 140;
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INFORMATION FOR SEQ ID NO: 3:
                                                                                                                           CORRESPONDENCE ADDRESS: ADDRESSEE: Evenson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: p: HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,
COMPUTER READABLE FORM
                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/915,795
                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 PLNPGKCAC-ECTESPQKCLLKGKKFHHQTCSC-----YRRPCTNRQKACEPGFSYSEE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 QCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQ 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 NTSTSYISKOLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                               253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 Q---CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC 291
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STATE: DC
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                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 DIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICM 125
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                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                     20005
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                                                                                                  E: Evenson, Mc
1200 G Street,
                                       United States
                                                                                                                                                                                                          Kari ALITALO
                                                                                                                                                                                                                              Andrew F. WILKS
Steven A. STACKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (202) 628-8844
                                                                                                                                                                                                                                                                          Marc G. ACHEN
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                                                                                                     McKeown, Edwards & Lenahan P.L.L.C
et, NW, Suite 700
                                         of America
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; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
US-08-915-795-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 30.2%; Score 704.5; DB 4 Best Local Similarity 38.9%; Pred. No. 1.1e-55; Matches 140; Conservative 61; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: N/A INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                 155 NTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIP
                                                                                                                             292
                                                                                                                                                                                                                                                                                                                                                         352 PLNPGKCAC-ECTESPQKCLLKGKKFHHQTCSC----YRRPCTNRQKACEPGFSYSEE 404
                                                                                                                                                                                                                                                                                         175 NTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLP 234
                                                                                                                                                                                                                                                                                                                                       95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                      41 EQQIRAASSLEELLRITHSEDWKLWRCRLRL-----KSFTSMDSRSASHRSTRFAATFY 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                   IETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICM 154
IQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKE
                                                                                                                                                                  EEDRCSHSKKLCPIDMLWDSNKCKCVLQE-----ENPLAGTED----HSHLQE---
                                                                                                                                                                                                        Q----CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC 291
                                                                                                                      QCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQ 351
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linear
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                                                                                 ------MMFDEDRCECVCKTPCPKDL
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Gaps

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Search completed: Job time: 194 sec October 17, 2001, 14:47:08

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Match Length
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Gapop 10.0 , Gapext 0.5
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2336
1 MHLLGFFSVACSLLAAALLP.....SYSEEVCRCVPSYWKRPQMS 419
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Copyright (c) 1993 - 2000 Compugen Ltd.
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jagged protein pre
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Notch homolog prot
Xotch protein - Af
tenascin-like prot
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fibrillin-2 precur
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16K vascular endot
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probable tenascin	T09070,	2	4006	6.2	144	5
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	A56125	N	158	6.2	144	ω
	T13954	2	1574	6.2	145	N
	T16408	N	565	6.2	145.5	Н
	T31070	2	2531	6.2	146	0
	S78549	ν	2321	6.3	147.5	9
	T09059	N	1964	6.3	147.5	8
	T42218	ν	1531	6.3	147.5	7
	A55567	N	2871	6.4	148.5	თ
	JC4679	2	207	6.4	148.5	01
	A47221	2	3002	6.4	149	-
	A55624	ν	2871	6.4	149	w
	A32160	N	2201	6.4	149	ະ
	T18355	ν	1187	6.4	149.5	
	A49175	N	1203	6.4	150.5	0

ALIGNMENTS

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Mclecule type: mRNA A;Mclecule type: mRNA A;Residues: 1-419 <mor> A;Cross-references: EMBL:U58111; NID:g1373426; PIDN:AAB02909.1; PID:g1373427 C;Genetics: C;Genetics: GBB:VEGFC; VRP A;Gene: GDB:VEGFC; VRP A;Gross-references: GDB:3890883; OMIM:601528 F;1-12/DOmain: signal sequence #status predicted <sig> F;1-10/Domain: propeptide #status predicted <pro></pro></sig></mor>	A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and A;Reference number: S69208 A;Accession: S69208 A;Molecule type: mRNA A;Residues: 1-419 <lee> A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989 R;Morris, J.C. R;Morris, J.C. A;Reference number: H01557 A;Reference number: H01557 A;Reference number: H01557 A;Reference number: H01557</lee>	A;Accession: \$61/95 A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Molecule type: mRNA A;Rosidues: 70-419 <jou1> A;Note: this sequence has been revised in reference \$69207 A;Accession: \$71443 A;Molecule type: protein A;Rosidues: 'X',104-120 <jou2> R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I. submitted to the EMBL Data Library. December 1995</jou2></jou1>	A; Accession: 189207 A; Accession: 189207 A; Accession: 189207 A; Status: nucleic acid sequence not shown A; Molecule type: mRNA A; Residues: 1-419 < JOUN A; Residues: 1-419 < JOUN A; Rocs: references: EMBL: X94216; NID: g1177488; PIDN: CAA63907.1; PID: e221096; PID: g118 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995 A; Note: only a part of the translation is shown A; Note: this is a revision to the sequence from reference 561795 R; Joukov, V.; Pajusola, K.; Raipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel EMBO J. 15, 290-298, 1996 A; Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 A; Reference number: S61795; MUID: 96178224	RESULT 1 S69207 vascular endothelial growth factor C precursor - human N;Alternate names: FLT4 ligand DHM C;Species: Homo sapiens (man) C;Date: 27-Apr:1996 #sequence_revision 01-Nov-1996 #text_change 08-Oct-1999 C;Accession: S69207; S61795; S71443; S69208; G02659 R;Joukov, V; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel EMBO J. 15, 1751, 1996 A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand A:Bereance number: S60207; MUTD-06203044

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C; Superfamilv.
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A;Title: The balbiani ring 3 gene in Chironomus A;Reference number: S08167; MUID:90172404
A;Accession: S08167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Balbiani ring 3 protein - midge (Chironomus tentans)
c;Speciles: Chironomus tentans
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C;Accession: S08167
R;Paulsson, G.; Lendahl, U.; Galli, J.; Ericsson, C.; Wieslander, L.
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                                            EITVPLSQGPKPVTISFANHTSCRCMSKLDV-----YRQVHSIIRRSLPATLPQCQA 238
                                                                                                                                      EVCIDVGKEFGVATNTFFKPPCVSVYRCGG---
                                                                                                                                                                                   KTCKCKCEKEMPTGGCENNKKWC-----DETCDCVCPQKNTCIAPKV---WDAKTCS-- 775
                                                                                                                                                                                                                               KMYKCQLRK---
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                                                                                                                                                                                                                                                                          Conservative
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                                                                                         CVNPPKCNSPQVLKDTCCCGCQNVKSCKAPQKFI-ENIC 815
                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                       Score 257; DB 2; Let Pred. No. 5.1e-11; 47; Mismatches 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                   -CCNSEGLQCMNTSTSYLSKTLF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tentans
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                  A; Title: Vascular endothelial growth factor A; Reference number: A40080; MUID: 90069608 A; Accession: A40080
                                                                                    A;Cross-references: GB:M27281; NID:g340300; PIDN:AAA36807.1; R;Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferscience 246, 1306-1309, 1989
                                                                                                                                                                                                                    A;Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63978 R;Keck, P.J.; Hauser, S.D.; Krivi, G.; Sanzo, K.; Warren, T.; Feder, J.; Connolly, D. Science 246, 1309-1312, 1999 A;Title: Vascular permeability factor, an endothelial cell mitogen related to PDGF. A;Reference number: A40079; MUID:90069609 A;Accession: A40079
                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-140,'N',183-232 <TI2>
A;Cross-references: GB:M63971; GB:M63972;
A;Accession: C40454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-141,227-23 <HOU>
R;Tischer, E; Mitchell, R; Hartman, T.; Silva, M.; Gos
J. Biol. Chem. 266, 11947-11954, 1991
J. Title: The human gene for vascular endothelial growth
A;Reference number: A40454; MUID:91268072
A;Accession: A40454
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                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-165, 183-232 <KEC>
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A; Residues: 1-141,227-232 <TI3>
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A; Residues: 1-165,183-232
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A; Residues: 1-140,'N',183-232 <HOU2>
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A; Residues: 1-232 <HOU1>
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                                                                 is a secreted angiogenic mitogen
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                                                                                                                                   PID: 9340301
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fourth

JQ1463;

189;

GB:M63977

GB:M63976

J.C.;

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R;Sharma, H.S.; Tang, Z.H.; Gho, B.C.G.; Verdouw, P.D.
Biochim. Biophys. Acta 1260, 235-238, 1995
A;Title: Nucleotide sequence and expression of the porcine vascular endothelial growth
A;Reference number: S52130; MUID:95143284
                                                                                                                                                                                  vascular endothelial growth factor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
C;Accession: S52130
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S52130
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J. Biol. Chem. 264, 20017-20074, 1999
A;Title: Human vascular permeability factor. Isc
A;Reference number: A34492; MUID:90062112
A;Accession: A34492
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Biochem. Biophys. Res. Commun. 183, 1167-1174, 1
A; Title: AIDS-associated Kaposi's sarcoma cells
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A; Residues: 27-36;43-49,'R';72-76,'Q',78-81;59-71 <CON>
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A;Cross-references: EMBL:X62568; NID:g37658;
A;Experimental source: AIDS-Kaposi's sarcoma
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A;Cross-references: GB:M32977; NID:g181970; PIDN:AAA35789.1; PID:g181971
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A; Residues: 1-140,'N',227-232 <WE2>
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Pred. No. 1.6e
33; Mismatches
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A;Molecule type: protein
A;Residues: 27-38 <ROS>
C;Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; glycoprotein;
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A; Residues: 1-116, 'ER', '119-190 <CLA>
A; Cross-references: GB:M95200; NID:g202350; PIDN:AAA40547.1;
A; Note: sequence extracted from NCBI backbone (NCBIN:110665,
R; Rosenthal, R.A.; Megyesi, J.F.; Henzel, W.J.; Ferrara, N.;
Growth Factors 4, 53-59, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Expression of vascular endothelial A;Reference number: A44881; MUID:92274860 A;Accession: B44881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Nov-1999
C;Accession: 844881; Asi3251; Asi3252
                                                                                                                                                                                                                         A;Title: Conditioned medium from mouse sarcoma 180 cells A;Reference number: A61029; MUID:91197543 A;Accession: A61029
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:107622, NCBIP:107623)
R;Claffey, K.P.; Wilkison, W.O.; Spiegelman, B.M.
J. Biol. Chem. 267, 16317-16322, 1992
J. Biol. Chem. 267, 16317-16322, 1992
A;Title: Vascular endothelial growth factor. Regulation by cell differentiation and A;Reference number: A43351; MUID:92355593
A;Accession: A43351
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A; Residues: 1-190 < BRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Breier, G.; Albrecht, U.; Sterrer, Development 114, 521-532, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-190 <SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status:
                                               Matches
                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 CSCKNT--DSRCKARQLELNERTCRC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 CVCKNKLFPSQCGANR-EFDENTCQC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 TISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145
  85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 LHHAKWSQAAPMAEGDQKPHEVVKFM--
LRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPL-----SQGPKPV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMSFLQHNKCECRPKKDRARQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKEL---DRNSCQ 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTEE-----FNITMQIMRIKPHQGQHIG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
62; Conserv
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.4%;
                                                                  8.9%;
22.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ENPCGPCSE----
                                               28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
                                        Score 207.5; DB 2;
Pred. No. 2:6e-08;
Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 218.5; DE Pred. No. 4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -DVYQRSYCRPIETLVDIFQEY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor during embryonic angiogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 190;
                                            Indels
                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -RRKHLFVQDPQTCK 161
                                                                                                                                                                                                                                                                     contains vascular endothelia
                                                                                                                                                                                                                                                                                                                                       PID:g202351
NCBIP:110675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:g249859
                                                                                                                                                                                                                                                                                                                  Folkman,
                                                                                         190;
                                            95;
                                          Gaps
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18

LHHAKWSQAAPTTEGEQKSHEVIKFM---

-DVYQRSYCRPIETLVDIFQEY

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A; Accesszon. A; Accesszon. A; Molecule type: protein
A; Residues: 27-33 <CLA>
R; Sugihara, T.; Kaul, S.C.; Mitsui, Y.; Wadhwa,
Biochim. Biophys. Acta 1224, 365-370, 1994
A; Title: Enhanced expression of multiple forms
                                                                      δÃ
                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 27-46 <SUG>
C; Comment: Homodimers could be demonstrated for recombinant VEGF-2 but not VEGF-3.
C; Keywords: alternative splicing; angiogenesis; disulfide bond; glycoprotein; homoginative splicing; angiogenesis; disulfide bond; angiogenesis; disulfide bond; glycoprotein; homoginative splicing; angiogenesis; disulfide bond; angiogenesis; disulfide 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:S38100; NID:g249860; PIDN:AAB22254.1; PID:g249861
A;Note: sequence extracted from NCBI backbone (NCBIN:107624, NCBIP:107625)
R;Clauss, M.; Gerlach, M.; Gerlach, H.; Brett, J.; Wang, F.; Familletti, P.C.; P
J. Exp. Med. 172, 1535-1545, 1990
A;Title: Vascular permeability factor: a tumor-derived polypeptide that induces
A;Reference number: A60932; MOID:91079755
       밁
                                                                                                                                                                                                                       Ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Contains: vascular endothelial growth factor-2; vascular perme C;Species: Mus musculus (house mouse) C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change C;Accession: A44881; C44881; A60932; S52136 R;Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W. Development 114, 521-532, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вb
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A; Accession: S52136
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A; Residues: 1-140,209-214 <BR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:S37052; NID:g249856; PIDN:AAB22252.1; PID:g249857 A;Experimental source: embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vascular endothelial growth factor-3 precursor - mouse N;Contains: vascular endothelial growth factor-2; vasc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: sequence extracted from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l-26/Domain: signal sequence #status
27-214/Product: vascular endothelial
                                                                              145
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                                                                                                                                                                                                                              LRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEF 144
PDEIEYIFKPSCVPLMRCAGCCNDEALECVPTSESNITMQIMRIKPHQSQHIG----EMS 120
                                                                      GVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLSQ--GPKPVTIS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --DSRCKARQLELNERTCRC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFPSQCGANR-EFDENTCQC
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                                                                                                                                                        LHHAKWSQAAPTTEGEQKSHEVIKFM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDF 262
                                                                                                                                                                                                                                                                                                                 59;
                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                            8.9%;
22.7%;
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                                                                                                                                                                                                                                                                                                         Score 207.5;
Pred. No. 2.9e
32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted <SIG>
growth factor-3
                                                                                                                                                                                                                                                                                                                                            207.5;
No. 2.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             forms of VEGF
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                                                                                                                                                                                                                                                                                                                                        .9e-08;
                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                    -DVYQRSYCRPIETLVDIFQEY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vascular permeability factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBIP: 104678
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R;Conn, G.; Bayne, M.L.; Soderman, D.D.; Kwok, P.W.; Sullivan, K.A.; Palisi, T.M.; Proc. Natl. Acad. Sci. U.S.A. 87, 2628-2632, 1990
A;Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen that A;Reference number: A35987; MUID:90207249
A;Accession: A35987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A35987
A;Cross-references: GB:M32976; NID:g163006; PIDN:AAA30502.1; PID:g163007 R;Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Blochem. Blophys. Res. Commun. 165, 1198-1206, 1989 A;Title: Vascular endothelial growth factor: a new member of the platelet.
                                                                                                                                                                                                                                  C;Species: Bos primigenius taurus (cattle) C;Date: 30-Jun-1992 #sequence_revision 30-C;Accession: B40080; B33787; A33255
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                                                                                  A; Molecule type: mRNA
A; Residues: 1-190 < LEU>
                                                                                                                                A; Accession:
                                                                                                                                                    A; Reference number: A40080;
                                                                                                                                                                          A; Title: Vascular endothelial growth factor
                                                                                                                                                                                             R; Leung, D.W.; Cachianes, G.; Kuang, Science 246, 1306-1309, 1989
                                                                                                                                                                                                                                                                                               vascular endothelial growth factor precursor (version
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A; Residues: 1-190 <CON>
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C;Date: 16-Nov-1990 #sequence_revision 16
C;Accession: A35987
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Best Local
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mes 62; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANR-EFDENTCQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --DSRCKARQLELNERTCRC
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Pred. No. 3.1e-08;
1; Mismatches 71;
                                                                                                                                                                                                                 W.J.; Goeddel,
                                                                                                                                                                                                                                                          30-Jun-1992
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                                                                                                                                                                       secreted angiogenic mitogen
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member of the platelet-derived
                                                                                                                                                                                                                                                          #text_change 05-Nov-1999
                                                                                                                                                                                                                 D.V.; Ferrara,
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A; Reference number: A33787; MUID: 90121225

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A; Molecule type: mRNA
A; Residues: 1-473 <INO>
A; Residues: 1-473 <INO>
A; Cross-references: GB:D43794; NID:9602767; PIDN:BAA07852.1;
C; Superfamily: unassigned EGF-related proteins; EGF homology
C; Keywords: duplication
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A;Molecule type: mRNA
A;Residues: 27-190 <TIS>
A;Cross references: GB:M31836; NID:g163808; PIDN:AAA30804.1; PID:g163809
A;Cross references: GB:M31836; NID:g163808; PIDN:AAA30804.1; PID:g163809
A;Ferrara, N.; Henzel, W.J.
Biochem. Biophys. Res. Commun. 161, 851-858, 1989
A;Title: Pituitary follicular cells secrete a novel heparin-binding growth factor special R;Reference number: A33255; MUID:89286596
A;Accession: A33255
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                                            Вp
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F;387-419/Domain: EGF homology <EGF1>
F;429-460/Domain: EGF homology <EGF>
F;429-460/Domain: EGF homology <EGF>
F;23,36,43,56,75,382,424,455,468,473/Modified site: 3',4'-dihydroxyphenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 270, 6698-6701, 1995
A;Title: Mussel adhesive plaque protein gene
A;Reference number: A56175; MUID:95204464
A;Accession: A56175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adhesive plaque protein Mgfp2 precursor - Mediterranean mussel C;Species: Mytilus galloprovincialis (Mediterranean mussel) C;Date: 27-Apr-1995 #sequence_revision 03-Oct-1995 #text_chang
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A;Residues: 27-31 <FER>
C;Keywords: alternative splicing; glycoprotein
C;Keywords: alternative splicing; glycoprotein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-190/Product: vascular endothelial growth factor #status predicted
F;100/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, J. Biol. Chem. 270, 6698-6701, 1995
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Best Local Similarity 22.8
Matches 60; Conservative
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Best Local
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GKEFG-VATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLSQGPKPV 199
                                                                                    YKCQLRKGGWQHUREQANLUSRTEETIKFAAAHYUTEILKSIDUEWRKTQCMPREVCIDV 140
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                                                 YKC-FCKGGYY---
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                                                                                                                                       100;
                                                                                                                                                       Similarity
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                                                                                                                                7.8%; Score 182.5; DB 2; 21.9%; Pred. No. 4.4e-06; tive 37; Mismatches 127;
                                            -----NLKNACKPNQCKNKSRCVPV
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Pred. No. 3.6e-08;
25; Mismatches 77;
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                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth
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RESULT
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Gene 88, 133-140, 1990
A;Title: Balbiani ring 3 in Chironomus tentans encodes a 185-kDa secretory protein wh A;Reference number: JQ0542; MUID:90269600
A;Accession: JQ0542
A;Accession: JQ0542
                                                                                                                                         Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M24160
A;Experimental source: salivary gland
C;Superfamily: unassigned Balbiani ring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Chironomus tentans
C;Date: 31-Dec-1991 #sequence_revision
C;Accession: J00342
                                                                      밁
                                                                                                      δÃ
                                                                                                                                                                         QΥ
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                                                                                                                                                                                                                                           QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-160 <DIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N; Alternate names: balbiani ring 3
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                         415
                                                                                                                                                                                                                                                                                                                        243
                                                                        158
                                                                                                                                                                                                                                                   303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
                                                                                                                                         102 RVCSCGCPVPRPDC-TNGQIYNINTCAC---GCGIDKPSCPKQQIYNWKTCDCECPNGMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256
                                                                                                                                                                                                                 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 GICSSDGSGGYRCRCKGGYSGPTCKVNVCKPTPCKNSGRCVNKGSSYNCICKGGYSGPTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                    ω
                                                                      ΕP
                                                                                            - RP
                                                                                                                                                                            GKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRC-VPSYWK 414
                                                                                                                                                                                                              NCGNKKFFDKPSCECKCKNN--PST--SPQVWDADDCECKCPKDKQKPQGGCDGGQKWND
                                                                                                                                                                                                                                                 SCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRT-----CPRNQPLNP 355
                                                                                                                                                                                                                                                                                                                      CPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCYR-----RPCTNRQKACEPGFSYSEEVCRCVPSY 4:12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIYTCKCAYGWRGRHCTDKAYKPNPCVVSKPCKNRGKCIWNGKAYRCKCAYGYGGRHCTK 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GGYTGPRC-----EVH-----ACKPNPCKNKGRCFPDGKTGYK-----CR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKTFKCVCRNGNFGRLCEKNVCSPNPCKNNG-KC----SPLGKTGYKCTCS-----
                                                                                                                                                                                                                                                                                      CKSPRQWTDSKCLC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSYKKNPCASRPCKNRGKCTDKGNGY --- VCKCARGY 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENVCKPNPCQNRGRCYPDNSDDGFKCRCVGGYKGPTCEDKPNPCNTKPCKNGGKCNYNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAN-----REFDENT-----CQCV-----CK---RTCPRNQPLNPGKC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVDGYSGPTCQENACKPNPCSNGGTCSADKFGDYSCECRPGYFGPECERYVCAPNPCKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CL-----AQEDFMF---SSDAGDDSTDGFHD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQ-CQAANKTCP---TNYMWNNHICR 255
                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                                         416
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---QCVCRAGLRPASC-----GPHKELDR-----NSCQCVCKNKLFPSQC
                                                                                                                                                                                                                                                                                                                                                                          7.7%;
26.4%;
                                                                                                                                                                                                                                                                                    -ECSTTPATCEGKQTWCG------EACQCICPGG--DK 45
                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                     Score 180.5; DB 2;
Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ICGPNKELDE 288
                                                                                                                                                                                                                                                                                                                                                                                          Length 160;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                         33;
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vascular endothelial growth factor-related
N;Alternate names: VRF 167 protein
C;Species: Mus musculus (house mouse)

factor 167

precursor -

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S57956
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                                                                                                                                                                                              Ωy
                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-146 < RED>
                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data A; Reference number: S57956 A; Accession: S57956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ovine vascular endothelial growth factor - sheep C;Species: Ovis orientalis aries, Ovis ammon aries C;Date: 13-Jan-1996 #sequence_revision Ol-Mar-1996 C;Accession: S57956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 137/2
F;1-21/Domain: signal sequence #status predicted <SIG>F;22-188/Product: vascular endothelial growth factor-r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:U43837; NID:g1314335; PIDN:AAC52553.1; PID:g1314336 C;Comment: This factor is a mitogen, that is selective for endothelial cells, ar endothelial growth factors 167 and VEGF 186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X89506; NID:g899350; PIDN:CAA61677.1; PID:g899351
                                                                                                                                                                                                                                                                                                                                                                                                  A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: vrf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-188 < TOW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Characterization of the murine VEGF-related factor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 19
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                              Query Match
Best Local
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Best Local Similarity
Matches 53; Conserv
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121
                                       203
                                                                                                                     145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 SRTEETI-KFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 YRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYR 219
                                                                              65
                                                                                                                                                             18
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                                                                                                                                                                                                  LRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEF 144
                                                                                                                                                                                                                                                                                                                                                                                                  preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.A.; Dai, Y.; Li, J.; Jones, S.C.; Moor, to the EMBL Data Library, July 1995
FLQHNKCECRPKKDKARQ 138
                                     FANHTSCRCMSKLDVYRQ 220
                                                                          PDEIEFIFKPSCVPLMRCGGCCNDESLECVPTEEFNITMQIMRIKPHQSQHIG----EMS 120
                                                                                                                 GVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLSQ--GPKPVTIS 202
                                                                                                                                                          LHHAKWSQAAPMAEGGQKPHEVMKFM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGFHDICGPNKELDEETCQC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKESAVKPDSPRILCPPCTQRRQRPDPRTCR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVHSIIRRSLPATL-PQCQAAN-----KTCPTNYMWNNHICRCLAQEDFMFSSDAGDDST 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QRCGGCCPDDGLECVPTGQHQVRMQILMIQYPSSQLGE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARTQAPVSQFDGPSHQKKVVPWIDVYARAT-CQPREVVVPLSMELMGNVVKQLVPSCVTV 75
                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lagercrantz, J.;
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Res. Commun.
                                                                                                                                                                                                                                                       7.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Grimmond, S.; Silins, G.; Nordenskjoeld, 220, 922-928, 1996
                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                         Score 173.5; DB 2
Pred. No. 6.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 175; DB 2;
Pred. No. 6.3e-06;
                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                          -DVYQRSFCRPIETLVDIFQEY 64
                                                                                                                                                                                                                                       61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (domestic sheep)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 188;
                                                                                                                                                                                                                                                                            Length 146;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                       19;
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                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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A; Molecule type: mRNA
A; Residues: 1-204, 'G', 206-221, 'A', 223-380, 'D', 382-386, 'H', 388-444, 'HN', 447-450, 'V', 45
A; Cross-references: GB:M23121; NID:g212746; PIDN:AAA49086.1; PID:g212749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Jones, F.S.; Hoffman, S.; Cunningham, B.A.; Edelma Proc. Natl. Acad. Sci. U.S.A. 86, 1905-1909, 1989 A;Title: A detailed structural model of cytotactin: A;Reference number: A32230; MUID:89184536 A;Accession: A32230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: cytotactin; hexabrachion
N;Contains: tenascin 190K; tenascin 200K
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A32230; B32230; A33379; B33379; C33379; S01292; A30903
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A;Title: Vascular endothelial growth factor: a new member of
A;Reference number: A33787; MUID:90121225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 05-Nov-1999
C:Accession: A33787
C:Accession: A3787
                                A; Cross-references: GB:M23121
                                                  A; Molecule type: mRNA
A; Residues: 1-204, 'G', 206-221, 'A', 223-380, 'D', 382-386, 'H', 388-444, 'HN', 447-450, 'V', 45
                                                                                                               A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
                                                                                                                                             A; Accession: C33379
                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',45
                                                                                                                                                                                                                            A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
                                                                                                                                                                                                                                                             A; Accession: B33379
                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Two contrary functions of tenascin: dissection A; Reference number: A33379; MUID:90030407 A; Accession: A33379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Spring, J.; Beck, K.
Cell 59, 325-334, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:J04519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-1044, 1318-1810 <JO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1810 < JON>
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A; Cross-references: GB:M33750; NID:g163810;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCMNT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STSYLSKTLFEITVPLSQ--GPKPVTISFANHTSCRCMSKLDVYRQ 220
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37; Conser
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phys. Res. Commun. 165, 1198–1206, 1989
Pearson,
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U.S.A. 86, 1905-1909, 1989
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34.9%;
  Shibahara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NID: g211717; PIDN: AAA48745.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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Pred. No. 6.2e-06;
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S.; Hofsteenge, J.; Chiquet-Ehrismann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIDN:AAA30805.1; PID:g163811
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F:223-249/Domain: EGF homology <EGFT>
F:316-342/Domain: EGF homology <EGFT>
F:316-342/Domain: EGF homology <EGFT>
F:592-673/Domain: fibronectin type III repeat homology <FN3B>
F:681-65/Domain: fibronectin type III repeat homology <FN3B>
F:773-857/Domain: fibronectin type III repeat homology <FN3C>
F:865-949/Domain: fibronectin type III repeat homology <FN3D>
F:957-1037/Domain: fibronectin type III repeat homology <FN3E>
F:1046-1128/Domain: fibronectin type III repeat homology <FN3E>
F:1137-1219/Domain: fibronectin type III repeat homology <FN3H>
F:128F-1310/Jomain: fibronectin type III repeat homology <FN3H>
F:1318-1399/Domain: fibronectin type III repeat homology <FN3I>
F:1407-1487/Jomain: fibronectin type III repeat homology <FN3I>
F:1495-1575/Domain: fibronectin type III repeat homology <FN3S>
F:1590-1798/Domain: fibronectin type III repeat homology <FN3S>
F:1590-1798/Domain: fibrinogen beta/gamma homology <FN3K>
F:1734-1747/Domain: calcium binding #status predicted <CAB>
16K vascular endothelial growth factor homolog A2R - Orf virus
C;Species: Orf virus
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
                                                                                                            RESULT
D49530
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A; Residues: 27-181,'R', 183-204,'G', 206-221,'A', 223-380,'D', 382-386,'H', 388-444,'HN', 447-A; Cross references: EMBE: X08030
A; Note: part of this sequence was confirmed by protein sequencing
A; Note: part of this sequence was confirmed by protein sequencing
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Best Local Similarity
Matches 90; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 FKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 GRLDTAPYCSGHGNYSTEICGCVCEPGWKGPNCSEPACPRN-CLNRGLCVRAKCICEEGF 213
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                                                                                                                                                                                                                                          QRGRCINGQCECHEGF 461
                                                                                                                                                                                                                                                                                                                                                                     RCVDGRCVCHEGYLGEDCGELRCPNDCHNRGRCINGQ-CVCDEGFIGEDCGELRCPNDCQ 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TIKFAAAH--YNTEILKSI-DNEWRKTQC----MPREVCIDVG----KEFGVATNTF 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANL-----NSRTEE 105
                                                                                                                                                                                                                                                                                                                                                                                                                                  PLNPGKCAC-----ECTE--SPQKCLLKGKKFHHQTCSC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INGTCFCEEGYTGEDCGELTCPNNCNGNGRCENGLCVCHEGFVGDDCSQKRCPKTCNNRG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----TGEDCNE---PLC-PNNCHNRGRCVDNECVCDEGYTGEDCGELICPNDCFDRGRC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MFSSDAGDDSTDGFHDICGPNKELDEETC---QCVCRAGLRPASCG----PHKELDRNSC 315
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    s; Score 172.5; DB 1; Length 1810;
    b; Pred. No. 9e-05;
    43; Mismatches 126; Indels 177; Gaps

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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-148 <4YT>
A;Cross-references: GB:S67522; NID:g456900; PIDN:AAB29223.1; PID:g456902
A;Note: sequence extracted from NCBI backbone (NCBIN:141422, NCBIP:141426)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: D49530
R;Lyttle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
J. Virol. 68, 84-92, 1994
A;Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus A;Reference number: A49530; MUID:94076465
A;Contents: NZ7
A;Contents: NZ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: D49530
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                       124 NEWRKT----OCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLOCMNTSTS 179
                                                             180 YLSKTLFEITVPLSQGPKP-----VTISFANHTSCRCMSK 214
95 NTTVTVSVTGVSSSSGTNSGVSTNLQRISVTEHTKCDCIGR 135
                                                                                                                             35 NDWMRTLDKSGCKPRDTVVYLGEEYPESTNLQYNPRCVTVKRCSGCCNGDGQICTAVETR 94
                                                                                                                                                                                                                                                       6.8%; Score 160; DB 2; ilarity 32.7%; Pred. No. 6.3e-05; Conservative 15; Mismatches 43
                                                                                                                                                                                                                                                                                                                 Length 148;
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Search completed: October 17, 2001, 14:48:34 Job time: 280 sec

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Result
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
                                                                                                                                                                                                                                                                                             %
Query
Match Length
BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93435 seqs, 34255486 residues
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2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHLLGFFSVACSLLAAALLP.....SYSEEVCRCVPSYWKRPQMS
 DB
                                                                                           VEGF_SHEEP
VWF_PIG
VEGH_ORFN2
TENA_CHICK
VEGH_ORFN7
NOTC_DROME
TENA_PIG
LMA5_MOUSE
VWF_CANFA
FBN2_HUMAN
FBN2_MOUSE
NOTC_ENARE
NOTC_XENLA
PLOF HUMAN
TENA_HUMAN
FBN1_MOUSE
FBN1_MOUSE
FBN1_BOVIN
NTC4_MOUSE
NTC1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     93435
                                                                          P15691 bos taurus
P26617 cavia porce
Q25464 mytilus gall
P52582 gallus gall
P49765 homo sapien
P49765 homo sapien
P49765 avis aries
Q28833 sus scrofa
P52584 orf virus (
P10039 gallus gall
P52585 orf virus (
P107207 drosophila
Q29116 sus scrofa
Q29116 sus scrofa
Q29116 sus scrofa
Q31001 mus musculu
Q28295 canis famil
P35556 homo sapien
Q61555 mus musculu
                P46530
P21783
P49763
P24821
P35555
Q61554
P98133
                                                                                                                                                                                                                         P49151 sus scrofa
Q00731 mus musculu
P16612 rattus norv
                                                                                                                                                                                                                                                           P49767 homo sapien
P97953 mus musculu
Q03376 chironomus
P46531
                                                                                                                                                                                                                                                    P15692 homo sapien
                                                                                                                                                                                                                                                                                              Description
                        homo sapien
homo sapien
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mus musculu
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xenopus lae
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                 bos taurus
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45	44	43	42	41	40	39	38	37	36	35	34
135.5	136.5	137	138	139	140	141	141.5	142	142.5	143	144
5.8	5. 8	5.9	5.9	6.0	6.0	6.0	6.1	6.1	6.1	6.1	6.2
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Q07008								P49764	P40798	Q21313	P04275
rattus norv	homo sapien	homo sapien	branchiosto	drosophila	mus musculu	mus musculu	caenorhabdi	mus musculu	drosophila	caenorhabdi	homo sapien

ALIGNMENTS

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Best Local
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15-JUL-1998 (Rel. 36, 1
30-MAY-2000 (Rel. 39, 1
VASCULAR ENDOTHELIAL GI
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CARBOHYD
SEQUENCE
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SIGNAL
               Mus musculus (Mouse Eukaryota; Metazoa;
                                                                                                    15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
30-MAY-2000 (Rel.
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PROSITE; PS00249; PDGF_1; 1.
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                                                                                                                                                                                                                                                                     ECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRCVPSYWKRPQMS
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U58111;
P15692;
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IPR002400;
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419
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ilarity 100.0%;
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(Mouse).
Tha⊠ca; Chordata;
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Last annotation of the computation of the c
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                                                                                       GROWTH
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N-LINKED (GLCNAC. ..) (
N-LINKED (GLCNAC. ..) (
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POTENTIAL.

VASCULAR ENDOTHELIAL GROWTH

4 X 24 AA TANDEM REPEATS.
               Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2336; DB 1;
Pred. No. 7.2e-174;
; Mismatches 0;
                                                                                                                                                                                  PRT;
                                                                                                      on update)
                                                                                       PRECURSOR
                                                                                                                                                                                415
             Vertebrata;
                                                                                     (VEGF-C)
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Best Local Similarity
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PRINTS: pR00438; GECYSKNOT.
PRINTS: pR00249; PDGE_1; 1.
PROSITE; pS00249; PDGE_2; 1.
PROSITE; pS50278; PDGE_2; 1.
PROSITE; PS50278; PDGE_2; 1.
POTENTIAL.
                                                                                                                                                                                                REPEAT
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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EMBL; U58112;
HSSP; P15692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97388482; pubMed=9247316;
Fitz L.J., Morris J.C., Towler P., Long A., Burgess P., G
Wang J., Gassaway R., Nickbarg E., Kovacic S., Ciarletta
Giannotti J., Finnerty H., Zollner R., Beier D.R., Leak L
Turner K.J., Wood C.R.;
"Characterization of murine Flt4 ligand/VEGF-C.";
Oncogene 15:613-618(1997).
                                                                                                                                                                                                                                                          REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                      SIGNAL
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "VEGF-C receptor binding and pattern of expression with suggests a role in lymphatic vascular development."; pevelopment 122:3829-3837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:109124; Vegfc.
InterPro; IPR000072; -.
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NCBI_TaxID=10090;
[1]
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Joukov V., Alitalo K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CELL GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION:
                                                                                  MHLLGFFSVACSLLAAALLPGPREAPAAAAAFESGLDLSDAEPDAGEATAYASKDLEEQL
            SIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSY
                                                RSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILK
                                    RSVSSVDELMSVLYPDYWKMYKCQLRKGGWQ----QPTLNTRTGDSVKFAAAHYNTEILK
IPR002400;
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236
415
                                                                                                                                     Conservative
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AAB46707.1; -.
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85.4%;
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TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
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                                                                                                                                     28;
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Pred. No. 1.4e
28; Mismatches
                                                                                                                                                                                                          4 (PARTIAL)
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N-LINKED (GI
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VASCULAR ENDOTHELIAL
4 X 24 AA TANDEM REPI
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
D9D3DD3CECC659D6
 2048; DB 1;
No. 1.4e-151;
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                                                                                                                                                                                                                                                                                                                                              Signal;
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                                                                                                                                       29;
                                                                                                                                                                                                                                                                                               REPEATS
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) (POTENTIAL).
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RESULT 3
BAR3_C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P SEQUENCE FROM N.A.

(C TISSUE-Salivary gland;

(X MEDLINE-90172404; pubMed=1689777;

(X MEDLINE-90172404; pubMed=1689777;

(X MEDLINE-90172404; pubMed=1689777;

(X Paulsson G., Lendahl U., Galli J., Ericsson C., Wieslander L.;

(Y The Balbiani ring 3 gene in Chironomus tentans has a diverged

(Y Trepetitive structure split by many introns.";

(L J. Mol. Biol. 211:331-349(1990).

(C - FUNCTION: USED BY THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR

(C - FUNCTION: USED BY THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR

(C - FUNCTION: THE LARVAL TUBE. BALBIANI RING PROTEIN 3 COULD PLAY A

(C - ROLE AS A TRANSPORT PROTEIN THAT BINDS TO OTHER PROTEINS

(C ROLE AS A TRANSPORT PROTEIN THAT BINDS TO OTHER PROTEINS

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(C ROLE AS A TRANSPORT PROTEIN THAT BINDS TO EARLY.

(C SUBCELLULAR LOCATION: SECUREFED.

(C - SUBCELLULAR LOCATION: SECUREFED.

(C - TISSUE SPECIFICITY: SALIVARY GLAND.

(C - TISSUE SPECIFICITY: SALIVARY GLAND.
      Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                               Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pterygota; Neoptera; Endopte
Chironomoidea; Chironomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q03376;
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01-OCT-1994
                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                      PRINTS;
                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7153;
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                                                                                                                                                                                                                                                                                                                             P18055;
                                                                                                                                                                                                                                                                                                                                                                                       X52263; CAA36506.1;
                                                                                                                                                                                                                                        Signal
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Neoptera; Endopterygota; Diptera; Nematocera;
Lea; Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tentans (Midge)
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(Rel. 27, Last sequence up
(Rel. 30, Last annotation
NG PROTEIN 3 PRECURSOR.
         Conservative
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                                                                                                                                                                                 1700
                                 11.0%;
22.8%;
                                                                                                                                                     186145
         47;
                                                                                                                                                  MW;
   Score 257; DB Pred. No. 3.1e
                                                                                                                                               POTENTIAL.
BALBIANI RING PROTEIN 3.
MW; 34202B28521B0815 CRO
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                                                             Length 1700;
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      110;
Gaps
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RESULT 4
VEGF_HUMAN
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                                                                                                                               MEDLINE=91268072; PubMed=1711045;
Tischer E., Mitchell R., Hartman
Fiddes J.C., Abraham J.A.;
                                                                                                                                                                                                                                 Connolly D.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR
            "AIDS-associated Kaposi's sarcoma endothelial growth factor.";
                                   MEDLINE=92231879; PubMed=1567395; Weindel K., Marme D., Weich H.A.;
                                                 SEQUENCE FROM N.A. MEDLINE=92231879;
                                                                                           "The human gene for vascular endothelial growth factor. protein forms are encoded through alternative exon spli J. Biol. Chem. 266:11947-11954(1991).
                                                                                                                                                                                                                                                                                                            Science 246:1306-1309(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEGF_HUMAN P15692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1041 DKCVV---ECAN-VKTCEGPQRWCDNQCKCI 1067
                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                    Science
                                                                                                                                                                                                                   PDGF.
                                                                                                                                                                                                                            "Vascular permeability factor,
                                                                                                                                                                                                                                                                    MEDLINE=90069609;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                  Leung D.W., Cachianes G., Kuang W.-J., "Vascular endothelial growth factor is
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90069608; PubMed=2479986;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -EETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKR-
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                                                                                                                                                                                                  246:1309-1312(1989)
Biophys.
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                                                                                                                                                                                                                                                     S.D., Krivi
                                                                                                                                                                                                                                                                   , AND PARTIAL SEQUENCE PubMed=2479987;
 Commun. 183:1167-1174(1992)
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Catarrhini; Hominidae
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                          cells
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                                                                                                                                                                                                                                                      Sanzo K.,
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                                                                                                                                               Silva M.,
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[5]
PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81.
MEDLINE-90062112; PubMed-2584205;
Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monsell R., Slegel N., Haymore B.L., Leingruber R., Feder J.;
"Human vascular permeability factor. Isolation from U937 cells.";
J. Biol. Chem. 264:20017-20024(1989).
                                                                                                                                                                                                                                                                                                                                                                                                           endothelial growth factor.";
Structure 6:637-648(1998).
-!- FUNCTION: GROWTH FACTOR ACTIVE
                                                                                                                        This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fairbrother W.J., Champe M.A., Christinger H.W.,
Starovasnik M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C., Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.; "Crystal_structure of the complex between VEGF and a receptor-blocking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.; "The crystal structure of vascular endothelial growth farefined to 1.93-A resolution: multiple copy flexibility binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98298440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "1H, 13C, and 15N backbone assignment and secondary structure of receptor-binding domain of vascular endothelial growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fairbrother W.J., Champe M.A., Christinger H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.
MEDLINE=99119204; PubMed=9922142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein Sci. 6:2250-2260(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 34-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Siochemistry 37:17765-17772(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Crystal structure of peptide.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Solution structure of the heparin-binding
                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
                                                                                                                                                                                         ALTERNATIVE PRODUCTS: FOUR FORMS ALTERNATIVE SPLICING OF THE SAME VEGF-189 AND VEGF-215).
                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMODIMER, DISULFIDE-LINKED. SUBCELLULAR LOCATION: SECRETED BUT RE
                                                                                                                                                                                                                                                                                                                                                                PERMEABILITY
                                                                                                                                                                                                                                                                                                                                                                                    CELL GROWTH. INDUCES ENDOTHELIAL
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                    non-profit institutions as long and this statement is not removed.
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license agreement (See http://www.isb-sib.ch/announce/
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PS50278; PDGF_2;
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BIOCHIM. BIOCHYS. ACTA 1260:235-238(1995).

-I- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND EN CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASSPERMEABILITY (BY SIMILARITY).

-I- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00341; PDGF; 1
PROSITE; PS00249; PDGF
PROSITE; PS50278; PDGF
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P49151;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         scrofa (Pig)
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                                           TISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQ 259
                                                                                     PDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTEE-----FNITMQIMRIKPHQGQHIG
                                                                                                                               GVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPL----
                                                                                                                                                                                                                                                                                 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00249; PDGF_1; 1. PS50278; PDGF_2; 1. Growth factor; Glyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000072; -
                                                                                                                                                                                                                                                                                                                                                                                                  190
                                                                                                                                                                                                                                                                               Conservative
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51
82
86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=7841203;
Z.H., Gho B.C.H., Verdouw P.D.;
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190
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127
129
76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                       9.4%;
23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                    22368
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                  ME.
                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                            Pred. No. 3.1e-10; 5; Mismatches 72;
                                                                                                                                                                                                                                                                                                                           Score 218.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VASCULAR ENDOTHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                               -LINKED (GLCNAC. . .) (F
04D40B8D7913047F CRC64;
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal
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                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       porcine vascular
                                                                                                                                                                                    -DVYQRSYCRPIETLVDIFQEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (VEGF) (VASCULAR
                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENDOTHELIAL
                                                                                                                                                                                                                                                                                                                           190;
                                                                                                                                                                                                                                                                               107;
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                                                                                                                                 SQGPKPV 199
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VEGF_MOUSE
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                                                                                            This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                      characterization of transcriptional and regulatory sequences.";
J. Biol. Chem. 271:3877-3883(1996).
-i- FUNCTION: GROWTH FACTOR ACTIVE IN AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96216498; PubMed=8632007;
Shima D.T., Kuroki M., Deutsch U., Ng Y., Adamis A.P., D'Amore P.A.;
"The mouse gene for vascular endothelial growth factor. Genomic structure, definition of the transcriptional unit, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claffey K.P., Wilkison W.O., Spiegelman B. "Vascular endothelial growth factor. Regul differentiation and activated second messe J. Biol. Chem. 267:16317-16322(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92274860; PubMed=1592003;
Breier G., Albrecht U., Sterrer S., Risau W.;
"Expression of vascular endothelial growth factor during embryonic
angiogenesis and endothelial cell differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel.
01-OCT-1996 (Rel.
01-OCT-2000 (Rel.
                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-3 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERMEABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q00731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92355593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Development 114:521-532(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEGF_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260
                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
SUBCELLULAR LOCATION: VEGF-1 AND VEGF-2 ARE SECRETED WHILE
VEGF-3 REMAINS CELL-SURFACE ASSOCIATED UNLESS RELEASED BY
                                                                                                                                        KIDNEY GLOMERULI. ALSO FOUND IN BRONCHIAL EPITHELIUM, ADRENAL GLAND AND IN SEMINIFEROUS TUBULES OF TESTIS. HIGH EXPRESSION OF TESTIS. HIGH EXPRESSION OF VEGF CONTINUES IN KIDNEY GLOMERULI AND CHOROLD PLEXUS IN ADULTS. SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: THREE FORMS (VEGF-1, VEGF-2 AND VEGF-3) ARE PRODUCED AS A RESULT OF ALTERNATIVE SPLICING OF THE SAME GENE. THE LONGEST FORM (VEGF-3, SHOWN HERE) CONTAINS A BASIC INSERT LINKED TO CELL-ASSOCIATION/HEPARIN-BINDING.
TISSUE SPECIFICITY: IN DEVELOPING EMBRYOS, EXPRESSED MAINLY IN THE CHOROLD PLEXUS, PARAVENTRICULAR NEUROEPITHELIUM, PLACENTA AND
                                                                                                                                                                                                                                                                                                                                                                         PERMEABILITY
                                                                                                                                                                                                                                                                                                                                                                                          CELL GROWTH.
                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CVCKNKLFPSQCGANR-EFDENTCQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSCKNT - - DSRCKARQLELNERTCRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKEL---DRNSCQ 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                         INDUCES ENDOTHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=1644816;
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34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (VEGF-1)
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Rodentia;
                                                           ormatics Institute. There are no resinstitutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Last sequence update)
, Last annotation update)
GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185
                                                                                                                                                                                                                                                                                                                                                                                       IN ANGIOGENESIS, AL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Regulation by messenger patl
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                                                                                                                                                                                                                                                                                                                                                                                       AND VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
; Murinae; Mus
                                                                           restrictions
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use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).

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Best Local S
Matches 59
                                                                                                           P16612;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; S37052; AAB2225;
EMBL; S38003; AAB2225;
EMBL; S38100; AAB2255;
EMBL; M95200; AAA4054;
EMBL; U41383; ', NOT_
PIR; A43351; A43351;
HSSP; P15692; 2VGH.
         Conn G.,
Palisi T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitogen;
SIGNAL
CHAIN
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
VARSPLIC
VARSPLIC
           SEQUENCE FROM N.A., AND SEQUENCE OF MEDILINE-90207249; PubMed=2320579; Conn G., Bayne M.L., Soderman D.D., Palisi T.M., Hope D.A., Thomas K.A.;
                                                            Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116;
                                                                     Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                VEGF_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:103178; Vegf.
InterPro; IPR000072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                     192
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                                                                                                                                                                                                                                                        LFPSQCGANR-EFDENTCQC
                                                                                                                                                                                                                                                                                                                                                                                                                       LRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEF 144
                                                                                                                                                                                                                                    --DSRCKARQLELNERTCRC
                                                                                                                                                                                                                                                                               LFVQDP.
                                                                                                                                                                                                                                                                                                                                                                           GVATNIFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLSQ--GPKPVTIS
                                                                                                                                                                                                                                                                                                                                                                                                         LHHAKWSQAAPTTEGEQKSHEVIKFM------DVYQRSYCRPIETLVDIFQEY
                                                                                                                                                                                                                                                                                                 MFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNK 322
                                                                                                                                                                                                                                                                                                                       FLQHSRCECRPKKDRTKPEKKSVRGK-----GKGQKRKRKKSRFKSWSVHCEPCSERRKH
                                                                                                                                                                                                                                                                                                                                          FANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDF
                                                                                                                                                                                                                                                                                                                                                                PDEIEYIFKPSCVPLMRCAGCCNDEALECVPTSESNITMQIMRIKPHQSQHIG----EMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; PS00249; PDGF_1; 1.
; PS50278; PDGF_2; 1.
; Growth factor; Glycol
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117
214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; AAB22252.1;
; AAB22253.1;
; AAB22254.1;
; AAA40547.1;
; -; NOT_ANNOT
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                                                                                                                                                                                 STANDARD;
cDNA sequences
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93
127
129
76
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100
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164
208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Alternative splicing; Signal.
BY SIMILARITY.
VASCULAR ENDOTHELIAL GROWTH FACTOR.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (PROBABLE).
K -> N (IN ISOFORM VEGF-1).
MISSING (IN ISOFORM VEGF-1).
MISSING (IN ISOFORM VEGF-2).
GE -> ER (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 207.5;
Pred. No. 2.5e
32; Mismatches
                                                                       Craniata; Ver
Sciurognathi;
                                                                                                                                                                                 PRT;
 of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B5540B51E4BB6E17 CRC64;
 vascular
                    Kwok P.W.,
                                         27-190
                                                                                                                                                                                 190
                                                                                   Vertebrata;
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hes 98;
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                                                                        Muridae;
 endothelial cell mitogen
                                                                                                                           (VEGF)
                    Sullivan K.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                           (VASCULAR
                                                                       Euteleostomi;
; Murinae; Rattus
                                                                                                                                                                                                                                                                              -QTCKCSCKNT
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RESULT VEGF_BOVIN
ID VEGF_BOVIN
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Matches 62
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DISULFID
DISULFID
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitogen;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00341; PDGF; 1
PROSITE; PS00249; PDGF
PROSITE; PS50278; PDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M32167; AAA41211.1;
PIR; A35987; A35987.
HSSP; P15692; 2VGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     that is homologous to platelet-derived growth factor.";
Proc. Natl. Acad. Sci. U.S.A. 87:25028-2533(1990).
-1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                      173
                                                                                                                              330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY). SIMILARITY: EXPRESSED IN THE PITUITARY, IN BRAIN, IN TISSUE SPECIFICITY: EXPRESSED IN THE PITUITARY, IN BRAIN, IN PARTICULARLY IN SUPRAOPTIC AND PARAVENTRICULAR NUCLEI AND THE CHOROID PLEXUS. ALSO FOUND ABUNDANTLY IN THE CORPUS LUTEUM OF THE OVARY AND IN KIDNEY GLOMERULI.

SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERMEABILITY.
SUBUNIT: HOWODIMER, DISULFIDE-LINKED
SUBCELLULAR LOCATION: SECRETED BUT RI
TO THE EXTRACELLULAR MATRIX UNLESS RI
                                                                                                    ANR-EFDENTCQC
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ARQLELNERTCRC
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                                                                                                                                                                                                                                                                   FKPSCVPLMRCAGCCNDEALECVPTSESNVTMQIMRIKPHQSQHIG----EMSFLQHSRC
                                                                                                                                                                                                                                                                                  FKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLSQ--GPKPVTISFANHTSC
                                                                                                                                                                                                                                                                                                                        HHAKWSQAAPTTEGEQK---AH---EVVKFMD-VYQRSYCRPIETLVDIFQEYPDEIEYI 71
                                                                                                                                                                                    DDSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCG
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62; Conser
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22396 1
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24.5%;
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BY SIMILARITY.
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BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLUNAC. .).
N-LINKED (GLUNAC. .).
N589374010441E377 CRC64;
                                                                                                                                                                                                               -----RTKP----
                                                                                                                                                                                                                                                                                                                                                                                         Score 206.5; DB 1
Pred. No. 2.6e-09;
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                    190
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                                                                                                                                                                                                                                                                                                                                                                             71;
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01-APR-1990 (Rel. 01-APR-1990 (Rel.

14, Created)
14, Last sequence update)

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Mitogen;
SIGNAL
CHAIN
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DISULFID
CARBOHYD
                    VARSPLIC VARSPLIC
                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                EMBL; M32976; AAA30502.1; -. EMBL; M31836; AAA30804.1; -. EMBL; M3750; AAA30805.1; -. PIR; A33255; A33255.
                                                                                                                                                                                                                                                                                           or send an
                                                                                                                                                                                                                                                                                                      entities
                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor specific for vascular endothelial cells.";
Biochem. Biophys. Res. Commun. 161:851-858(1989);
-!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS.
CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tischer E., Gospodarowicz D., Mitchell R., Silva I Lau K., Crisp T., Fiddes J.C., Abraham J.A., "Vascular endothelial growth factor: a new member derived growth factor gene family."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 27-MEDLINE=90069608; PubMed=2479986; Leung D.W., Cachianes G., Kuang W.-J., "Vascular endothelial growth factor is
                                                                                                                                                                         Pfam; PF00341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrara N., Henzel W.J.;
"Pituitary follicular cells secrete a novel heparin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, VASCULAR ENDOTHELIAL
                                                                                                                                                                                     [nterPro;
                                                                                                                                                                                                HSSP; P15692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89286596; PubMed=2735925;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90121225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 246:1306-1309(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERMEABILITY
                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                          TO THE EXTRACELLULAR MATRIX UNLESS
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                                                                                                                                                                                                           в40080; в40080.
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                                                                                                                                     PS00249; PDGF_1; 1.
PS50278; PDGF_2; 1.
Growth factor; Glyc
                                                                                                                                                                                                                                                                                        requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               non-profit institutions as long and this statement is not removed
                                                                                                                                                                                   IPR000072;
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                                                                                                                                                                         PDGF; 1.
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IAL GROWTH FACTOR PRECURSOR (VEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=2610687;
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                                                                                                                                     Glycoprotein;
          WW;
                                                                            VASCULAR ENDOTHELIAL (
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MISSING (IN ISOFORM BETA).

R -> K (IN ISOFORM BETA).

EDBF903E46E24789 CRC64:
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                                          INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POT
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                                                                                                                                     Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                          RELEASED
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                                          (POTENTIAL)
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Best Local s
Matches 60
                                                                        Pfam; PF00341; PDGF; 1.
Pfam; PF00341; PDGF; 1.
PROSITE; PS00249; PDGF_1;
PROSITE; PS50279.
             Mitogen;
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01-AUG-1992 (Rel. 23, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
VASCULAR ENDOTHELIAL GROWTH FACTOR (VE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEGF_CAVPO ST/
P26617;
01-AUG-1992 (Rel.
                                                                                                                                 EMBL; M84230; AAA37057.1; HSSP; P15692; 2VGH.
                                                                                                                                                                    entities requires a license agreement or send an email to license@isb-sib.ch
                                                                                                                                                                                           modified and this statement
                                                                                                                                                                                                     the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                              Berse B.;
Submitted (XXX-1992)
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAVPO
  CARBOHYL
                                                                                                                                                                                                                                 between
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                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID*10141;
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                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation auropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                    GROWTH
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azoa; Chordata;
eria; Rodentia;
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                                                                                  PDGF_1;
PDGF_2;
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BY SIMILARITY.

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O INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. . . ) (POTEN
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Hystricognathi; Cavii
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No. 3.1
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RESULT 10
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Q25464;
30-MAY-2000
30-MAY-2000
01-OCT-2000
                                                                                                                                                                                                         "Mussel adhesive plaque protein gene is a novel member of epi
growth factor-like gene family.";
J. Biol. Chem. 270:6698-6701(1995).
-i- FUNCTION: PROVIDES ADHESIVENESS TO THE MUSSEL'S FOOT. MUS
PRODUCE ONE OF THE STRONGEST WATER INSOLUBLE GLUE. THE MU
ADHESIVE IS A BUNDLE OF THREADS, CALLED A BYSSUS, FORMED
FIBROUS COLLAGENOUS CORE COAFED WITH ADHESIVE PROTEINS.
-i- SUBCELLULAR LOCATION: SECRETED.
-i- SUBCELLULAR LOCATION: SECRETED.
-i- SUBCELLULAR LOCATION: SECRETED.
InterPro; IPRO Pfam; PF00008;
                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruct use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            MEDLINE=95204464; PubMed=7896812; Inoue K., Takeuchi Y., Miki D., C
                                                                                                                                                                                                                                                                                                                                                                                                          Mytilus galloprovincialis (Mediterranean mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID-29158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                        EMBL; D43794; BAA07852.1;
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30-MAY-2000 (Rel. 39, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
ADHESIVE PLAQUE MATRIX PROTEIN 2 PRECURSOR (FOOT
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                         DIHYDROXYPHENYLALANINE)
SIMILARITY: CONTAINS 11
                                                                                                                                                                                   FORMATION, STAGE.
PTM: SOME TYROSINES ARE HYDROXYLATED
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56; Conservative
           IPR000561;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                 license agreement (See http://www.isb-sib.ch/announce/
license@isb-sib.ch).
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22.5%;
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Mismatches
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IE MUSSEL'S
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                                                                            81 YKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDV 140
                                         GKEFG-VATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLSQGPKPV
               TISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQ-CQAANKTCP---TNYMWNNHICR
                              GKTFKCVCRNGNFGRLCEKNVCSPNPCKNNG-KC----
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PS00022;
PS01186;
-GGYTGPRC----
                                                                                            Conservative
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EGF_1; 11.
EGF_2; 10.
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51772
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461
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21
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BY SIMILA
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                                                                                           Score 182.5; DB 1
Pred. No. 4.9e-07;
7; Mismatches 127
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DOPA.
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POTENTIAL.
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                                                                                                         DB 1;
                              -SPLGKTGYKCTCS-----
                                                                                            127;
                                                                                                                                  CRC64
                                                                                            Indels
                                                                                                          Length
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                                                                                                           473;
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RESULT
VEGF_CH
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P52582; Q91420;
01-OCT-1996 (Rel. 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHICK
                                                                                                                                                                                                           differentiation in the quail embryo.";
Dev. Biol. 169:699-712(1995).
-i- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS,
CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEGF.
Gallus (Chicken), and
Gallus gallus (Chicken), and
Coturnix coturnix japonica (Japanese quail).
Coturnix coturnix japonica (Japanese quail).
Coturnix coturnix japonica (Japanese quail).
Coturnix gallus (Chicken), and
Coturnix coturnix japonica (Japanese quail).
                                                                                                                                                                                                                                                                                                              SPECIES=C.c.japonica;
MEDLINE=95301109; PubMed=7781909;
Flamme I. Breier G., Risau W.;
"Vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 60-187 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFECIES=C.C.japonica;
MEDLINE=96005007; Publ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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15-DEC-1998 (Rel. 37, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
                                                                                                                                                                                                                                                                                        "vascular endothelial growth factor (VEGF) and VEGF receptor (\text{Ik-1}) are expressed during vasculogenesis and vascular
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RETENTION SIGNAL.

RETENTION SIGNAL.

TISSUE SPECIFICITY: ABUNDANTLY AND EQUALLY EXPRESSED IN HEART LIVER. IN KIDNEY GLOMERULI, BRAIN AND YOLK SAC, VEGF-166 FORM.

5- TO 10- TIMES MORE ABUNDANT THAN THE VEGF-190 FORM.

DEVELOPMENTAL STAGE: THE VEGF-166 FORM IS EXPRESSED EARLY AT I
                                                                                                            SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
ALTERNATIVE PRODUCTS: THREE ISOFORMS (VEGF-190, VEGF-146 AND VEGF-
166) ARE PRODUCED AS A RESULT OF ALTERNATIVE SPLICING OF THE SAME
GENE. THE LONGER FORM CONTAINS A BASIC INSERT WHICH ACTS AS A CELL
                                                                                                                                                                                         PERMEABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSYKKNPCASRPCKNRGKCTDKGNGY---VCKCARGY 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIYTCKCAYGWRGRHCTDKAYKPNPCVVSKPCKNRGKCIWNGKAYRCKCAYGYGGRHCTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GICSSDGSGGYRCRCKGGYSGPTCKVNVCKPTPCKNSGRCVNKGSSYNCICKGGYSGPTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCYR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENVCKPNPCQNRGRCYPDNSDDGFKCRCVGGYKGPTCEDKPNPCNTKPCKNGGKCNYNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CVDGYSGPTCQENACKPNPCSNGGTCSADKFGDYSCECRPGYFGPECERYVCAPNPCKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ACECT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CL-----AQEDFMF---SSDAGDDSTDGFHD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----REFDENT-----CQCV-----CK---RTCPRNQPLNPGKC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPCTNRQKACEPGFSYSEEVCRCVPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -QCVCRAGLRPASC-----GPHKELDR-----NSCQCVCKNKLFPSQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=7556923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216
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                                                                                                                                                                                                                                AND ENDOTHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -ICGPNKELDE 288
                  EARLY AT DAY
                                                        IS
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                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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VARSPLIC
VARSPLIC
VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
           Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 40, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR
                                                                                                                        VEGB_HUMAN P49765;
                                               VEGFB OR VRF.
                                                             FACTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00249; PDGF_1; 1. PROSITE; PS50278; PDGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00341; PDGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB011078; BAA24925.1; -. EMBL; S79680; AAB35371.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000072;
                                                                                                                                                                                                                         320
                                                                                                                                                                                                                                                 175
                                                                                                                                                                                                                                                                                                  119
                                                                                                                                                                                                                                                                                                                                                                          145
                                                                                                                                                                                               191 -- KFTDSRCKSRQLELNERTCRC
                                                                                                                                                                                                                                                                          260
                                                                                                                                                                                                                                                                                                                           200
                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                                           90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND IS UPGRADED DURING GASTRULATION. EXPRESSION OF THE VEGF-19 FORM IS DETECTABLE ONLY FROM DAY 2. SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                        KNKLFPSQCGANR-EFDENTCQC
                                                                                                                                                                                                                                                                                                                                                                                                   WIHWGLAALLYLQSAELSKAAPALGDGERKPNEVIKFLE-VYERSFCRTIETLVDIFQEY 65
                                                                                                                                                                                                                                                 RKHLFVQ---
                                                                                                                                                                                                                                                                                                 HMSFLQHSKCDCRPKKDVKNKQEKKSKRGKGKGQKRKRKKGRYKPPSF---
                                                                                                                                                                                                                                                                                                                          TISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQ
                                                                                                                                                                                                                                                                                                                                                                         GVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLS-----QGPKPV 199
                                                                                                                                                                                                                                                                                                                                                                                                                          WQHNREQANLNSRTEETIKFAAA-----HYNTEILKSIDNEWRKTQCMPREVCIDVGKEF
                                                                                                                                                                                                                                                                         EDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVC
                                                                                                                                                                                                                                                                                                                                                 PDEVEYIFRPSCVPLMRCAGCCGDEGLECVPVD-----VYNVTMEIARIKPHQSQHIA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P15692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216
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83
87
77
101
142
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                                    (Human)
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                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216
128
130
177
86
101
142
142
166
166
210
25203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor;
            Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.6%;
20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Alternative splicing; Signal.
BY SIMILARITY.
VASCULAR ENDOTHELIAL GROWTH FACTOR.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
                                                                                                                                                                                                                                                 ----DPQTCKCSC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . ) (POTENTIAL).
K -> N (IN ISOFORM VEGF-166).
MISSING (IN ISOFORM VEGF-146).
MISSING (IN ISOFORM VEGF-146).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 178.5; DB
Pred. No. 4.4e-07
1; Mismatches 9
                                                                                                                                                                                                 211
                                                                                                                                                                                                                        341
            Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (BY SIMILARITY).
                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82E669C2F6FC6DA7 CRC64;
                                                                                                                                    188
                                                                                                                                    ΑA
            Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  98;
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                                                                        (VEGF-B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bу
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                                                                         (VEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216;
                                                                                                                                                                                                                                                                                                 -HCEPCSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 13
VEGB_MOUSE
ID VEGB_MOUSE
AC P49766;
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                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitogen;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pollock P., Gotley D., Carson E., Rakar S., Nordenskjoeld M. Hayward N., Weber G.;
"Cloning and characterization of a novel human gene related vascular endothelial growth factor.";
Genome Res. 6:124-131(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=97077124; PubMed=8919691;
Grimmond S., Lagercrantz J., Drin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=96197355; PubMed=8637916;

Olofsson B., Pajusola K., Kaipainen A., von Euler G.,

Saksela O., Orpana A., Pettersson R.F., Alitalo K., Er

"Vascular endothelial growth factor B, a novel growth
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U48801; AAB06274.1; -. EMBL; U43369; AAA91463.1; -. HSSP; P15692; 1VPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000072; -
Pfam; PF00341; PDGF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                +
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                                                                                               149
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                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.
HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.
SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREETHER HONORIMER, DISULFIDE-LINKED. CAN ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WITH VEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
                                                                                                                           CQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQC
                                                                                                                                                                                                                                                                                                                    AAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601398;
                                                                                                                                                                                         ATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEET
                                                                                                                                                                                                                                                                                   APGHQRKVVSWIDVYTRAT-CQPREVVVPLTVELMGTVAKQLVPSCVTVQRCGGCCPDDG
                                                                                                                                                                                                                      LECVPTGQHQVRMQILMIRYPSSQLGE---MSLEEHSQCECRPK---
                                                                                                                                                                                                                                                    LQCMNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLP 230
                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00249; PDGF_1; 1.
PS50278; PDGF_2; 1.
Growth factor; Signal; Heparin-binding.
1 21 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                              188 AA;
                                                                                                                                                                                                                                                                                                                                                   Conservative
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                              188 v
21261 MW;
                                                                                             -HQRPDPRTCRCRCRRRSFLRCQGRGLELNPDTCRC
                                                                                                                                                                                                                                                                                                                                                                7.5%; Score 175.5; DB 1; 22.5%; Pred. No. 6.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A. 93:2576-2581(1996)
                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                                           VASCULAR ENDOTHELIAL GROWTH F04654D5A3727194 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drinkwater C.,
n E., Rakar S.,
                                                                                                                                                           RCTQH - -
              PRT;
                                                                                                                                                                                                                                                                                                                                                 Mismatches
                188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Silins G.,
                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                        --KKDSAVKPDSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Townson
                                                                                               183
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SEQUENCE
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VASCULAR ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
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Olofsson B., Pajusola K., Kalpainen A., von Euler G.,
Saksela O., Orpana A., Pettersson R.F., Alitalo K., E
"Vascular endothelial growth factor B, a novel growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
Mitogen; Growth factor; Signal; Heparin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U48800; AAB06273.1; -. EMBL; U43837; AAC52553.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS
TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
-!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN HEART, BRAIN, KIDN
AND SKELETAL MUSCLE.
-!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Townson S., Lagercrantz J., Grimmond S., Silins G., Nordenskjoeld M., Weber G., Hayward N.K.; "Characterization of the murine VEGF-related factor Biochem. Biophys. Res. Commun. 220:922-928(1996).
-i- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. E-i-SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endothelial cells.";
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                                               QVHSIIRRSLPATL-PQCQAAN-----KTCPTNYMWNNHICRCLAQEDFMFSSDAGDDST
                                                                                                                                                        YRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYR 219
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KKESAVKPDSPRILCPPCTQRRQRPDPRTCR--
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P15692;
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                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VASCULAR ENDOTHELIAL GROWTH FACTOR ; D52A055FB995E9CA CRC64;
                                                                                                                                                                                                                                                                                                                                               Score 175;
Pred. No. 7.
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FORM HETERODIA
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DISULFID
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SIGNAL
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Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Mammalia; Eutheria; Ceta
Bovidae; Caprinae; Ovis.
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01-NOV-1997 (Rel. 35, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF)
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                                                                                                                                                                                                                                                                                         HSSP; P15692; 1VPF.
                                                                                                                                                                                                                                                                                                   EMBL; x89506; CAA61677.1; -.
                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization and expression of vascular endothelial growth factor (VEGF) in the ovine corpus luteum.";
J. Reprod. Fertil. 108:157-165(1996).
-I- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reynolds L.P., Moor R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redmer D.A., Dai Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Kidney;
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LHHAKWSQAAPMAEGGQKPHEVMKFM----
                       LRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEF 144
                                                l Similarity 29.0
                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.ch).
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PS50278; PDGF_2; 1.
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Cetartiodactyla; Ruminantia; Pecora;
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W; 4E792CB557F91760 CRC64;
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                                               Score 173.5; DB 1; Pred. No. 7.2e-07; B; Mismatches 61;
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VASCULAR ENDOTHELIAL GROWTH
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                  PRINTS; PRO0365; ENDOTHELIN.
PRINTS; PRO0453; VWFADOWAIN.
PROSITE; PS50234; VWFA; 3.
PROSITE; PS501208; VWFC; 3.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01125; CTCK_2; 1.
                                                                                                                                                               InterPro; IPR002919; -. Pfam; PF00007; Cys_knot; 1. Pfam; PF00092; vwa; 3. Pfam; PF00093; vwc; 3. Pfam; PF00094; vwd; 3. Pfam; PF01826; TIL; 3.
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Q28833;
Q1-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Primary Structure of the factor VIII binding domain of human, po and rabbit von Willebrand factor.";
Biochem. Biophys. Res. Commun. 194:1019-1024(1993).

-i- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEOSTASIS, IT PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics Institute. The European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF VASCULAR INJURY (BY SIMILARITY) SUBUNIT: MULTIMERIC (BY SIMILARITY).

SUBUNIT: MULTIMERIC (BY SIMILARITY)

FTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR INTERCHAIN DISCUFIDE BONDS (BY SIMILARITY).

SIMILARITY: CONTAINS 3 WAFC DOMAINS.

SIMILARITY: CONTAINS A C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).

SIMILARITY: SOME, TO SILKWORM HEMOCYTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    email to license@isb-sib.ch).
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Platelet; Glycoprotein; Extracellular matrix;
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the EMBL/GenBank/DDBJ
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CELL ATTACHMENT SITE (POTENTIAL).

BY SIMILARITY.

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| :|:|
CCGKCLPSACKVVIGSFRGDSVSYWK 2184
                               VC-RCVP-----SYWK 414
                                                                 PVGQFWEEGCDVCTCTD-----LEDAVMGLRVAQCAQKPC---EDSCRPGFTYVLHEGE 2158
                                                                                                                                TPALRKTQCCDEYECACNCVNTTLSCPLGYLASTVTNDCGCT-TTTCLPDKVCVHRGTVY 2107
                                                                                                                                                                                                   VCDLVSCDLPPVPHCEGGLQPTLTNPGECRPN----FTCACRKEECPRGPLP-SCPPHR
                                                                                                                                                                                                                                                                     -----CTCLSG-----RRVNCTLQPCPTARAPACGLCEVARLRQEAHQCCP-----EYEC
                                                                                                  PRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSY---SEE
                                                                                                                                                                 E-----LDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTC------
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Search completed: Job time: 464 sec October 17, 2001, 14:51:38

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Result
No.
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 2092.5
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1: sp_archea:*
2: sp_bacteria
3: sp_fund:*
4: sp_human:*
5: sp_human:*
5: sp_mammal:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_plant:*
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11: sp_rodent:
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13: sp_vertebr
14: sp_virus:**
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Match Length DB
 89.6
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Copyright (c) 1993 - 2000 Compugen Ltd.
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057352 coturnix co
043915 homo sapien
p97946 mus musculu
035251 rattus norv
035757 rattus norv
094446 chironomus
094448 chironomus
09449 homo sapien
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ALIGNMENTS

Qу 60	Db 1	0у 1	Query Match Best Local Matches 37		FT CHAIN										RP SEQU										AC 09XS50	XS5	RESOLI
0 LRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEIL 119	1 MHLLGFCSVACSLLAAALLPGPRRAPAAAAAAFESGLGFSDTEPDAGENKAYAGKEMEEQ 60	1 MHLLGFFSVACSILAAALLPGPREAP-AAAAAFESGLDLSDAEPDAGEATAYASKDLEEQ 59	/ Match 89.6%; Score 2092.5; DB 6; Length 420; Local Similarity 88.1%; Pred. No. 5.5e-191; res 370; Conservative 19; Mismatches 30; Indels 1; Gaps	NCE 420 AA; 46681 MW;	ATN 21 420 FOTENTIAL.	SMART; SM00141; PDGF; 1.	TROSTIE; F300249; FDGT_1; I.	Pfam; PF00341; PDGF; 1.	InterPro; IPR000072;	HSSP; P15692; 1VPP.	EMBL; AB004275; BAA77687.1;	Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.	 Liu X., Yonekura H., Yamaqishi S., Yamamoto Y., Yamamoto H.:	TTSSHE=HEART:	SEQUENCE FROM N.A.	[1]	BOVIDAE; BOS.	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Bos taurus (Bovine).	HTWO	(TrEMBLrel. 16,	(TrEMBLiel. 12,	01-NOV-1999 (Trematical 12 Created)	O9XS50: FRELLMINARI; FRI; 4ZO AA.		-
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Best Local
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InterPro; IPR00200; -.
Pfam; PF00341; PDGF; 1.
PRINTS; PR00438; GFCYSKNOT.
PrODOM; PD001629; -; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS00249; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
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01-JUN-1998 (TREMBLTEL 06, C
01-JUN-1998 (TREMBLTEL 06, L
01-MAR-2001 (TREMBLTEL 16, L
VASCULAR ENDOTHELIAL GROWTH F
VEGF-C
                                                                                                                                                                                                                                                                                                    Signal.
SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Development 125:743-752(1998).
EMBL; Y15837; CAA75799.1; -.
HSSP; P15692; IVPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eichmann A., Corbel C., Jaffredo T., Breant V., Joukov V., Kumar V., Alitalo K., Le Douarin N.M.; "Avian VEGF-C: cloning, embryonic expression pattern and stimulation of the differentiation of VEGFR2-expressing endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Archosauria; Aves; Neognathae; Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 057352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursors.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=98167900; PubMed=9435294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=93934;
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76.28;
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FACTOR C PRECURSOR.
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Pred. No. 5.3e
88; Mismatches
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VASCULAR ENDOTHELIAL GROWTH
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mes; Phasianidae; Phasiani
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                                                    "Vascular endothelial growth factor D (VEGF-D) is a l tyrosine kinases VEGF receptor 2 (FlX1) and VEGF
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O43915;
O1-JUN-1998 (TrEMBLrel. 0
O1-JUN-1998 (TrEMBLrel. 0
O1-MAR-2001 (TrEMBLrel. 1
GROWTH FACTOR FIGF.
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[2]
                  Pfam;
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MEDLINE=98140120; PubMed=9479493;
Rocchigiani M., Lestingi M., Luddi A.,
Rossi E., Ballabio A., Zuffardi O., Ol.
                                                                                                                                                                                                                                                                                                                                         Achen M.G., Jeltsch M., Alitalo K., Stacker S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics 42:483-488(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=LUNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Human FIGF: cloning, gene structure, between the PIGA and the GRPR genes."; Genomics 47:207-216(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamada Y., Nezu J.,
"Molecular cloning
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rPro; IPR000072;
; PF00341; PDGF;
cm; PD001629; -;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J., Shimane M., Hirata
ing of a novel vascular
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ch M., Kukk E.,
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16,
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                                                                                                                                                                                                                                                                                                                                                            Maekinen
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Oliviero S.;
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endothelial
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DR DR SQ

PROSITE; PS00249; PI PROSITE; PS50278; PI SMART; SM00141; PDGI SEQUENCE 354 AA;

9; PDGF_1; 8; PDGF_2; PDGF; 1.

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Best Local Similarity
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VEGE-D OR Fior.
Mus musculus (Mouse).
Mus musculus (Motazoa; Chordata; Metazoa; Rodentia; Rodentia;
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01-MAY-1997 (TrEMBLrel.
01-MAY-1997 (TrEMBLrel.
                  InterPro; IPR000072; -. Pfam; PF00341; PDGF; 1. ProDom; PD001629; -; 1.
                                                                                                                       EMBL; X99572; CAA67892.1;
EMBL; D89628; BAA14002.1;
HSSP; P15692; 1VPP
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ordandini M., Marconcini L., Ferruzzi R., Oliviero S.; "Identification of a c-fos-induced gene that is related to platelet-derived growth factor/vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997 (Tremblrel. 03, 01-MAY-1997 (Tremblrel. 03, 01-MAR-2001 (Tremblrel. 16, VASCULAR ENDOTHELIAL GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P97946
                                                                                             MGD; MGI:108037; Figf.
                                                                                                                                                                                               Genomics 42:483-488(1997).
                                                                                                                                                                                                                            VEGF-D."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             Yamada Y., Nezu J.,
                                                                                                                                                                                                                                                                                                    MEDLINE=97349118; PubMed=9205122;
                                                                                                                                                                                                                                                Yamada Y., Nezu J., Shimane M., Hirata Y.;
Molecular cloning of a novel vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                              family."
                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 114
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PS00249; PDGF_1;
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Last annotation update)
FACTOR D (C-FOS INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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Pred. No. 6.
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Sciurognathi; Muridae;
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DR
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Best Local Sin
Matches 134;
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Best Local
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01-JAN-1998 (TrembLrel. 05, C
01-JAN-1998 (TrembLrel. 05, L
01-MAR-2001 (TrembLrel. 16, L
VASCULAR ENDOTHELIAL GROWTH F
                                                                                                                    HSSP; p15692; 1VPP.
Interpro; IPR000072;
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; -; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
SWART; SW00141; PDGF; 1.
SWART; SW00141; PDGF; 1.
SEQUENCE 326 AA; 37112 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50278; I
SMART; SM00141; PD0
SEQUENCE 358 AA;
                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                 Genomics 42:483-488(1997).
EMBL; AF014827; AAB66557.1;
                                                                                                                                                                                                                                                                       Yamada Y., Nezu J., Shimane M., Hirata Y.; "Molecular cloning of a novel vascular endothelial growth factor,
                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE DAWLEY;
MEDLINE-97349118; PubMed-9205122;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             VEGF-D
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EQQIRAASTLEELLQVAHSEDWKLWRCRLKL-----KSLANVDSRSTSHRSTRFAATFY
                         EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPENCSCFECKESLESCCQKHKIFHPDTCSCEDRCPFHTRTCASRKPACGKHWRFPKE 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETCQC:| : | | | : : | : | : | | | | | | |
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139; Conserv
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PDGF; 1.
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Last annotation updat
FACTOR D.
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                                                  Score 675.5; DB
Pred. No. 3.2e-50
3; Mismatches
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Pred. No. 7.8e-59;
8; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                      1261AFA373596C00 CRC64;
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                                                    3.2e-56;
nes 79;
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01-JAN-1998 (TrEMBLrel. 05, Cr
01-JAN-1998 (TrEMBLrel. 16, Li
01-MAR-2001 (TrEMBLrel. 16, Li
VASCULAR ENDOTHELIAL GROWTH F.
Rattus norvegicus (Rat).
  Q94446;
Q94446;
01-FEB-1997
01-FEB-1997
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PROSITE; PS50278; PDGF_2;
SMART; SM00141; PDGF; 1.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY; TISSUE-LUNG; Mandriota S.J., Pepper M.S.; Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF010302; AAB63248.1; -. HSSP; P15692; 2VPF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        111;
                                                                                                                                                                                                                                                                                                                                                              VSVYRCGGCCNSEGLQCMNTSTGYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLD
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126
126 ‡
  (TrEMBLrel.
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                                                                     PRELIMINARY;
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FACTOR-C (FRAGMENT).
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Pred. No. 9.4e-53;
0; Mismatches 5
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Sciurognathi;
                                                                     PRT;
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Murinae; Rat
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В
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                   Q94438 PRELIMINARY;
Q94438;
01-FEB-1997 (TrEMBLrel. 02, C
01-FEB-1997 (TrEMBLrel. 02, L
01-OCT-2000 (TrEMBLrel. 15, L
185 KDA SILK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=SALIVARY GLAND,
Case S.T., Cox C., Be
Submitted (APR-1996)
                                                                                                            Chironomus pallidivittatus (Midge).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Chironomoidea; Chironomidae; Chironominae; Chironomus.
NCBI_TaxID=7151;
          TISSUE-SALIVARY GLAND;
Case S.T., Cox C., Bell W.C.,
Submitted (APR-1996) to the E
EMBL; U54640; AAA99803.1; -.
InterPro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                   1354
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                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                       SP185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00022; EGF_1; UNKNOWN_2.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

SEQUENCE 1704 AA; 185745 MW; 3A3F20247C8F1E28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000561; -.
InterPro; IPR000853; -.
PRINTS; PR00876; MTNEMATODE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chironomus thummi thummi (Midge).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Chironomoidea; Chironomidae; Chironominae; Chironomus.
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U54641; AAA99804.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TremBLrel.
220 KDA SILK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                              363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity hes 79; Conserv
                                                                                                                                                                                                                                                                                                                                                S-GTQTC-PAGQSWDSQTCQC-SCPATGK---CTGAQFWCAKQCKCV
                                                                                                                                                                                                                                                                                                                                                                            TESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRCV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QIFDKNTCKCKCPNEKPGDSCGKGKDFCPVDCSCKCKSPKPANGCPGVQEWNEDKCKCEC 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INCPAKQTFIESECECGCET----RPKCLDGFRFSNLECGCVCDEKKCQ------GK 1125
                                                                                                                                                                                                                                                                                                                                                                                                      KWNKNTCACECPPGKATPASCGDKKSWNPDSCSCQCKSKMPGGGCPSNQQWNCETCKCEC
                                                                                                                                                                                                                                                                                                                                                                                                                                    ELDRNSCQCVC-KNKLFPSQCGANREFDENTCQCVCKRT----CPRNQPLNPGKCACEC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WCENSCQCVCPKNMEKPADN------CG-NKWWNDKACECECKPGCPEAGCKGVQ 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKDKSKTTCEGGQKWNDNQCQCGCPTPAPTCSASQKYSNVTCSCGCNPGMPAKGCPGNQV 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLDVYRQV-----KTCPTNYM 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TQCMPREVCIDVGKEFGVATNTFFKPPCVSVYR-----CGGCCNSEGLQCMNTSTSYLSK 183
IPR000853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                Created)
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Pred. No. 1e
                                                      Hoffman
                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                            1698
                                                       R.T.,
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                                                       Martin J., Hamilton
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                                                                                                                                                                                                                   update)
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                                          databases
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                                                       R.;
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Best Local
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Best Local
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PROSITE;
SEQUENCE
                                                                                                                                                                                                                          WILLIAMS S.;
Williams S.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL136131; CAC19512.1;
SEQUENCE 232 AA; 27042 MW; FB49F364446F4D01 CRC64;
                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1117
                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TEEMBLrel. 16, Created)
01-MAR-2001 (TEEMBLrel. 16, Last sequence update)
01-MAR-2001 (TEEMBLrel. 16, Last annotation update)
DJ261G23.6.3 (VASCULAR ENDOTHELIAL GROWTH FACTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9H1W9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1387
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                 189
                                                                        129
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                                            50
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                                                                                                                               69
                                                                                                                                                                     Local
TVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYM
                                                            TQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEI 188
                                         SYCHPIETLYDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTEESNITMQIMRI 109
                                                                                                                          LMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPAQKKCDSPKTWDESSCSC----QCPKNMRPPKGGCNAGRTWDDATCSEKCAAVP 1438
                                                                                                   LLLYLHHAKWSQAAPMAEGGGQNHH-----EVVKFM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKGKK----FHHQTCSCYRRPCTNRQK----ACEPGFSYSE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSQCGANREFDENTCQCVC--KRTCPRNQPLNPGKCACECTESPQ------KCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKMCQCECKPGCPEGGCKGVMKWNANTCACECPAGKPASCGDIKSWNDDSCSCQCKSKMP 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEWNEEKCQC-----ECPKDKPK-----KQCPGGQDWNNHLCQCGCPTP 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q-----GKQVFDKNTCQCKCPNQKPGDTCGNGKDFCPLDCSCKCKSPKPANGCPGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNEWR-----KTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYR-----CGGCCNSEGL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGCPPNQQWNEKTCECECSAKGNCPAGQTWNSQTCQCSCPASGTCTGAQVWCSKACKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APTCSNKQKYSNVSCSCGCKPGKPKEGRPGKQIWCENTCRCVCPKNMDKPANNCGSKWWN
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                                                                                                                                                      h 10.2%;
Similarity 24.7%;
70; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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186164 MW; 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.8%;
                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                     Score 238.5; DB 4;
Pred. No. 8.6e-15;
33; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 252; DB 5;
Pred. No. 4.6e-15
0; Mismatches 12
                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; I Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- RPASCGPHKELDRNSCQCVCKNKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
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123;
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                                                                                                                                                                                 Length
                                                                                                                                                        Indels
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                                                                                              ------DVYQR 49
                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -EVCRCVP 410
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Q16889
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01-NOV-1996 (TrEMBLrel. 01, Cr
01-NOV-1998 (TrEMBLrel. 08, La
01-MAR-2001 (TrEMBLrel. 16, La
01-MAR-2001 (TrEMBLREL. 16, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S85192; AAC63102.1; -
EMBL; S85224; AAC63101.1; J
EMBL; S85199; AAC63101.1; J
EMBL; S85201; AAC63101.1; J
EMBL; S85201; AAC63101.1; J
EMBL; S85222; AAC63101.1; J
EMBL; S85222; AAC63101.1; J
EMBL; S85222; AYE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00249; PROSITE; PS50278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of RNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00341; PDGF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fourth molecular species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92168017; PubMed-1791831; Houck K.A., Ferrara N., Winer J., Cachianes G., The vascular endothelial growth factor family:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                     132
209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187
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CSERRKHLFVQDPQTCKCSCKNT--DSRCKARQLELNERTCRC
                                                                                                                                                                                                                                                                                                                                                                                                                          LMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endocrinol. 5:1806-1814(1991).
                                                                                          WSVYVGARC---
                                                                                                                                       WNNHI-CRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGL-RPASCGP
                                                                                                                                                                                     KP--HQGQHIGEMSFLQHNKCECRPKKDRARQEKKSVRGK----
                                                                                                                                                                                                                                                                              SYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTEESNITMQIMRI
                                                                                                                                                                                                                                                                                                                          TQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEI 188
                                                                                                                                                                                                                                                                                                                                                                              LLLYLHHAKWSQAAPMAEGGGQNHH------
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                                                                                                                                                                                                                               TVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HKE-----LDRNSCQCVCKNKLFPSQCGANR-EFDENTCQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WSVYVGARC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KP--HQGQHIGEMSFLQHNKCECRPKKDRARQEKKSVRGK-----GKGQKRKRKKSRYKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 AA;
                                            ---LDRNSCQCVCKNKLFPSQCGANR-EFDENTCQC
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pDGF_2;
pDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.2%;
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JOINED.
JOINED.
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Last annotation updat
FACTOR (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 238.5; DB 4
Pred. No. 9.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            069DFE9B9723DBA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101;
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249
                                            341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227
                                                                                                                                                                                     -GKGQKRKRKKSRYKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341
                                                                                          -CLMPWSLPGPHPCGP
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                                                                                                                                                                                                                                                                                                                                                                              -DVYQR
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RESULT
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Best Local (
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EMBL: AJ010438; CAA09179.1; -
EMBL: AL0562645; AAC16730.1; -
EMBL: AL136131; CAC19514.1; -
HSSP: P15692; 2VPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       060720;
01-AUG-1998
01-MAY-1999
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                   CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        Signal.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VEGF183 PROTEIN PRECURSOR (VASCULAR ENDOTHELIAL GROWTH FACTOR 183)
(DJ261G23.6.6) (VASCULAR ENDOTHELIAL GROWTH FACTOR).
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Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-RETINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 114-209 FROM
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                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jingjing
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                                             166
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           12
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                                                                                                                                                           TVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYM 248
                                                                                                                                                                                              TQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEI 188
                                             ERRKHLFVQDPQTCKCSCKNT - - DSRCKARQLELNERTCRC
                                                                                                              WNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHK 308
                                                                                                                                       KP--HQGQHIGEMSFLQHNKCECRPKKDRARQEKKSVR----
                                                                                                                                                                                 SYCHPIETLYDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTEESNITMQIMRI 109
                                                                                                                                                                                                                             LLLYLHHAKWSQAAPMAEGGGQNHH-----EVVKFM-----
                                                                                                                                                                                                                                                                                                                                                                                                    PD001629;
                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                              PS50278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L., Roque R.
(MAY-1998)
                                                                                                                                                                                                                                                                                                                              27
209
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                 LDRNSCQCVCKNKLFPSQCGANR-EFDENTCQC 341
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                                                                                                                                                                                                                                                                                                                                                                            PDGF_1;
PDGF_2;
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209
24422
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                                                                                                                                                                                                                                                                                     Score 231;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
VEGF183 PROTEIN.
; F01CCEACD945D6CA CRC64;
                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n of a new splicing variant VEGF183.";
                                                                                       -GKGKGQKRK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expr.
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                                           204
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                                                                                        RKKSRP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                            ----- DVYQR 49
                                                                                                                                                                                                                                                                          98;
                                                                                        -CGPCS
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RESULT 13
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Best Local S
Matches 66
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Pfam; PF00341; PDGF; 1.

ProDom; PE001629; .; 1.

PROSITE; PS00249; PDGF_1; 1.

PROSITE; PS50278; PDGF_2; 1.

SMART; SM00141; PDGF; 1.

SEQUENCE 208 AA; 24400 MW;
                                                                                                                                                   01-OCT-2000
01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9XSF4;
Q9XSF4;
01-NOV-1999
01-NOV-1999
01-MAR-2001
                                                                                                                                                                                 Q9MYV3;
                                                                                           Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Carnivora;
                   Scheidegger P., Weiglhofer W., Suare
Ballmer-Hofer K., Jaussi R.;
"Vascular endothelial growth factor
bearing dog
Biol. Chem.
                                                                                                                               VEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jingjing L., Roque R.S.;
Submitted (MAR-1999) to the
EMBL; AF133249; AAD29683.1;
HSSP; P15692; 2VPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora; MCBI_TaxID=9615;
                                                  MEDLINE=20125516; PubMed=10661874;
                                                             SEQUENCE FROM N.A.
                                                                                    NCBI_TaxID=9615;
                                                                                                                                        VASCULAR
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                                                                                                                                                                                                                                                 QTCKCSCKNT - - DSRCKARQLELNERTCRC
                                                                                                                                                                                                                                                             NSCQCVCKNKLFPSQCGANR-EFDENTCQC
                                                                                                                                                                                                                                                                                                                                                      TISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQ
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                                                                                                                                                                                                                                                                                                            EDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKE-
                                                                                                                                                                                                                                                                                                                                    EMSFLQHSKCECRPKKDRARQEKKSVR-----
                                                                                                                                                                                                                                                                                                                                                                             PDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTEE----FNITMQIMRIKPHQGQHIG
                                                                                                                                                                                                                                                                                                                                                                                                 GVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPL----
                                                                                                                                                                                                                                                                                                                                                                                                                      LHHAKWSQAAPMAGGEHKPHEVVKFM------DVYQRSYCRPIETLVDIFQEY
         dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                          ENDOTHELIAL
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380:1449-1454(1999).
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                                                                                                                                         GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.7%;
24.4%;
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16,
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16,
                                                                                                                                                                                                                                                                                          GKGKGQKRK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                          FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FACTOR 182.
                                                                                                                                      Last sequence update)
Last annotation update)
FACTOR 188 PRECURSOR.
                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                            Craniata; Vertebrata; ; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                          Suarez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
Fissipedia; Canidae;
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                      (VEGF)
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                                                                                                                                                                                             214
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                                          s;
                                                                                                                                                                                                                                                                                          -RKKSRP--CGPCSERRKHLFVQDP
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                                          Kaser-Hotz B.,
                      and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              81;
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                     receptors in tumor-
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Canis.
                                                                                               Canis
                                                                                                         Euteleostomi;
                                          Steiner
                                                                                                                                                                                                                                                                                                                                                                                                 -SQGPKPV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                              97;
                                                                                                                                                                                                                                                                                                               LDR
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                                          R.
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RESULT 14
Q9XSF5
ID Q9XSF5
AC Q9XSF5
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                                                                                                                         Query Match
Best Local
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Best Local Similarity
Matches 67; Conserv
                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9XSF5 PRELIMINARX;
Q9XSF5;
Q9XSF5;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Q1-MAR-2001 (TREMBLEL GROWTH FACTOR 188.
                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEGE. (Dog).
Canis familiaris (Dog).
Cunis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF133250; AAD29684.1; -. HSSP; P15692; 2VPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
                                                                                                                                                                                                                                                                     pfam; PF00341; PDGF; 1.
proDom; PD001629; -; 1.
prOSITE; PS00249; PDGF_1;
pROSITE; PS50278; PDGF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Ve;
Mammalia; Eutheria; Carnivora; Fissipedia;
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ133758; CAB82426.1; InterPro; IPR000072; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00341; PDGF; 1.
PROSITE; PS00249; PDGF_1;
PROSITE; PS50278; PDGF_2;
                                                                                                                                                                                                                                                                                                                                                                       HSSP; P15692; 2VPF.
InterPro; IPR000072; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247
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     18
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                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 LRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEF 144
                                                 LRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HKEL---DRNSCQCVCKNKLFPSQCGANR-EFDENTCQC
     LHHAKWSQAAPMAGGEHKPHEVVKFM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMSFLQHSKCECRPKKDRARQEKKSIRGKGKGQKRKRKKSRYKPWSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKHLFVQDPQTCKC$CKNT--DSRCKARQLELNERTCRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISFANHTSCRCMSKLDVYRQVHSIIR------RSLPATLPQCQAANKTCPTN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPL-----SQGPKPV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHHAKWSQAAPMAGGEHKPHEVVKFM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTEE-----FNITMQIMRIKPHQGQHIG 117
                                                                                                                                                                                                                         SM00141; PDGF; 1.,
CE 214 AA; 25151 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
214 AA;
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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214
25175
                                                                                                                         9.5%;
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                                                                                                  29;
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                                                                                       Score 221.5; DB o;
Pred. No. 3.3e-13;
""omatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 226.5; DB 6;
Pred. No. 1.1e-13;
6; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VASCULAR ENDOTHELIAL GROWTH FACTOR 188
                                                                                                                                                                                                                         2269981AFBC60058 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0AC980A158C44B27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -CGPCSE----
-DVYQRSYCRPIETLVDIFQEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -DVYQRSYCRPIETLVDIFQEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209
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                                                                                                  Indels
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                                                                                                  91;
                                                                                             Gaps
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RESULT
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Best Local S
Matches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GKRO PRELIMINARY;
Q9GKRO;
Q1-MAR-2001 (TrEMBLrel. 16, L
01-MAR-2001 (TrEMBLrel. 16, L
01-MAR-2001 (TrEMBLrel. 16, L
                                                                                                                                                                                                                                                                                                                                                                                          Miura N., Misumi K., Kawahara K., Nakashima'M., Fukumitsu S., Kawabata H., Uto N., Oka T., Maruyama I., Sakamoto H.; "Cloning of cDNA and High-Level Expression of Equine Vascular Endotherial Growth Factor (VEGF)."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AB053350; BABZ0890.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Perissodactyla; Equidae; Equus. NCBI_TaxID=9796; [1]
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VASCULAR ENDOTHELIAL GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                             320
                                                                                                                      121
                                                                                                                                                  203
                                                                                                                                                                                                            145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 NSCQCVCKNKLFPSQCGANR-EFDENTCQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 QTCKCSCKNT--DSRCKARQLELNERTCRC
                                                                                                                                                                                                                                         18
                                                                                                                                                                                                                                                                       85
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                 KNKLFPSQCGANR-EFDENTCQC
                                                                                                                                                 FANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDF 262
KNT - - DSRCKARQLELNERTCRC
                                                                                      MFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKEL---DRNSCQCVC
                                                                                                                      FLQHSKCECRPKKDKARQ-----
                                                                                                                                                                                              GVATNIFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLSQ--GPKPVTIS 202
                                                                                                                                                                                                                                         LHHAKWSQAAPMAEGEHKTHEVVKFM-------DVYQRSYCRPIETLVDIFQEY 64
                                                                                                                                                                             PDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTAEFNITMQIMRIKPHQSQHIG----EMS
                                                                                                                                                                                                                                                                     LRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKE-----LDR 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMSFLQHSKCECRPKKDRARQEKKSVR---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTEE - - - - - FNITMQIMRIKPHQGQHIG
                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                             190 AA;
                                                                                                                                                                                                                                                                                                     Conservative
                                                          --- ENPCGPCSE----
                                                                                                                                                                                                                                                                                                                 9.48;
                                                                                                                                                                                                                                                                                                                                                                             22312 MW; 87E9E161439E5F87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKGKGQKRKRKKSRYKSWSVP--CGPCSERRKHLFVQDP
                                                                                                                                                                                                                                                                                                     27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FACTOR 165
                                                                                                                                                                                                                                                                                                   Score 220.5; DB 6;
Pred. No. 3.5e-13;
7; Mismatches 73;
                          341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                              DB 6;
                                                        -RRKHLFVQDPQTCKCSC
                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                   Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                 190;
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                        319
                                                          164
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Search completed: Job time: 415 sec

October

17,

2001,

14:50:49

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                    score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                         Score
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2: /SIDS8/gcgdata,
3: /SIDS8/gcgdata,
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6: /SIDS8/gcgdata,
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                         Length
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                                          AAW00932
AAW11478
AAW75751
AAW75740
AAY30518
AAY22320
AAW86203
                                                                                                                                                                                                       AAW86237
AAW17837
                          AAB10648
                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Search time 115.93 Seconds
(without alignments)
53.339 Million cell updates/sec
                                                                                     Human vascular end
Vascular endotheli
Human vascular end
Vascular endotheli
                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                          Human VEGF-C full
Human foetal liver
Human Flt4 recepto
                                          Full length human
Human vascular end
VEGC protein
VEGF-C prote
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28.8 354 22 AAY9757	28.8 354 21 AAY709	28.8 354 21 AAY7075	28.8 354 21 AAB2904	28.8 354 21 AAB1064	28.8 354 19 AAW4429	28.8 354 19 AAW5324	28.8 354 19 AAW4903	28.8 325 22 AAY9757	28.8 325 19 AAW53	29.9 318 20 AAY0828	29.9 113 20 AAY0828	30.1 358 18 AAW1499	30.2 358 19 AAW4429	30.2 358 19 AAW5324	30.2 337 20	30.2 321 19 AAW5324	30.2 178 20 AAY0828	30.6 326 19 AAW4429	63.5 350 16 AAR8268	64.4 350 22 AAY9757	64.4 350 21 AAY9714	64.4 350 20	64.4 350 20 AAY3051	76.4 418 19 AAW7574	76.4 418 18 AAW0093	78.8 415 19 AAW7574	78.8 415 18 AAW009	98.3 419 18 AAW1383	100.0 419 22 AAB3760	100.0 419 22 AAY9757	0 419 21 AAY7098	100.0 419 21 AAY707	100.0 419
Human VEGF-D1 prot	p	pro-	VEGF-		n vascula	sapiens	zvegf2			growth		ne c-Fos	Mouse vascular end		an growth		an growth	vascular endo	endo		Truncated vascular	Truncated human VE	5	5	l Flt4 rec	e vascu	Flt4 rece	vascular	VEGF-C.	VEGF-B p	vascular en	prepro-vasc	Vascular endotheli

ALIGNMENTS

RESULT AAW86237

AAW86237 standard; protein; 399 AA

AAW86237;

16-FEB-1999

(first entry)

New truncated vascular endothelial growth factor-related protein subunits - lack part of the N-terminal sequence, used to stimulate

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RESULT
AAW17837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 102;
Lyman SD;
                                                    (IMMV ) IMMUNEX CORP
                                                                                                         08-NOV-1995;
                                                                                                                                                              05-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Foetal liver kinase 1 binding protein; human; flk-1bp; receptor tyrosine kinase; vasculogenesis; angiogenesis; wound healing; tumour; therapy; antagonist; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW17837 standard; Protein; 419 AA
                                                                                                                                                                                                                15-MAY-1997.
                                                                                                                                                                                                                                                                       W09717442-AJ
                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human foetal liver kinase A binding protein flk-1bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Fig 2D; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                         95US-0554374
                                                                                                                                                              96WO-US17584
                                                                                                                                                                                                                                                                                                                                                                              /label= Mat_protein
/note= "(Claim 10)"
21..35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21..419
                                                                                                                                                                                                                                                                                                                                                     /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 539; DB 20;
Pred. No. 1.1e-55;
No. Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This polypeptide comprises a human foetal liver kinase 1 binding protein (flk-lbp) (see AAW17837) that binds to the receptor tyrosine kinase flk-l expressed on vascular endothelial and other cells.

The mature flk1-bp can be secreted from host cells transformed with an expression vector including an isolated flk-lbp cDNA clone (see AAT68811). Flk-lbp can be used to isolate cells to which it binds, for use in studying the roles of such cells and of flk-l in vasculogenesis and angiogenesis. Angiogenesis inhibition or increased vascularisation may be clinically desirable (e.g. to suppress solid tumour growth or in wound healing, respectively). The flk-lbp can be administered to treat conditions with defective or insufficient flk-l. Polypeptides may also act as carriers to deliver diagnostic/therapeutic agents to cells to which flk1-bp binds, to generate antibodies, and to identify flk-lbp antagonists useful for treating flk-lbp mediated conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 102
                                                                                                                                                                                                                                                              vascular endothelial growth factor receptor-3; ligand;
anglogenesis; wound healing; lymph vessel; lymphangloma;
cancer; metastasis; therapy; diagnosis; antibody; inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW00932 standard;
              Peptide
                                                            Peptide
                                                                                                         Peptide
                                                                                                                                                     Peptide
                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                            VEGF-C; Flt4;
                                                                                                                                                                                                                                                                                                                                         Human Flt4 receptor tyrosine kinase ligand VEGF-C.
                                                                                                                                                                                                                                                                                                                                                                       10-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                         AAW00932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding a human foetal liver kinase 1 binding protein - use to treat conditions with insufficient protein, deliver agents to cells and identify antagonists to treat protein-mediated conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-281031/25
N-PSDB; AAT68811.
                                                                                                                                                                                     Peptide
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mes 102; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                            receptor tyrosine kinase; VEGFR-3; human;
               103..227
                                                              103..225
                                                                                                          103..217
                                            /note=
                                                                          /note= "preferred retaining
                                                                                                                       /note= "preferred active fragment of VEGF-C,
    retaining Flt4 ligand activity (Claim 15)"
                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                   'label= Prepro_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 539; DB 18; 100.0%; Pred. No. 1.1e-55; tive 0; Mismatches 0;
                           "preferred retaining
"preferred active fragment of VEGF-C
                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                              active fragment of VEGF-C, Flt4 ligand activity (Clai
                                                                          active frage
Flt4 ligand
                            ligand activity (Claim
                                                                       fragment of VEGF-C,
lgand activity (Claim 12)*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131
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Matches 102
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01-AUG-1995;
12-JAN-1996;
14-FEB-1996;
                                                                                                                                                                                                                                                     claimed methods for detecting endothelial cells (e.g. to image lymphatic vessels, endothelial venules, Flt4 receptor in histochemical tissue) and also to maintain the growth of mammalian endothelial cells (e.g. to accelerate angiogenesis and to promote endothelial function of lymphatic vessels). Inhibitors of VEGF-C, such as antibodies, can be used to control endothelial
                                                                                                                                                                                                                                                                                                                                         This polypeptide comprises the pre-pro sequence of human VEGF-C, a novel ligand that binds specifically to human F1t4 receptor tyrosine kinase (VEGFR-3), stimulating phosphorylation of the receptor. Its sequence was deduced from a cDNA clone (AAT84276) obtd. from a PC-3 prostatic adenocarcinoma cell (ATCC CRL 1435) library. The polypeptide, or its active fragments, can be expressed in transformed or transfected host cells for use in
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                            cell proliferation, e.g. lymphangioma or metastatic cancer.
Mouse and quail VEGF-C sequences (see AAW00934-35) have also been
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 112-113; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \tt Flt4 receptor tyrosine kinase ligand and related nucleic acid to modulate growth of endothelial cells and for diagnosis of endothelial cell diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1996;
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                             61
90 wqhnreqanlnsrteetikfaaahynteilksidnewrktqc 131
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             WQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQC
                                                    {\tt aafesgldlsdaepdageatayaskdleeqlrsvssvdelmtvlypeywkmykcqlrkgg}
                                                                    AAFESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGG 60
                                                                                                                             Similarity
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                                                                                                                                                                                     .419
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llarity 100.0%;
Conservative 0
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95US-0510133.
96US-0585895.
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retaining Flt4 ligand activity (Claim 8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retaining Flt4 ligand activity (Claim 14)"
                                                                                                               0;
                                                                                                            Score 539; DB 18;
Pred. No. 1.1e-55;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                active fragment of VEGF-C, Flt4 ligand activity (Claim
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                            102
                                                                                                                                         Length 419;
                                                                                                               Indels
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                                                                                                            Gaps
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RESULT AAW11478

AAW75751 ID AAW

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AAW75751 standard; Protein; 419

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Best Local
                                                                                                                                                                                       Human vascular endothelial growth factor 2 (VEGF2) (AAW11478) is structurally related to the VEGFYDDGF family and is a potent mitogen for vascular endothelial cells, stimulating their growth and angiogenesis. The amino acid sequence of VEGF2 was deduced from a cDNA clone (AAT51371) obtd. from an early stage human (week embryo cDNA library. VEGF2 polypeptides can be produced in transformed host cells and used to promote angiogenesis e.g., to stimulate the growth of transplanted tissue following coronary bypass surgery, or to promote endothelialisation in vascular graft surgery. It can also be used to screen for antagonists (useful e.g. for tumour therapy) and agonists of VEGF2 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor 2; VEGF2; angiogenesis; endothelialisation; coronary bypass surgery; vascular graft surgery; agonist; antagonist; therapy; diagnosis.
                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig
                                                                                                                                                                                                                                                                                                                                                                            promote angiogenesis or endothelialisation in vascular graft surgery
                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding human vascular endothelial growth factor 2 - used to
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-043137/04.
N-PSDB; AAT51371.
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 90
                         61 WQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQC 102
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                                                                                                               Local Similarity
                                               102;
                                                                                                                                                                   419 AA;
                                                                                                   Conservative
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47..419
/label= Mat_protein
/note= "the mature protein is separately claimed
(Claim 5)"
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                                                                                                   0;
                                                                                                               Score 539; DB 18;
Pred. No. 1.1e-55;
                                                                                                   Mismatches
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131
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               AAW75740 standard; Protein;
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated vascular endothelial growth factor polypeptide(s) - used to develop products for treating, e.g. cancers, inflammation, pedema, granulocytopenia or for wound healing or tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flt4; vascular endothelial growth factor C; vascular endothelial cell; lymphatic endothelial cell; myelopoiesis; angiogeneses; inflammation; lymphangiogenesis; oedema; elephantiasis; Milroy's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alitalo K, Joukov V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-FEB-1997;
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                                                                                                                                                                                                                                                    102;
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                                                                                                                                                                                                                                                                                                                                             419 AA;
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 The vascular endothelial growth factor C (VEGF-C) polypeptides have activities affecting growth and migration of vascular endothelial cells, promoting growth of lymphatic endothelial cells and lymphatic vessels, increasing vascular permeability, and affecting myelopolesis. The products can be used for stimulating angiogenesis, for inhibiting angiogenesis, for stimulating lymphangiogenesis, treatment or prevention of inflammation, oedema, elephantiasis, or Milroy's disease. They can also be used to modulate myelopolesis, e.g. treating granulocytopenia. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating of leucocytes between tissues and lymphatic vessels or to affect migration in and out of the thymus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated vascular endothelial growth factor polypeptide(s) - used to develop products for treating, e.g. cancers, inflammation, oedema, granulocytopenia or for wound healing or tissue
Vascular endothelial growth factor-2 (VEGF-2).
                               16-NOV-1999
                                                                                           AAY30518 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 112-115; 177pp; English.
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N-PSDB; AAV52576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flt4; vascular endothelial growth factor C; vascular endothelial cell; lymphatic endothelial cell; myelopoiesis; angiogeneses; inflammation; lymphangiogenesis; oedema; elephantiasis; Milroy's disease.
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                                                                                                                                                                                                           61 WQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQC 102
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                             (first entry)
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                                                                                                                                                                                                                                                                                                         0;
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Pred. No. 1.1e-55;
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Human vascular endothelial growth factor-2; VEGF-2;

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. Examples of immunologic deficiency syndromes include blood protein disorders, ataxia telangiectasia, common variable immunodeficiency, Digeorge syndrome, HTV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich disorder, anemia, thrombocytopenia, or hemoglobinuria. They can also be used to modulate emostatic or thrombolytic activity.
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                            Similarly allergic reactions and conditions such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           medical condition. The VEGF-2 polypeptides or polynucleotides may be useful in treating deficiencies or disorders of the immune system, by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents vascular endothelial growth factor-2 (VEGF-2). The VEGF-2 polypeptides have activities similar to VEGF. The VEGF-2 polypeptides have activities similar to VEGF. The VEGF-2 polypeptides stimulate the growth of vascular endothelial cells, stimulate endothelial cell migration, stimulate angiogenesis, decrease blood pressure, and increase blood flow. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vascular endothelial cell growth; endothelial cell migration; angiogenesis; blood pressure; blood flow; immune system disorder; immune cell; cancer; autoimmune disorder; blood protein disorder; ataxia telangiectasia; common variable immunodeficiency; pigeorge syndrome; HIV infection; HTLV-BLV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Fig 1A-E; 222pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human vascular endothelial growth factor-2, used for treating, e.g. immune disorders and cancers \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-551399/46.
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30-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allergy; asthma; allergic asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAR-1999;
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                  WQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQC
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98US-0107997.
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                                                                                                                                                       100.0%; Score 539; DB 20; 100.0%; Pred. No. 1.1e-55; tive 0; Mismatches 0;
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thrombocytopenia; hemoglobinuria;
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Best Local Similarity
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08-MAR-1994;
06-JUN-1995;
VEGF; VRP; vascular endothelial growth factor; VEGF-related protein; recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia; coronary; collateral vessel development; cell growth; migration; heart; lower limb ischaemia; stroke; peripheral vascular disease; intestine; wound healing; skin; vascular permeability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the vascular endothelial growth factor 2 (VEGF2), of the invention. The isolated polypeptide is useful for stimulating angiogenesis, by promoting the proliferation of endothelial cells, for the treatment of a wound, or for the treatment of tissue or bone damage the content of the content 
                                                                                                                                                            Human vascular endothelial growth factor (VEGF)-C sequence
                                                                                                                                                                                                                                                                                                                       AAW86203 standard; protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 1; 49pp; English.
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                                                                                                                                                                                                                    16-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vascular endothelial growth factor 2 for wound healing and vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-443606/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endothelial cell proliferation; tissue damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEGF2; vascular endothelial growth factor 2; angiogenesis; bone damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Full length human VEGF2 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY22320 standard; Protein; 419 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 WQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQC, 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAFESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                              (first entry)
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94US-0207550.
95US-0465968.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 539; DB 20;
Pred. No. 1.1e-55;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                       AA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 102;
                                       VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth; VEGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transformed or transfected with expression vectors containing nucleic acids encoding the truncated VRP subunits are used to produce the truncated proteins recombinantly. The truncated VRP subunits, optionally expressed from gene therapy vectors, have in vivo and in vitro angiogenic activity and are used to stimulate angiogenesis, particularly coronary collateral vessel development in cases of cardiac isohaemia; to stimulate endothelial cell growth and migration in vitro; to treat heart disease; to treat ischaemia (e.g.cardiac, chronic coronary or chronic lower limb ischaemia; stroke and peripheral vascular disease); to promote healing of wounds (of skin or intestines), and to increase vascular permeability.
                Homo sapiens
                                                                                                                                                                    Human VEGC protein.
                                                                                                                                                                                                                                          AAB10648
                                                                                                                                                                                                                                                                          AAB10648 standard; Protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This represents the amino acid sequence of human vascular endothelial growth factor (VEGF)-C protein. The invention provides truncated VRP (VEGF-related protein) subunits that have at least one amino acid N-terminal to the first Cys of the core sequence deleted. Host cells
                                                                                                                                                                                                        19-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             angiogenesis, e.g. for treating heart disease and ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New truncated vascular endothelial growth factor-related protein subunits - lack part of the N-terminal sequence, used to stimulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-009426/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COLL-) COLLATERAL THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAFESGIDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGG 60
                                                                                                                                                                                                                                                                                                                                                          aafesgldlsdaepdageatayaskdleeqlrsvssvdelmtvlypeywkmykcqlrkgg 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 539; DB 20;
Pred. No. 1.1e-55;
^. wismatches 0;
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Best Local S
Matches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGC protein used to illustrate the method of the invention.
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18-MAR-1999;
08-NOV-1999;
                                      Human; Elen .... -... Vascular endothelial growth factor receptor vascular endothelial growth factor receptor VEGF-C; Milroy-Nonne syndrome; lymphoedema praecox; VEGF-C;
                                                                                                Human; Flt4;
                                                                                                                                 Human VEGF-C
                                                                                                                                                                  31-JAN-2001
                                                                                                                                                                                                   AAB29048;
                                                                                                                                                                                                                                  AAB29048 standard; Protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 11; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New vascular endothelial growth factor protein, useful for treating preventing diseases associated with inappropriate angiogenesis activ such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-442669/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gordon RD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 539; DB 21; ilarity 100.0%; Pred. No. 1.1e-55; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sprengel JJ,
                                                                                                                                 protein sequence.
                                                                                                fms-like tyrosine kinase 4; lymphoedema;
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98GB-0028377.
99US-0124967.
99US-0164131.
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                                                                                 VEGFR-3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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Homo sapiens

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the protein sequence for the human vascular endothelial growth factor C (VEGF-C). It was used to demonstrate the methods of the invention, which involve the screening of individuals to determine which vascular endothelial growth factor receptor 3 (VEGFR-3, also known as Flt4 or fms-like tyrosine kinase 4) alleles they possess and thus their likelihood of developing hereditary lymphoedema. Conditions associated with lymphoedema include Milroy-Nonne syndrome,
         07-FEB-2000; 2000WO-US03047
                                                          WO200045835-A1
                                                                                                            age-related macular
                                                                                                                     Vascular endothelial growth factor 2; VEGF-2; retina; angiogenesis; treatment; injury; degeneration; photoreceptors; eye; angioid streaks; retinitis; pigmentosa; human;
                                                                                                                                                                        Vascular endothelial growth
                                                                                                                                                                                                  22-DEC-2000
                                                                                                                                                                                                                                              AAY97144 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 60-61; 76pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening a human subject for increased risk of developing a disorder, comprises assaying a nucleic acid to determine a mulaturing the sequence of a vascular endothelial growth factor receptor-3
                                    10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which is early onset lymphoedema and lymphoedema praecox, which is late
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING (UYPI-) UNIV PITTSBURGH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419
                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
llarity 100.0%;
Conservative 0
                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
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                                                                                                           degeneration; diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Finegold DN,
                                                                                                                                                                                                                                                  419
                                                                                                                                                                        factor-2 (VEGF-2).
                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 539; DB 21; Pred. No. 1.1e-55; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
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                                                                                                         retinopathy
                                                                                                                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 419;
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                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 1
AAY70749
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Best Local Similarity
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12-FEB-1999;
03-JUN-1999;
22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Administration of vascular endothelial growth factor 2 (VEGF-2) to a patient can be used for treating injury or degeneration of photoreceptors associated with e.g. angioid streaks, retinitis pigmentosa, age-related macular degeneration, diabetic retinopathy, etc. VEGF-2 promotes angiogenesis, the formation of new blood vessels in the retina.
                                                                                                                                                               Key
                                                                                                                                                                                                             cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis; neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma; sarcoma; malignancy; VEGF-C; vascular endothelial growth factor C.
                                       Peptide
                                                                Protein
                                                                                                                           Peptide
                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                 Human; receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4; VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35;
                                                                                                                                                                                                                                                                                       Human prepro-vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                 AAY70749 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 31; Fig la-e; 252pp; English
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                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      injury or degeneration of photoreceptors comprises ering to a subject vascular endothelial growth fact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alderson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0119179.
99US-0119926.
99US-0137796.
99US-0171505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                         /label N-terminal_peptide
/note "cleavage of this peptide from partially processed
VEGF-C produces a fully processed mature form of VEGF-C
of 21-23 kD which has high affinity to VEGFR-2"
/label= C-terminal_peptide
/note= "Has a pattern of spaced cysteine
reminiscent of a Balbiani ring 3 protein
                                                                                                                            32..103
                                       228..419
                                                  /label= Mature_VEGF-C
                                                                                                                                     /label= Signal_peptide
                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Melder
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(BR3P) se
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  sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Vascular endothelial growth factor-C; VEGF; human; re-endothelialisation vascular endothelial growth factor receptor; VEGFR; vascular trauma; blood vessel; cardiovascular surgery; anti-restenosis agent; prevention;

re-endothelialisation;

Human vascular endothelial growth factor (VEGF)-C protein.

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RESULT
AAY70982
   BX8XE
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                                                                                                                                                                                                                                                                                                                                        CC by expression of fms-like tyrosine kinase 4 (Fit4) receptor (also cendothelial cells of blood vessels adjacent to malignant neoplasm. The method involves administering a compound that inhibits binding of a compound that inhibits binding of a compound that the compound to Fit4 thereby inhibiting Fit4 mediated proliferation of vascular compound to Fit4 thereby inhibiting Fit4 mediated proliferation of vascular compound to Fit4 thereby inhibiting Fit4 mediated proliferation of vascular compounds can be used to treatment of malignancies characterised by Fit4-expressing blood cells. The compounds cell carcinomas, lymphomas, melanomas compounds can be used for manufacturing medicament useful for diagnostic screening, imaging and compounds can be used treatment of malignancies characterised by Fit4-expressing blood cells. The Fit4 gene maps to chromosomal region 5q35 and is expressed as 5.8 kb compounds to a subfamily of class III receptor tyrosine kinases (RTKs). It is used as a target for tumour imaging and anti-tumour therapy. CC The present sequence is a human prepro-vascular endothelial growth continued the compound.
                                                                                                                                                                                                                                                              Matches
   09-AUG-2000
                                 AAY70982;
                                                              AAY70982
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating neoplastic diseases such as lymphoma, carcinomas, melanomas and sarcomas, involves administering a compound capable of inhibiting binding of ligand proteins to fms-like tyrosine kinase-4 receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-1998;
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                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               patent discloses a method to treat neoplastic disease characterised
                                                                                                                                    AAFESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGG 60
                                                                                                                                                                                                aafesgldlsdaepdageatayaskdleeqlrsvssvdelmtvlypeywkmykcqlrkgg 89
                                                                                                                                                                                                                                                              102;
                                                            standard;
                                                                                                                                                                                                                                                                                                                                        419
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaipainen
 (first
                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 140-142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "binds and stimulates at position 156 is essential 165 is essential for VEGFR-2 at 131. 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cleavage of signal peptide and the C-terminal peptide produces a partially processed form of VEGF-C about 29 kD which has high affinity to Flt4 (VEGFR-3)'113..213
                                                            Protein;
entry)
                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "important for VEGF-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148pp; English.
                                                                                                                                                                                                                                                                          Score 539;
Pred. No. 1
                                                            A
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                                                                                                                                                                                                                                                                          DB 21;
l.1e-55;
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for VEGFR-2 binding
and VEGFR-3 binding
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                                                                                                                                                                                                                                                             Indels
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The present amino acid sequence is the complete human prepro-vascular endothelial growth factor (VEGF)-C. VEGF-C has the ability to stimulate re-endothelialisation of an injured blood vessel, without significant stimulation of smooth muscle cell proliferation. It can bind to and stimulate VEGFR-2 (vascular endothelial growth factor receptor) and/or VEGFR-3 phosphorylation in cells that express such receptors. An anti-restenosis agent comprising either a VEGF-C gene or protein is used in a method to reduce or prevent restenosis and stenosis of a blood vessel following vascular trauma e.g., cardiovascular surgery and
                                                                                                                                                                                                                                                                                                                                                                              (LUDW-)
                                                                                                                                                                                         Claim
                                                                                                                                                                                                                       Preventing stenosis and restenosis endothelial growth factor proteins
                                                                                                                                                                                                                                                                               N-PSDB;
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                                                                                                                                                                                                                                                                                            .2000-350584/30
                                                                                                                                                                                                                                                                                                                                                              LUDWIG INST CANCER RES. UNIV HELSINKI LICENSING YLA-HERTTUALA S.
                                                                                                                                                                                       Page 51-53;
transluminal coronary angioplasty.
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156
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228..419
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137
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131..2
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/note= "Cleavage results
----tain (29 kD)"
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/note= "Cleavage results in fully-processed
VEGF-C protein (21-23 kD)"
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/notein (29 kD)"
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"Cleavage results in part
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"Processed vascular
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or
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Query Match

Length 419;

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RESULT 1
AAY97570
ID AAY97570
ID AAY97570
AAY97570
AAY97570
AAY970
AAY97
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(lymph)angiogenesis. The proteins are also used to identify specific binding agents (potential therapeutic agents) and to raise antibodies. The antibodies are useful as therapeutic (ant)agonists; for detection, purification and targeting of proteins for in vivo or in vitro diagnosis (including imaging) or for therapy (including when linked to e.g. a label or cytotoxin); and for immunotyping of cells, e.g. for detecting minimal residual disease or haematopoietic progenitor/stem cells. It is also contemplated that the sequences might be useful for treating a very wide
                                                                                                                                                                                                                                                               ameliorate disease and to detect diseases, or susceptibility, by detecting mutations or the presence or amount of angiogenic protein expression. Particularly they are used to stimulate wound healing, growth of damaged bone and tissue, and for repair of vascular tissue, especially peripheral arterial disease, critical limb ischaemia or coronary disease. Antagonists of the sequences are used to inhibit angiogenesis in tumours and to treat inflammation (where associated with increased vascular permeability), diabetic retinopathy, rheumatoid arthritis or psoriasis. Agonists are also useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding angiogenic proteins, useful e.g. for promoting healing of wounds and treating peripheral arterial disease, critical limb ischaemia or coronary disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which is an angiogenic protein of the invention. The angiogenic proteins and the DNA sequences encoding them, are used to prevent, treat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Fig 1; 244pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1999;
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Best Local :
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October 17, 2001, 14:45:59
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FELEPAX: (202)371-2540
FELEPAX: (202)371-25
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Best Local Similarity

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Score 539; DB 2 Pred. No. 1e-60;

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Query Match

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-999-811-2 uence 2, Appli ent No. 593254 NERAL INFORMAT APPLICANT: RO APPLICANT: CA CITY: WASHI STATE: DC COUNTRY: US ZIP: 20005 COMPUTER READA COMPUTER READA COMPUTER READA COMPUTER READA COMPUTER: I OPERATING TYPE: COMPUTER: PARTICATION FILING DATE: APPLICATION FILING DATE: FILING D	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
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APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
RUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
CARDESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
ADDRESSEE: STERNE, VASSLER, GOLDSTEIN & FOX
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NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,
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APPLICATION NUMBER:
FILING DATE: 24-DEC-
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
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                                                                              Local Similarity
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Pred. No. 1e-60;
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997
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NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 0
FILING DATE: 06-JUN-1995
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MEDIUM TYPE: Floppy COMPUTER: IBM PC com.
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APPLICANT: ROSEN, CRA
APPLICANT: CAO, LIANG
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               61 WQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQC 102
90 WQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQC 131
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CLASSIFICATION:
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                                                                                                                                   Conservative
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                                                                                                                                                 100.0%; Score 539; DB 3 100.0%; Pred. No. 1e-60;
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                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/5:
FILING DATE: 01-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F196/00427
FILING DATE: 01-AUG-1996
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C) TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses I NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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APPLICANT: Joukov, Vladimir
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APPLICATION NUMBER:
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                  61 WQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQC
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TOPOTION
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REGISTRATION NUMBER: 38,153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/671,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                              1 AAFESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGG 60
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WQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQC 131
                                                                           AAFESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGG 89
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                                    102
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                      TITLE OF INVENTION: HUNUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                     APPLICANT:
COMPUTER READABLE FORM:
                  COUNTRY: UZIP: 07068
                                                      CITY: ROSELAND
STATE: NEW JERSEY
                                                                                              STREET:
                                                                                                              ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                           90 WQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQC 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAFESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGG 60
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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LENGTH: 419 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alitalo, Kari
Joukov, Vladomir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gass, David A. REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gass, David
                                                                                              E: CECCHI, STEWART
6 BECKER FARM ROAD
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                                                                                                                                                                     HU, ET AL.
WENTION: Human Vascular EndothelialGrowth Factor
                                   USA
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100.0%; Pred. No. 1e-60;
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CURRENT APPLICATION DATA:

WORD PERFECT 5.1

MS-DOS

OPERATING SYSTEM:

TYPE:

3.5 INCH DISKETTE

IBM PS/2

APPLICATION NUMBER:

PCT/US96/09001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 11, Application US/08795430
Patent No. 6130071
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular
TITLE OF INVENTION: Protein
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                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                              COMPUTER READABLE FORM:
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REFERENCE/DOCKET NUMBER: 321
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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APPLICATION NUMBER: 0:
FILING DATE: 6 JUN 95
APPLICATION NUMBER: 0:
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ATTORNEY/AGENT INFORMATION:
             APPLICATION NUMBER: PCT/
FILING DATE: 01-AUG-1996
                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                     FILING DATE:
                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                      STATE:
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TOPOLOGY: LI
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APPLICATION DATA
                                                                                                                                                                                                                                  RY: United States of America 60606-6402
                                                                                                                                                                                                                                                                                   Chicago
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                                                                                                                                                                                                                                                                  Illinois
                                                                                                                                                                                                                                                                                                    E: Marshall, O'Toole, 6300 Sears Tower, 233
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                                                                                                                                                                                                                                                                                                                                                         Vascular Endothelial Growth Factor C (VEGF-C)
Protein and Gene, Mutants Thereof, and Uses T
57
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                                 PCT/F196/00427
                                                                                                      US/08/795,430
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Pred. No. 5.9e-60;
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South Wacker Drive
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular
TITLE OF INVENTION: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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APPLICATION NUMBER: 08/5
FILING DATE: 01-AUG-1995
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APPLICATION NUMBER:
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TELEFAX: 25-3856
                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 312/474-0448
                                                                   FILING DATE:
                                                                                                                                                                                                                       STATE: Illinois
COUNTRY: United States of America
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APPLICATION NUMBER: PCT/
FILING DATE: 01-AUG-1996
                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                               CITY: Chicago
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00 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-NOV-1994
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                                                                                                                                                                                                                                                                                                                                   Vascular Endothelial Growth Factor C (VEGF-C)
Protein and Gene, Mutants Thereof, and Uses Thereof
57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.8%;
78.4%;
                PCT/FI96/00427
                                                                                  US/08/795,430
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Pred. No. 3.8e-46;
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                                                                                                                                                                                                                                                                                South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
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PRIOR APPLICATION DATA:

FILING DATE:

28-JUN-1996

08/671,573

APPLICATION NUMBER: FILING DATE: 14-FE

08/601,132

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 25-3856
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 amin
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/999,811
                                                                                                                                                                                                                                                                                                       VASCULAR ENDOTHELIAL GROWTH FACTOR NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HU, JING-SHAN APPLICANT: ROSEN, CRAIG APPLICANT: CAO, LIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/56
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                                  CLASSIFICATION:
                                                                                                                                                                                                                             CITY: WASHINGTON STATE: DC
 APPLICATION NUMBER:
                                                    FILING DATE:
                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 WQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.4%; Score 412; DB 4; Length 418; Local Similarity 75.2%; Pred. No. 1.8e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 01-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 AAYESGHGYYEEEPGAGEPKAHASKDLEEQLRSVSSVDELMTVLYPEYWKMFKCQLRKGG 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 14-NOV
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                                                                                                                                                                                                                                                                                ADDRESSEE:
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TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAFESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGG 60
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                                                    HEREWITH
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14-NOV-1994
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LIANG
us 08/207,550
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RESULT 11 US-09-042-105-4

Sequence 4, Application US/09042105

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US-08-824-996-2
; Sequence 2, Application US/08824996B
; Patent No. 5935820.
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                                                                                                           Query Match
Best Local Similarity 100.
Thinks 62; Conservative
                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 350
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: 08/207,550
EARLIER FILING DATE: 1994-03-08
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Polynuc TITLE OF INVENTION: Factor FILE REFERENCE: PF112D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hu, Jing-Shan
APPLICANT: Rosen, Craig A.
APPLICANT: Cao, Liang
                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202)371-2540 INFORMATION FOR SEQ ID NO:
101 QC 102
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61 QC 62
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REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 QC 102
                                                                    41 MTVLYPEYWKMYKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTVLYPEYWKMYKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.4%; Score 347; DB 2; ilarity 100.0%; Pred. No. 2.8e-36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucelotides Encoding Vascular Endothelial Growth Factor \mathbf 2
                                                                                                                                      64.4%; Score 347; DB 2; 100.0%; Pred. No. 2.8e-36; tive 0; Mismatches 0;
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                                                                                                                                        Indels
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US-08-510-133A-33
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                         ; Sequence 33, Application US/08510133A
Patent No. 6221839
; GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
Joukov, Vladomir
                                                                                                                  RESULT 12
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                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                      Query Match
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APPLICANT:
                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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APPLICATION NUMBER: |
FILING DATE: 8-MAR-1
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APPLICATION NUMBER: US
FILING DATE: HEREWITH
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                 Match 64.4%; Score 347; DB 3; I Local Similarity 100.0%; Pred. No. 2.8e-36; DS 3; I Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 24-DE CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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TITLE OF INVENTION: Receptor Ligand NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                               : (202)371-2600
(202)371-2540
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ROSEN, CRAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER: TO BE ASSIGNED 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRAIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VASCULAR ENDOTHELIAL GROWTH FACTOR 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Applicat Patent No. 6245530 GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Joukov, Vladimir TITLE OF INVENTION: Receptor NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 QC 102
||
61 QC 62
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alitalo, Kari APPLICANT: Joukov, Vladi
ATTORNEY/AGENT INFORMATION:
                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                            STREET: 6300 Sears Tower, 233 Sou
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                      CLASSIFICATION:
                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 MTVLYPEYWKMYKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKT 100
                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PBETENTIA Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: CLASSIFICATION: 
ATTORNEY/AGENT IMPORMATION:

ATTORNEY/AGENT IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 350 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08585895
                                                                                                                                                                                                                                                                                                E: Marshall, O'Toole, 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.4%; Score 347; DB 4;
100.0%; Pred. No. 2.8e-36;
tive 0; Mismatches 0;
                                                               US/08/585,895
                                                                                                                                                                                                                                                                                                  Gerstein, Murray & Borun
South Wacker Drive
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REGISTRATION NUMBER: 38

38,153 TER: 28113/33072

Gass, David A.

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RESULT 14
US-08-915-795-9
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                                                                    TELEX: N/A
TELEX: N/A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
FENGTH: 321 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                       TELEPHONE: (202) 628-8800
                                                                                                                                                                                                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TISSUE TYPE:
                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
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                                                                                                                                                                                                                                                                                                                                                                                       United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kari ALITALO
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Steven A. STACKER
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Mouse Lung
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100.08; Pr
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                                                                                                       Matches
                                                                                                                  Query Match
Best Local Similarity
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APPLICANT: Marc G
                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
86 NTEILKSIDNEWRKTQC 102
                                             46
                                                                                                                                                                                                                                                                                                                                                                                          NAME: EVANS, Joseph D. REGISTRATION NUMBER: 26 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 NTEILKSIDNEWRKTQC 102
                                                                         28 EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 85
                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                  TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
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                                             EQQIRAASSLEELLQIAHSEDWKLWRCRLKL---
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1200 G Street, NW, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andrew F. WILKS
Steven A. STACKER
                                                                                                                                                                                                                                                                                                                                             (202) 628-8844
                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         United States of America
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                                                                                                                     30.2%;
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                                                                                                                   Score 163; DB 4
Pred. No. 1e-12;
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                                                                                                       Mismatches
                                             ---KSLASMDSRSASHRSTRFAATFY 99
                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --KSLASMDSRSASHRSTRFAATFY 94
                                                                                                       16;
                                                                                                                                 Length 358
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Db 100 DTETLKVIDEEWQRTQC 116

Search completed: October 17, 2001, 14:47:09 Job time: 195 sec

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being primard is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
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Query
Match Length DB
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length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
   October 17, 2001, 14:48:34; Search time 78.16 Seconds (without alignments) 99.409 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219241 seqs, 76174552 residues
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Copyright (c) 1993 - 2000 Compugen Ltd.
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pir2:*
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1,3-beta-glu
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	hypothetical prote	hypothetical prote	probable lipoprote	cysteine synthase	Ran-binding protei	unknown protein (i	transferrin-bindin	hypothetical prote	alliin lyase (EC 4	probable cytochrom	translation elonga	probable carbamoyl	hypothetical prote	splicing factor PR	hypothetical prote	phenylalaninetRN	-

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A; Cau, L.; Zhang, L.; Ruiz-Lozano, P.; Yang, Q.; Chien, K.R.; Graham, R.M.; Zhou, M.; Biol. Chem. 273, 21077-21083, 1998
A;Title: A novel putative protein-tyrosine phosphatase contains a BRO1-like domain A; Reference number: Z18004; MUID:98361981
A; Accession: T14355
A; Accession: T14355
                                                                                                                A;Molecule type: DNA
A;Residues: 1-1729 <ISH>
A;Cross-references: EMBL:D78352; PIDN:BAA11369.1
                                                                                                                                                                                                                                                                                              C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C;Accession: T43403; T39836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t
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T14355
                A; Reference number: A; Accession: T39836
                                     A; Experimental source: strain L972
R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Devlin,
submitted to the EMBL Data Library, February 1998
A; Reference number: Z21884
                                                                                                                                                                                                    A;Description: A fission yeast gene A;Reference number: Z22487 A;Accession: T43403
                                                                                                                                                                                                                                                                                   C;Accession: T43403; T3: R;Ishiguro, J.; Saitou,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-1494 <CAO>
A; Cross-references: EMBL
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                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                              submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                               1,3-beta-glucan synthase (EC 2.4.1.34) [similarity] - fission yeast (Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity 29.4%;
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preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANVQYAAVR --- RVLSELDQKWNST 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEQQLRELIQKDDITASLVTTDHSEMKKLFEEQLKKYDQLKVYLEQNLAAQDNVLRALTE 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETIKFAAAHYNTEILKSIDNEWRKT 100
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Pred. No. 11;
L7; Mismatches
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Pred. No. 1.7e-48;
; Mismatches 0;
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alpha-helical coiled coil protein TlpA - Salmonella typhimurium C;Species: Salmonella typhimurium C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
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A;Cross-references: GB:m88208; NID:g968910; PIDN:AAA74964.1; PID:g968911 A;Experimental source: large virulence-associated plasmid pEX102
                                                 A; Molecule type: DNA
A; Residues: 1-371 < KOS>
                                                                                                A; Status: preliminary
                                                                                                                    J. Biol. Chem. 267, 12258-12265, 1992
A;Title: A new alpha-helical coiled coil protein
A;Reference number: A44122; MUID:92291112
A;Accession: A44122
                                                                                                                                                                                                                    R; Koski,
                                                                                                                                                                                                                                          C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:U32693; GB:L42023; NID:g1573021; PIDN:AAC21750.1; PID:g1573022 C;Superfamily: heat shock protein grpE
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A; Residues: 1-234 <TIGR>
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C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Nov-1999
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Best Local Similarity
Watches 29; Conserv.
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C; Keywords: glycosyltransferase;
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A; Residues: 1-1729 <LYN>
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A; Accession: I64046
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C;Species: Haemophilus influenzae
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Best Local Similarity
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                                                                                                                                                                                                                    P.; Saarilahti, H.;
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27.48;
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Pred. No. 6.7;
3; Mismatches 1
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No. 61;
                                                                                                                                                                                                                    Taira,
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                                                                                                                                                                                                                    S.; Riikonen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 234;
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                                                                                                                                                                     Salmonella typhimuriu
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                                                                                                                                                                                                                 P.;
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A; Note: sequence

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A,Gene: GDB:IGHG4
A,Gene: GDB:IGHG4
A,Cross-references: GDB:119340; OMIM:147130
A,Cross-references: GDB:119340
glycine dehydrogenase homolog
C; Species: Bacillus subtilis
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F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental F;27-83,141-201,247-305/Disulfide bonds: #status predicted F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; hemorotetramer; immunoglobulin C;Keywords: immunoglobulin homology <IMI> F;20-85/Domain: immunoglobulin homology <IMI> F;99-110/Region: hinge
                                                                                   A69959
                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses.
A;Reference number: A90249; MUID:70207560
A;Accession: A90249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: the sequence was determined from the germline gene R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C. Biochem, J. 117, 33-47, 1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene A;Reference number: A90933; MUID:83157104
A;Accession: A90933
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C;Accession: A90933; A90249; A02150
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C; Species: Homo sapiens (man)
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A; Residues: 1-30;81-326 <PIN>
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Best Local (
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   144 VDVSQEDPEVQENWYVDGVEVHNAKTKPREEQENSTYRVVSVLTVLHQDWLNGKEYKCKV 20:
                                                                                                                                                                                                                                       204 SNKG
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                                                                                                                                                                                                                                                                                                           RKGGWQHNREQANLNSRTEETIKFA 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGEQTAQAERELADAAQTVDDLEEKLDELQDRYDSLTLALESERSLRQ---QHDVEMAQL 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                   -LPSSIEKTISKA 219
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Pred. No.
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Pred. No. 11;
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                                           Bacillus
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RESULT
T49093
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Accession: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
T16509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F59A6.3 - Caenorhabditis elegans C;Speckes: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t.C;Accession: T16509
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                                                                                                                                                                                                                                                  A; Introns: 106/1; 620/1; 634/3; 675/3; 775/1
                                                                                                                                                                                                                                                                                  A; Gene: CESP:F59A6.3
                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-786 <NHA>
A; Cross-references: EMBL:U41994; NID:g1123047;
                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T16509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: The sequence A; Reference number: Z18526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, December 1995 A;Description: The sequence of C. elegans cosmid F59A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Nhan,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Kunst, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.9
Best Local Similarity 28.4
Matches 23; Conservative
                                                                                                                 Matches
                                                                                                                                         Query Match
Best Local Similarity
719 YTSSPTSSQIKSSYSVGELITQVCPQSYVFEIALQPVKIYKC-LKTGKWAGSPE 771
                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 FAA-----AHYNTEILKSI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 KDKQEMLATIGVSSIDDLFADI-PENVKYKKEHQIKKAKSETELTRELTKLASKNRDTVQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 KDLEEQLRS--VSSVDELMTVLYPE---YWKMYKCQLRKGGWQHNREQANLNSRTEETIK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YqhJ
                                                       YASKDLEEQLRSVSSVDELMTVLYPEYW-----KMYKCQLRKGGWQHNRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YASFLGAGVYDHYQPVIVDHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
                                                                                                              18;
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.9%;
                                                                                                                                         12.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                      Score 69; DE
Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 69.5;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence not shown; translation not
                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-Sep-1999 #text_change
                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                   PID:g1123052; PIDN:AAA83456.1; CESP:F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                   2;
                                                                                                              17;
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                                                                                                                                                                Length 786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (decarboxylating)
                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.; Fabret, C.; Ferrari,
                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-Sep-1999
                                                       66
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                                                                                                           2;
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N;Contains: dynein ATPase (EC 3.6.1.33)
C;Species: Rattus norvegicus (Norway rat)
C;Decies: Rattus norvegicus (Norway rat)
C;Date: 15-Apr-1994 #sequence_revision 02-May-1994 #text_change 19-Jan-2001
C;Accession: A38905; I58139
C;Accession: A38905; I58139
A;Orc. Natl. Acad. Sci. U.S.A. 90, 7928-7932, 1993
A;Title: The primary structure of rat brain (cytoplasmic) dynein heavy chain, a cytopla: A;Accession: A38905; MUID:93376715
A;Accession: A38905
                                                                                                                 C;Keywords: ATP; blocked amino end; heterotetramer; hydref;1904-1911/Region: nucleotide-binding motif A (P-loop) F;2222-2229/Region: nucleotide-binding motif A (P-loop) F;2593-2600/Region: nucleotide-binding motif A (P-loop) F;2935-2942/Region: nucleotide-binding motif A (P-loop) F;2935-2942/Region: nucleotide-binding motif A (P-loop) F;1910/Binding site: ATP (Lys) #status predicted F;2228/Binding site: ATP (Lys) #status predicted F;2599/Binding site: ATP (Lys) #status predicted F;2941/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                    C;Superfamily: dynein heavy chain, cytosolic C;Keywords: ATP; blocked amino end; heterotetramer; hydrolase; microtubule binding; nuc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: I58139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuron 10, 787-796, 1993
A;Title: Molecular cloning of the retrograde transport motor cytoplasmic dynein
A;Reference number: I58139; MUID:93264075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F4F15.250 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000 C;Accession: T49093
                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-1023,'MP',1026-1771,'D',1773-2097,'A',2099-2138,'V',2140-2174,'A',2176-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-4644 <ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A38905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1403 <ALC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: T49093
                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:L08505; NID:g294542; PIDN:AAA41103.1;
                                                                                                                                                                                                                                                                                                                                                                                        44 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:D13896; NID:g402527; PIDN:BAA02996.1; R;Mikami, A.; Paschal, B.M.; Mazumdar, M.; Vallee, R.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: ATSP: F4F15.250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown
Ouery Match 12.8%;
Best Local Similarity 25.0%;
Matches 27; Conservative 2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KCQLR-KGGWQHNREQANLNSRTEE----TIKFAAAHYNTEILKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESGLDLSDAEPDAGEATAY-----ASKDLEEQLRSVSSVDELMTVLY--PE--YWKMY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESQVENNDAQPKQGELRLYPVSVKTQSGGKMELQLNPGDSVMDIRQFLLDAPETCYFTCY 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y chain, cytosolic - rat
dynein ATPase (EC 3.6.1.33)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123/3; 187/1;
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    21;
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Score 69; DB 1; L
Pred. No. 2.7e+02;
L; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286/2; 351/1;
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68;
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                                              Length 4644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1403
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  22;
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  Gaps
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  5
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Best Matches

Local

Similarity 23; Conserv

Conservative

21;

37; ۲,

Indels

11;

Gaps

2

Score 68.5; Di Pred. No. 51; 21; Mismatches

DB

Length 984;

12.7%;

8

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DLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQ 67

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-984 <PAR>
                                                                                                                                                    A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A; Reference number: A81250; MUID:20150912 A; Accession: F81299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Xenopus laevis (African clawed frog)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997
C;Accession: S70644
C; Superfamily: Neisseria meningitidis hypothetical protein
                    A; Gene:
                                      C; Genetics:
                                                        A;Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73943.1; PID:g696
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: annexin VII; annexin repeat homology F;212-282/Domain: annexin repeat homology <AX1>F;283-355/Domain: annexin repeat homology <AX2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-512 <SRI>
A;Cross-references: EMBL:U16365; NID:g790543; PIDN:AAB18145.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: S70644; MUID:96265035
A;Accession: S70644
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Srivastava,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;443-512/Domain: annexin repeat homology <AX4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S70644
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                                                                                                                                                                                                                                                                                                                                                                                                                            310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 TAY-GKDLIKDLKSELSGNVEELIIALFMPSTYYDAWSLYNA-MKGAGTQERVLIEILCT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAYASKDLEEQLRSVSS--VDELMTVL----YPEYWKMYKCQLRKGGWQHNREQANLNS 72
                                                                                                                                                                                                                                                                                                                                                                                                                            RTNSEIRNIVACYKQEFGREIEKDIR 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a, M.; Zhang-Keck, Z.Y.; Caohuy, H.; McPhie, P.; Pollard, H.B. 316, 729-735, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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Pred. No. 24;
l3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homology <AX3>
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                                                                        Qy
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A;Description: Localization of the Ran-GTP binding protein RanBP2 at the cytoplasmic si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ran-binding protein 2 - mouse (fragment)
N;Alternate names: RanBP2 protein
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C;Accession: S57968
R;Wilken, N.; Senecal, J.L.; Scheer, U.; Dabauvalle, M.C.
                                                                                                                                                                                                                    A;Gene: CESP:Y87G2A.p
A;Introns: 198/1; 265/3; 407/3
                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AL110500; PIDN:CAB54490.1; A;Experimental source: clone Y87G2A
                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: T27468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
A; Gene: RanBP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-1265 <WIL>
A;Cross-references: EMBL:X87337; NID:g899335; PIDN:CAA60778.1;
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                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S57968
A; Accession: S57968
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Best Local Similarity 19.6
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                                     ESDSDYSDGE----EATPEQWKELDKELDKVVALLKEYEAAKVTETDPVKRYRNLCQLST 116
                                                                          ESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSV---DELMTVLYPEYWKMYK--CQL-- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVVFSHRAKLYRYDKDVGQWKERGIGDIKILQNYDNKQVRIVMRRDQVLKLCANHRITPD 1242
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-----RKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSI 93
                                                                                                                      Conservative
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                                                                                                                                       12.6%; Score 68; 29.8%; Pred. No.
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Pred. No. 68;
                                                                                                                    Mismatches
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A;Status: preliminary
A;Molecule type: DNA
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A.Molecule type: DNA
A.Residues: 1-611 <WIL>
A.Cross-references: EMBL:X85964; NID:g757760; PIDN:CAA59942.1; PID:g757763
A.Experimental source: strain Q1182, plasmid QpDV
R.Thiele, D.; Willems, H.; Haas, M.; Krauss, H.
submitted to the EMBL Data Library, October 1993
A.Reference number: S38215
A.Recession: S38224
Search completed: October 17, 2001, 14:48:36 Job time: 282 sec
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Result
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Listing first 45 summaries
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Perfect score:
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Match
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000
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                        OM70_NEUCR
YPX2_CAEEL
YZ28_METJA
EF1G_XENLA
ALLN_ALLAS
SYE2_THEMA
YGJ9_YEAST
VPA_BPP2
                                                                 EF1H_XENLA
ALLCE
TBPB_NEIMB
RBP2_HUMAN
Y309_MYCPN
EAEH_ECOLI
PHPA_PLACH
MY16_MOUSE
SYGB_AQUAE
RBP2_BOVIN
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SYFA_YEAST
PRO8_YEAST
FOS_CYPCA
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ANX7_XENLA
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Kukk E., Lymboussaki A., Taira S.,
Joukov V., Alitalo K.;
"VEGF-C receptor binding and patter
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Development 122:3829-3837(1996).
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N-LINKED (GLCNAC. . .)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 425; DB 1;
Pred. No. 4.1e-37;
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VASCULAR ENDOTHELIAL GROWTH
4 X 24 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                      subdivision;
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                                                                                                                                                                                                                      Pasteurellaceae;
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127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 415
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(POTENTIAL).
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RESULT GCZ - TH CCC TH 
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15-JUL-1999
IG GAMMA-4 C
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P01861;
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Homo sapiens (Human).
Homo sapiens (Human).
""barvota; Metazoa; Chordata;
""barvota; Primates;
                                                             constant red
Biochem. J.
                                                                                                                                                              Pink J.R.L.,
                                                                                                                                                                                                                                                                                  MEDLINE=83157104; PubMed=6299662; Ellison J.W., Buxbaum J.N., Hood L.E.; Ellison J.W., Hood immunoglobulin "Nucleotide sequence of a human immunoglobulin DNA 1:11-18(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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PRINTS; PR00773; GRPEPROTEIN.
PROSITE; PS01071; GRPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U32693;
HSSP; P09372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 269:496-512(1995).

-!- FUNCTION: STIMULATES, JOINTLY WITH DNAJ, TO DNAK. HELPS TO RELEASE ADP FROM DNAK THUS MORE EFFICIENTLY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fine L.D., Fritchman J.L.,
Gnehm C.L., McDonald L.A.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; HI0071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                          "Human immunoglobulin subclasses. Partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                 MEDLINE=70207560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Utterback T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36
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   SWISS-PROT entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVEKAHKFALEKFSKDILNTIDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TI----KFAAAHYNTEILKSIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEEAIARVQELEEQL---
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                                                             region of a gamma 4 chain.";
J. 117:33-47(1970).
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(Rel.
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                                                                                                                                                          Buttery S.H., de Vries G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., I., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., itchman J.L., Fuhrmann J.L., Geoghagen N.S.M., ICDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1DKG.
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01,
38,
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27.7%;
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   copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70; DB
Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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ALLOWING DNAK TO RI
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   a collaboration
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GCS1_BACSU
P54376;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
PROBABLE GLYCINE DEHYDROGENASE (DECARBOXYLATING] SUBUNIT
14.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SY
                                         Submitted
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MIM;
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Pfam; PF00047; 1g; 3.

PFam; PF000290; IG_MHC;
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                                                                                 STRAIN=168 / JH642;
                                                                                                                Submitted
                                                                                                                          Mizuno M.,
Kobayashi
                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus.
                                                               Takeuchi M.;
                                                                     Kobayashi Y., Mizuno M.,
                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                NCBI_TaxID=1423
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InterPro; IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                                       7 LDLSDAEP------DAGEATAYASKDLEEQLRSVSSVDELMTVLYPEY--WKMYKCQL 56
FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATIC GLYCINE. THE P PROTEIN BINDS THE ALPHA-AMINO GROUP OF GLYCINE THROUGH ITS PYRIDOXAL PHOSPHATE COFACTOR; CO(2) IS RELEASED AN THE REMAINING METHYLAMINE MOIETY IS THE THEN TRANSFERRED TO TILIPOAMIDE COFACTOR OF THE H PROTEIN (BY SIMILARITY).
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                                                   (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                (MAR-1996) to
                                                                                                                                  Masuda
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29.4%;
                                                                                                                                   Takemaru K.,
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                                                                                                                the EMBL/GenBank/DDBJ
                                                                        Masuda
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CH2.
CH3.
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 69.5;
Pred. No. 4
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                                                                                                                                    Hosono
                                                                      Takemaru K.,
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DYHC_MOUSE
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Best Local
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01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                         Sasaki S., Shionoya A., Hirotsune S.;

"Complete cDNA sequence of murine cytoplasmic dynein heavy chain.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS

MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND

MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND

MOTOR FOR THE INTRACELLULAR TOO HEAVY CHAINS AND A NUMBER OF

INTERMEDIATE AND LIGHT CHAINS.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                              DYNELL.

DNCHC1 OR DNcnr.

Mus musculus (Mouse).

Metazoa; Chordata; (Mouse)

Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U1-UCT-2000 (Rel: 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (CYTOPLASMIC DYNEIN HEAVY CHAIN).
DNCHC1 OR DNCH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 295110; yghJ.
SubtiList; BG11510; yghJ.
Hypothetical protein; Oxidoreductase; Pyridoxal
Hypothetical protein A9497 MW; 7C75330F233056B8
                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYHC_
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D84432; BAA12547.1; -. EMBL; Z99116; CAB14387.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was use by non-profit institutions as long as its content is in no was
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                                                                                                                                                                                                                                                                                                                                                                           STRAIN-FVB;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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DIHYDROLIPOYLPROTEIN + CO(2).
COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                          SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: THE GLYCINE CLEAVAGE P, T, L, AND H.
                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDLEEQLRS--VSSVDELMTVLYPE---YWKMYKCQLRKGGWQHNREQANLNSRTEETIK 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
             AY004877; AAF91078.1;
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Pred. No. 6.6;
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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SYSTEM IS COMPOS
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L outstation -
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P38650; 063178:
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation updat
                                                                                                                             Mikami A., Paschal B.M., Mazumdar M., "Molecular cloning of the retrograde t dynein (MAP 1C).";
                                  Neuron 10:787-796(1993).

- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNI-
- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNI-
- FUNCTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VES-
ORGANELLES ALONG MICROTUBULES.
- SUBJUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A INTERMEDIATE AND LIGHT CHAINS.
- INTERMEDIATE AND LIGHT CHAINS.
- SUBCELLULAR LOCATION: CYTOPLASMIC.
- SUBCELLULAR LOCATION: CYTOPLASMIC.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBI_TaxID=10116;
               This SWISS-PROT entry
                                                                                                                                                                                                                                          a cytoplasmic
                                                                                                                                                                                                                                                                                            STRAIN=WISTAR; TISSUE=Brain; MEDLINE=93376715; PubMed=7690137;
                                                                                                                                                                                                                                                                                                                                                                                 DNCHC1 OR DNCH1 OR DNEC1 OR MAP1C. Rattus norvegicus (Rat).
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                                                                                                                                                                                                      SEQUENCE FROM N.A
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27; Conservative
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ci. U.S.A. 90:7928-7932(1993).
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25.0%;
                                                                                                                                                                                                                                                                               Nonaka S., Aizawa H., Kawasaki
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COILED COIL (POTENTIAL).
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Pred. No.
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l; Mismatches
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gnt. It is produced through Bioinformatics and the EM
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(CYTOPLASMIC
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transport motor cytoplasmic
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                                                                                                                                                                                                                                                                               H., Nakata
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                                                                                                     DYNEIN ACTS AS
F VESICLES AND
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                                                                             NUMBER
                                                                                                                                                                                                                                                      heavy chain,
      a collaboration
MRL outstation -
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Best Local
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ANX7_XENLA STANDARE
092125;
01-NOV-1997 (Rel. 35, 01-NOV-1997 (Rel. 35, 101-OCT-2000 (Rel. 40, 10
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MEDLINE=96265035; PubMed=8670145;
Srivastava M., Zhang-Keck Z.Y., C
                                    TISSUE=Brain;
                                                                                                                 Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; M
                                                                                                                                                ANNEXIN A7 (ANNEXIN VII) (SYNEXIN).
ANXA7 OR ANX7.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                        3520
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                                                                                   NCBI_TaxID=8355;
                                                                                                    Xenopodinae;
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                                                  EQUENCE FROM N.A.
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COILED COIL (POTENTIAL).
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Pred. No. 1.1e
21; Mismatches
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 McPhie P.,
                                                                                                                  Pipoidea; Pipidae;
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Best Local S
Matches 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                            STRAIN-CV. BRIGHT YELLOW 2;
Philipps G., Chaboute M.E., Clement B., Gigot C.;
Submitted (OCT-1995) to the EMBL/GenBank/DDDI databases.
-!- FUNCTION: PROVIDES THE PRECURSORS NECESSARY FOR DNA SYNTHESIS.
-!- CATALYTIC ACTIVITY: 2'DEOXYRIBONUCLEOSIDE DIPHOSPHATE + OXIDIZ
THIOREDOXIN'+ H(2)0 = RIBONUCLEOSIDE DIPHOSPHATE + REDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT).

NICOCLIANA TABACUM (COMMON tobacy)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spei
Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
Solanales; Solanaceae; Nicotiana.
                               -!- COFACTOR: CONTAINS TWO IRON IONS (BY SIMILARITY).
-!- PARTHWAY: FIRST REACTION IN THE DNA REPLICATION PAT
-!- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE RIBONUCLEOSIDE DIPHOSPH
SMALL CHAIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem.
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27; Conser
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218 277 ANNEXIN 2
290 350 ANNEXIN 2
373 433 ANNEXIN 3
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SWISS-PROT entry is copyright. It is produced through a collaboration

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RESULT 10
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                                                                       STRAIN-AR39;
MEDLINE-20150255; PubMed=10684935;
MEDLINE-20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
White O., Hickey E.K., Peterson J., Whouri H., Craven B.,
Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B.,
Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J.,
Bowman C., Dodson R., Gwinn M., Fraser C.M.,
                                                                                                                                                                                                                                                                                                   01-OCT-2000 (Rel. 40, Last sequence uportherICAL PROTEIN CPN0137/CP0635. CPN0137 OR CP0635.
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STRAIN=J138;
MEDLINE=20330349;
                      SEQUENCE FROM N.
                                                                MCClarty G., Salzberg S.L., Eisen J., Fraser "Genome sequences of Chlamydia trachomatis Mc
                                                                                                                                                                                           "Comparative genomes of Chlamydia
                                                                                                                                                                                                        Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
                                                                                                                                                                                                                                                                           Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
NCBI_TaxID=83558;
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                                                                                                                                                                                                                                 MEDLINE=99206606; PubMed=10192388;
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                                              Nucleic
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iae AR39.";
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21:385-389(1999).
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                                             Res.
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 PubMed=10871362;
                                             28:1397-1406(2000).
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RESULT 11
CPSM_HUMAN
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P31327; 043774;
p31327; 043774;
01-JUL_1993 (Rel. 26, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
CARBAMOYL-PHOSPHATE SYNTHETASE I) (CPSASE I).
                                                                                                                                                    Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T "Comparison of whole genome sequences of Chlamydia pn from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                 synthetase
                                                                                                                                                                                                   MEDLINE=92084128; Pul
Haraguchi Y., Uchino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002678; -. Pfam; PF01784; DUF34; 1.
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EMBL; AE002221; AAF38450.1;
EMBL; AP002545; BAA98347.1;
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                      identification of a missense mutation in CPS1.";
Hum. Mutat. 12:206-211(1998).
-!- FUNCTION: INVOLVED IN THE UREA CYCLE OF UREOTELIC ANIMALS WHERE
                                                                         Gal A.;
                                                                                     Finckh U., Kohlschuetter A.,
                                                                                                 MEDLINE-98375696;
                                                                                                                          SEQUENCE FROM N.A., VARIANT CPS1
                                                                                                                                                                                           Matsuda I.;
                                                                                                                                                                                                                                            SEQUENCE FROM
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SEQUENCE 2
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                                                                                                                                                                             "Cloning and sequence of
                                                            Prenatal diagnosis of carbamoyl
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107:335-340(1991).
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CELL
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Pred. No. 7.7;
19; Mismatches
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ation in CPS1.";
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InterPro; IPR002474; -.
Pfam; PF00289; CPSase_sm_chain; 2.
Pfam; PF00988; CPSase_sm_chain; 1.
Pfam; PF00117; GATase; 1.
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PRINTS; PRO0099; CPSGATASE.
PROSITE; PS00866; CPSASE_1;
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EMBL; Y15793; CAA75785.1; -.
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HSSP; P00968; 1JDB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: PRIMARILY IN THE LIVER AND SMALL INTESTINE.
DISEASE: DEFECTS IN CPS1 ARE THE CAUSE OF AN AUTOSOMAL RECESSIVE
METABOLIC DISORDER THAT CAUSE A TYPE OF HYPERAMMONEMIA. CLINICAL
SYMPTOMS ARE VOMITING IN INFANCY, PROTEIN INTOLERANCE,
INTERMITTENT ATAXIA, SEIZURES, LETHARGY, AND MENTAL RETARDATION.
SIMILARITY: TO OTHER CARBAMOYL-PHOSPHATE SYNTHETASES. ALSO
CONTAINS A GLUTAMINE AMIDOTRANGFERASE-LIKE DOMAIN BUT THE CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: 2 ATP + NH(3) + CO(2) + H(2)O = 2 ADP ORTHOPHOSPHATE + CARBAMOYL PHOSPHATE.
ENZYME REGULATION: REQUIRES N-ACETYLGLUTAMATE AS AN ATLACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIVATOR. SUBCELLULAR LOCATION: MITOCHONDRIAL
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                  RLSRS -> KMSPN (IN REF. 1)
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E -> G (IN REF. 1).
EH -> AT (IN REF. 1).
GD -> EN (IN REF. 1).
I -> N (IN REF. 1).
F -> S (IN REF. 1).
H -> U (IN REF. 1).
A -> V (IN REF. 1).
A -> N (IN REF. 1).
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RLSRS -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMOLOG
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E53A22D77563961D CRC64;
                                                                                                                                                                                                                                                                                                   M (IN CPS1 DEFICIENCY).
1=VAR_006835.
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RESULT 12
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Best Local S
Matches 24
                                                                                                 Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender Volpe T., Watner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to the SWISS-PROT data bank.
-!- CATALYTIC ACTIVITY: ATP + L-PHENYLALANINE + TRNA(PHE) = AM PYROPHOSPHATE + L-PHENYLALANYL-TRNA(PHE).
-!- SUBURIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE PHE-TRNA SYNTHETASE ALPHA CHAIN SUBFAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN (EC 6.1.1.20) (PHENYLALANINE-TRNA LIGASE ALPHA CHAIN) (PHERS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYFA_YEAST
P15625;
use by non-profit institumodified and this statement entities requires a license
                                                                                                                                                                                                                                                                                             Fasiolo F., Sanni A., Potier S., Ebel J.-P., Boulanger Y., "Identification of the major tRNA(Phe) binding domain in the tetrameric structure of cytoplasmic phenylalanyl-tRNA synthetase from
                                                                                                                                                                                                                                                                                                                                                                                           Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chromosome VI from
                              the European
use by non
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                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE,
MEDLINE=89121098;
                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae."; Nat. Genet. 10:261-268(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Murakami Y., Naitou M., Hagiwara H., Sasanuma S.-I., Sasanuma M., Tsuchiya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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Sanni A., Mirande
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                                                           between
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MEDLINE=95400292; PubMed=7670463;
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                           SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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263:15407-15415(1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                        AND TRNA-BINDING
                                                                                                                                                                                                                                                                                                                                           PubMed=2644133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetaceae;
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l3; Mismatches
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                and
                                                           a collaboration
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license agreement (See http://www.isb-sib.ch/announce,

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Best Local Similarity
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01-FEB-1994 (Rel. 28, Last sequence update 01-NOV-1995 (Rel. 32, Last annotation update PRE-MRNA SPLICING FACTOR PRP8.
PRP8 OR RNA8 OR DBF3 OR DNA39 OR YHR165C.
PRP8 OR RNA8 OR DBF3 OR DNA39 OR YHR165C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
               Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=95304847; PubMed=7785334;

Hodges P.E., Jackson S.P., Brown J.D., E

"Extraordinary sequence conservation of
"Extraordinary sequence conservation of
"Extraordinary sequence conservation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEPD; 7545; -.

**SGD; **S000197; FRS2.*

**InterPro; IPR002106; -.

InterPro; IPR002319; -.

Pfam; PF01409; tRNA-synt_2d; 1.

PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.

Aminoacyl-trNa synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                 STRAIN=S288C / AB972;
MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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23.5%;
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f the PRP8 s
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RESULT 1.
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Matches
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P79702;
01-NOV-1997
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CONFLICT
SEQUENCE
                    SEQUENCE FROM N.A. Chang M.S., Huang C.J.; Submitted (FEB-1997) to
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Cyprininae; Cyprinicum; Cyprininae; Cyprinidae; Cyprininae; Cyprini
                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
30-MAY-2000 (Rel.
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"Cloning of the RNA8 gene of Saccharomyces cerevisiae, detection the RNA8 protein, and demonstration that it is essential for nucl pre-mRNA splicing.";
pre-mRNA splicing.";
Mol. Cell. Biol. 8:1067-1075(1988).
HOL. Cell. Biol. 8:1067-1075(1988).
HOL. CELL CYCLE BINDS RNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is greenent (See http://www.isb-sib.ch/an
                                                                                                                                                                                                   Cyprinus carpio (Common carp)
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SIMILARITY: STRONG, TO C.ELEGANS PROTEIN C50C3.6.
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S48905;
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S48905.
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28.3%;
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                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
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LIYIIPGPVQCAYHGIIIQCRVLSRTMRSTTRL
(IN REF. 2).
T -> S (IN REF. 2).
W -> C (IN REF. 2).
MW; 8F4F6F89D34D3508 CRC64;
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Pred. No. 1.4e+02;
""amatches 20;
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POLY-PRO.
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(CELLULAR ONCOGENE
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FUNCTION: NUCLEAR

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COVALENTLY LINKED COMPLEX WITH THE C-JUN/AP-1 TRANSCRIPTION FACTOR. C-FOS HAS A CRITICAL FUNCTION IN REGULATING THE DEVELOPMENT OF CELLS DESTINED TO FORM AND MAINTAIN THE SKELETON. IT IS THOUGHT TO HAVE AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION, CELL PROLIFERATION AND DIFFERENTIATION (BY SIMILARITY).

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YGEW_ECOLI
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Best Local Similarity
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01-NOV-1997
01-NOV-1997
EMBL; U28375; AAA83051.1;
                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         YGEW_ECOLI
Q46803;
                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                       Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                 Science
                                                                                                                                                                                                                                                  STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS: PRO0042; LEUZIPPRFOS.
PROSITE; PS00036; BZIP_BASIC; 1.
Proto-oncogene; Nuclear protein; Phosphorylation; DNA-binding.
DNA_BIND 115 136 BASIC MOTIF.
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-!- SUBCELLULAR LOCATION: NUCLEAR
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY. FOS SUBFAMILY.
                                                                                                                                                                                            Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                               Escherichia coli
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                                                                                                                                                -!- SIMILARITY: SOME, TO ORNITHINE CARBAMOYLTRANSFERASE.
                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                  Escherichia
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141
347 AA;
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(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
L 40.2 KDA PROTEIN IN KDUI-LYSS INTERGENIC REGION
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InterPro; IPR002029; -.
Pfam; PF00185; OTCace; 2.
Hypothetical protein.
SEQUENCE 363 AA; 40212 MW; F8436BC00BF2DC83 CRC64;
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             October 17,
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23.6%; Pred.
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             2001,
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Post-processing: Minimum Match 0%
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                                                                                                      SPTREMBL_16:*

1: sp_archea:*
2: sp_bacteria.
3: sp_fungi:*
4: sp_human:*
5: sp_human:*
5: sp_mammal:*
7: sp_mhc:*
8: sp_organel1
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclass:
13: sp_vertebra
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sp_vertebrate:*
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SUMMARIES
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DB ID 6 Q9X550 13 057352 11 035251 11 P97946 4 043915 4 043915 11 088902 4 Q9P257 4 Q9P257 11 060482 3 Q10287 11 0962482 3 Q10287 11 0962481 2 Q56080 5 Q21027 10 Q9SUZ1
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
64.5	65	65	65	65	65.5	66	66	66.5	66.5	67	67	67	67	67	67	67	67	67	67.5	83	68	83	68	68.5	68.5
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	Q22184 caenorhabdi		Q9ufy5 homo sapien	Q9rvi5 deinococcus	O80941 arabidopsis	Q9h993 homo sapien	Q9flp3 arabidopsis	Q9fcs2 neisseria m	Q9w397 drosophila	Q9steO brassica na	Q9kqz2 vibrio chol	Q9ryvl deinococcus	001798 caenorhabdi	Q9jv08 neisseria m	Q9jzy9 neisseria m	023566 arabidopsis	O55722 chilo iride	Q54882 s putative	Q9vmy5 drosophila	052870 coxiella bu	Q45932 coxiella bu	. Q45855 coxiella bu	Q9na28 caenorhabdi	Q9eru9 mus musculu	Q61992 mus musculu

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Best Local Similarity
Matches 87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure and expression of bovine VEGF family."; submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AB004275; BAA77687.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea,
Bovidae; Bovinae; Bos.
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Liu X., Yonek
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61 WQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQC 102
                                                                                                              31
                                                                                                                                                 1 AAFESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGG
                                                                                                          AAFESGLGFSDTEPDAGENKAYAGKEMEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGG
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420 /
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85.3%;
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  of bovine 'VEGF family.";
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Pred. No. 8.4e-41;
5; Mismatches 10
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VASCULAR ENDOTHELIAL GROWTH FACTOR
; 58BA84317A3C8E2D CRC64;
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WQHSTEQANTNIRTGETLKFAAAHYNTEILRSIDNEWRKTQC 132

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Best Local S
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01-JAN-1998 (TrEMBLrel. 05, C
01-JAN-1998 (TrEMBLrel. 05, L
01-MAR-2001 (TrEMBLrel. 16, L
VASCULAR ENDOTHELIAL GROWTH F
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057352;
01-JUN-1998
STRAIN=SPRAGUE DAWLI
MEDLINE=97349118; Pu
Yamada Y., Nezu J.,
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                                   SEQUENCE FROM N.A
                                                       NCBI_TaxID=10116;
                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                         Rattus norvegicus (Rat).
                                                                                                      VEGF-D.
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PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
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Alitalo K., Le Douarin N.M.:
"Avian VEGF-C: cloning, embryonic expression
of the differentiation of VEGFR2-expressing (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coturnix coturnix japonica (Jap
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Development 125:743-752(1998).
EMBL; Y15837; CAA75799.1; -.
HSSP; P15692; 1VPP.
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                                                                                                                                                                                                                                                                                                                     Similarity 75.5
77; Conservative
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                          DAWLEY;
             PubMed=9205122;
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418
 Shimane
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ta; Craniata; Vertebrata;
hae; Galliformes; Phasian.
                                                                                                               Last sequence update)
Last annotation update)
FACTOR D.
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Last annotation updat
FACTOR C PRECURSOR.
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Pred. No. 6.6e
l3; Mismatches
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                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                         PRT;
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 Hirata
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.6e-36;
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                                                                              Euteleostomi
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idae; Phasianinae;
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Matches 31
                                                      MGD; MGI:108037; Figf.
InterPro; IPR000072; -.
Pfam; PF00341; PDGF; 1.
ProDom; PD001029; -; 1.
PROSITE; PS00249; PDGF_1; 1
PROSITE; PS50278; PDGF_2; 1
SMART; SM00141; PDGF; 1.
SEQUENCE 358 AA; 40908 M
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P97946;
01-MAY-1997 (TIEMBLICAL. 0:
01-MAY-1997 (TIEMBLICAL. 0:
01-MAR-2001 (TIEMBLICAL. 1:
                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J;
MEDLINE=97030254; PubMed=8876195;
                                                                                                                                                              Genomics 42:483-488(1997).
EMBL; X99572; CAA67892.1;
EMBL; D89628; BAA14002.1;
                                                                                                                                                                                                    Yamada Y., Nezu J., Shimane M., Hirata Y.;
"Molecular cloning of a novel vascular endothelial growth factor
VEGF-D.";
                                                                                                                                                                                                                                                                                                          platelet-derived growth
                                                                                                                                                                                                                                                                                                                    Ordandini M., Marconcini L., Ferruzzi "Identification of a c-fos-induced gen
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
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EMBL; AF014827; AAB66557.1;
HSSP; P15692; 1VPP.
                                                                                                                                                       HSSP; P15692; 1VPP
                                                                                                                                                                                                                                    MEDLINE=97349118; PubMed=9205122;
                                                                                                                                                                                                                                                  TISSUE=LUNG;
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                                                                                                                                                                                                                                                                                     Proc.
                                                                                                                                                                                                                                                                                               family.";
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03,
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fos-induced gene that is related
factor/vascular endothelial grow
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Last annotation updat
FACTOR D (C-FOS INDUC
Score 163; DB 11;
Pred. No. 4.3e-09;
3; Mismatches 16
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Pred. No. 2.4e
22; Mismatches
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Best Local
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                                                                            SEQUENCE
                                                                                  Pfam; PF00341; PDGF; 1.
ProDom; PD001629; -; 1.
PROSITE: PS00249; PDGF_1; 1.
PROSITE: PS50278; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                             MEDLINE=98118549; PubMed=9435229; Achen M.G., Jeltsch M., Kukk E., Alitalo K., Stacker S.A.;
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                                                                                                                                                                                                                                                                                                                                           MEDLINE=97349118; PubMed=9205122;
Yamada Y., Nezu J., Shimane M., Hirata Y.;
"MOLecular cloning of a novel vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                      "Human FIGF: cloning, gene structure, and mapping between the PIGA and the GRPR genes."; Genomics 47:207-216(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-JUN-1998
                                                                                                                                            EMBL; Y12863; CAA73370.1; HSSP; P15692; 1VPP.
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        EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 85
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EQQIRAASSLEELLQIAHSEDWKLWRCRLKL-----KSLASMDSRSASHRSTRFAATFY 99
                                                                                                                                                                AJ000185;
                             l Similarity
29; Conser
                                                                            354 AA;
                            Conservative
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                                                                            40444 MW;
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37.7%;
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16,
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Last sequence update)
Last annotation updat
                                    Score 155; DB 4;
Pred. No. 2.9e-08;
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Best Local
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SEQUENCE FROM N.A.
MEDLINE=20277482; PubMed=1
Nagase T., Kikuno R., Ishi
"Prediction of the coding
                                                                                                                   01-OCT-2000 (Trembirel. 15, 01-OCT-2000 (Trembirel. 15, 01-MAR-2001 (Trembirel. 16, KIAA1471 PROTEIN (FRAGMENT).
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Q9P257;
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Pfam; PF00102; Y_phosphatase; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
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O88902;
O1-NOV-1998 (TrEMBLrel. 08,
O1-NOV-1998 (TrEMBLrel. 16,
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Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10116;
                                                           NCBI_TaxID=9606
                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                             Homo sapiens (Human)
                                                                                                          KIAA1471
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SEQUENCE
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              PubMed=10819331;
R., Ishikawa K.,
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Pred. No. 22;
17; Mismatches
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Sciurognathi; Muridae;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=20549011; PubMed=11095967;
MEDLINE=20549011; PubMed=11095967;
Toyooka S., Ouchida M., Jitsumori Y., Tsukuda K.,
Toyooka S., Ouchida M., Shimizu K.;
Nakamura A., Shimizu N., Shimizu K.;
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Homo sapiens (Human).
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SEQUENCE
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01-MAR-2001 (TrEMBLrel.
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Biochem. Biophys. Res. Commun. 278:671-678(2000).
EMBL; AB025194; BAB19280.1; -.
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EMBL; AB040904; BAA95995.1; ...
InterPro; IPR000242; ...
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1345 AA;
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Pred. No. 50;
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Catarrhini; Hominidae
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                                          TRANSMEM TRANSMEM
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"Cps1+, a Schizosaccharomyces pombe gene homolog of Saccharomyces cerevisiae FKS genes whose mutation confers hypersensitivity to cyclosporin A and papulacandin B.";
J. Bacteriol. 179:7653-7662(1997).
                                                                                                                                                                                                                   EMBL;
                                                                                                                                                   Pfam; PF02364; Glucan_synthase; Transferase; Glyc
                                                                                                                                                                                                                                                                                                 Lyne M., Rajandream M.A., Barrell B.G., Devlin K., Churcher C.M.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-i- CATALYTIC ACTIVITY: UDP-GLUCOSE + (1,3-BETA-D-GLUCOSYL)(N) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLUCAN-UDP GLUCOSYLTRANSFERASE). CPS1 OR DRC1 OR SPBC19G7.05C.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
1,3-BETA-GLUCAN SYNTHASE COMPONENT CPS1 (EC 2.4.1.34) (1,3-BETA-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q10287;
01-NOV-1996
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TISSUE-OFGAN OF CORTI;
MEDLINE-961094991; PubMed-8622957;
Luebke A.E., Dahl G.P., Roos B.A.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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  TRANSMEM
                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4896;
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
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                                                                                                                                                                                                                                         D78352; BAA11369.1;
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nilarity 33.3%;
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Pred. No. 6.5;
L2; Mismatches
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                                                                                                                                         PROSITE; PS50011,
PROSITE; PS50090;
PROSITE; PS50090;
ATP-binding; Heli
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DOMAIN
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SEQUENCE
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Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Branc Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams Somerville C.R., Venter J.C.;
                                                                                                                                                                                                                               Pfam; PF00271; helicase_C
Pfam; PF00385; chromo; 1.
Pfam; PF00628; PHD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        physically assigned P1 and TAC cl
DNA Res. 5:379-391(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of Arabidopsis thaliana of Sequence features of the regions of 1,081,958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Embryophyta; Tracheo Magnoliophyta; eudicotyledons; core eudicots; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TIEMBLIEL. 06, Last sequence update)
01-MAR-2001 (TIEMBLIEL. 16, Last annotation update)
HUMAN MI-2 AUTOANTIGEN-LIKE PROTEIN (HELICASE-LIKE PROTEIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99156233;
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9 LSDAEPDAGEATAYASKDLEEQLRSVSSVDELM--TVLYPEYWKMYKCQLRKGGWQHNRE 66
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IPR001650;
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Pred. No. 1.7e
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W; B3CABD2960201AC1 CRC64;
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dicots; Rosidae;
                                           .7e+02;
.es 46;
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.2e+02;
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e; eurosids II;
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RESULT
Q9QZH1
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Best Local
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Q9QZH1;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
LEFT-RIGHT DYNEIN.
DNAHC11 OR LRD.
                                                                                                               01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                              SMART; SP
SEQUENCE
                                                                                                                                              Q56080;
Q56080;
                                                                                                                                                                                                            1312
SEQUENCE FROM N.A.
MEDLINE=92291112; PubMed=
Koski P., Saarilahti H.,
Osterlund K., Hurme R., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Supp D.M., Brueckner M., Kuehn M.R., WGGrath J., Corrales J.M., Potter S.S. "Targeted deletion of the ATP binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                              Salmonella
                                                                       Bacteria;
                                                                                 Salmonella
                                                                                             TLPA
                                                                                                       TLPA.
                                                                                                                                                                                                                                                    1263 LDKANQELEA
                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNO
PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  confirms its role in
                                                  NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1100864; Dnahc11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Development 0:0-0(1999).
EMBL; AF183144; AAF07922.1;
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                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003593;
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                                                                                                                                                                                                                                                                                             26;
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                                                                       a typhimurium.
Proteobacteria;
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                                                                                                               (TrEMBLrel.)
(TrEMBLrel.)
                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                              AAA;
AA;
                     PubMed=1601892;
                                                                                                                                                                                                                                                                                                     13.1%;
                                                                                                                                                                                                                                                    -----LEEEMEQMQNSARLFEVALPEYKQMKQCRQEIRLLKGLW- 1311
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Rhen M.;
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Last sequence up
Last annotation
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Last annotation updat
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Pred. No. 3.9e
L5; Mismatches
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 development of left-right
                                                                       subdivision; Enterobacteriaceae;
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           Riikonen
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RESULT 15
005206
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Best Local S
Matches 24
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Best Local Sim
Matches 24;
   005206
005206;
01-JUL-1997
01-JUL-1997
01-JAN-1998
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Q9EUI5;
01-MAR-2001
01-MAR-2001
01-MAR-2001
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Plasmid 50k virulence.
Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AB040415; BAB20549.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                              "50 kb virulence plasmid of Salmonella enterica serovar Choleraesuis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=RF-1;
Okada N., Haneda T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coiled coil protein.";
J. Biol. Chem. 269:10675-1
EMBL; M88208; AAA74964.1;
SEQUENCE 371 AA; 41523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A new alpha-helical coiled coil protein encoded by the Salmonella typhimurium virulence plasmid."; J. Biol. Chem. 267:12258-12265(1992). [2]
                                                                                                                                                                                                                                                                                                                                                                                              Plasmid
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Hurme R., Namork E., Nurmiaho-Lassila E.L., Rhen M.;
"Intermediate filament-like network formed in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=119912;
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                                                                                                                                                          166 KER-----LAAAEENT 176
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                                                                                                                                                                                                                         AGEQTAQAERELADAAQTVDDLEEKLDELQDRYDSLTLALESERSLRQ----QHDVEMAQL 165
                                                                                                                                                                                                                                                         AGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKM-----YKCQLRKGGWQHNREQANL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGEQTAQAERELADAAQTVDDLEEKLDELQDRYDSLTLALESERSLRQ----QHDVEMAQL 165
                                                                                                                                                                                                                                                                                            24;
 (TrEMBLrel.)
(TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                             371 AA; 41479 MW;
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l (TrEMBLrel. 16,
l (TrEMBLrel. 16,
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                                                                        PRELIMINARY;
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31.2%;
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                                                                        124 AA
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22;
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EMBL; U92492; AAB51153.1; -.
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NON_TER 1 124 124
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Bacteria; Firmicutes; B
Streptococcus.
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                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                    STRAIN-STI4935;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1314;
                                                              58 KD--QEEREKIELNYLKKLDKNQEEREKL-----ELDYLKKLDHEHKEHQ 100
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                                                                                                                                            1 AAFESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMY---KCQLR 57
                                                                                                                   AGFANQTEVKAAGPDSSPQNVSSDRDIYE------LHEELWKEYDILKEKLD 57
                                                                                       KGGWQHNREQANLN-----SRTEETIKFAAAHYNTEILKSIDNEWRKTQ 101
                                                                                                                                                                      l Similarity 25.5
28; Conservative
                                                                                                                                                                                                                                        124 124
124 AA; 14716 MW;
                                                                                                                                                                                  12.8%;
                                                                                                                                                                                                                                                                                                                                                                                   Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                        15;
                                                                                                                                                                    Score 69; DB 2
Pred. No. 7.6;
15; Mismatches
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                                                                                                                                                                      37;
                                                                                                                                                                                              Length 124;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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2: /SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIDSB/gcgdata/geneseq/geneseqp/AA198B.DAT:*

(*SIDSB/gcgdata/geneseq/geneseqp/AA198D.DAT:*

(*SIDSB/gcgdata/geneseq/geneseqp/AA199D.DAT:*

(*SIDSB/gcgdata/geneseq/geneseqp/AA200D.DAT:*

(*SIDSB/gcgdata/geneseq/geneseqp/AA200D.DAT:*

(*SIDSB/gcgdata/geneseq/geneseqp/AA200D.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
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		•			SUMMARIES	
Result		Query				
No.	Score	Match	Match Length DB	DВ	ID	Description
1		100.0	. 399	20	AAW86237	Human VEGF-C full
2	375	100.0	419	18	AAW17837	Human foetal live
ω	_	100.0	419	18	AAW00932	Human Flt4 recept
4	_	100.0	419	18	AAW13833	Human vascular er
S	-	100.0	419	18	AAW11478	Human vascular er
6		100.0	419	19	AAW75751	Vascular endothel
7	-	100.0	419	19	AAW75740	Human vascular er
8		100.0	419	20	AAY30518	Vascular endothel
9		100.0	419	20	AAY22320	Full length humar
10		100.0	419	20	AAW86203	Human vascular er
11		100.0	419	21	AAB10648	Human VEGC protei

44 5	42	40 41	ა ა 9	37	ა ა ნ თ	34	ωú	ຸ່ພ	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
8 4 8	86 6	8 8 8	8 7	87	87 87	87	87	87	87	87	87	88	191	191	191	191	191	276	276	284	284	375	375	375	375	375	375
22	22.9		ν.	ω.	ω ω ·	ω	ωι	υ	ω	ω.	ω	ω.	0	0	0	0	0	ω	ω	ŗ		00.	00.	00.	0	00.	100.0
358	358	32	35, 178	354	ωw	354	ω c	ıω	35,	32	32	320	35(35	350	35	35	41	41!	411	411	41	41	41	41	41	41
	3 19 19																								N	9 21	2
G (C	40	AAY08286	AAB37606 AAY08287	AAY97573	AAY70750 AAY70983	AAB29049	AAB10649	AAW53241	03	AAY97572	AAW53240	AAW44296	AAY97577		AAY22321	AAY30519	AAR82686	4	AAW00933	AAW75743	AAW00934	AAB37605	AAY97570	960	AAY70749	AAY97144	AAB29048
																						:					
ne	vascula	growth f	Human VEGF-D. Hom Human growth facto	VEGF-D1	Human prepro-vascu	VEGF-	Human VEGD protein	sapiens		_		lar	Ŧ	vascul	Truncated human VE	A truncated vascul	\mathbf{L}	vascu	Ø	l vascu	Flt4 rece	G	Human VEGF-B prote		Human prepro-vascu	0	Human VEGF-C prote

ALIGNMENTS

AAW86237

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AAW86237 standard; protein; 399

AA

AAW86237;

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WPI; 1999-009426/01.
                                                                                                                                                                                                              VEGF; VRP; vascular endothelial growth factor; VEGF-related protein; recombinant; truncated; gene therapy; anglogenesis; cardiac ischaemia; coronary; collateral vessel development; cell growth; migration, heart; lower limb ischaemia; stroke; peripheral vascular disease; intestine;
                                                                                                                                                                                                                                                                                         16-FEB-1999 (first entry)
                                                                                                                 20-APR-1998;
                                                                                                                                      05-NOV-1998
                                                                                                                                                           WO9849300-A2
                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                     wound healing;
                                                                                                                                                                                                                                                                    Human VEGF-C full length sequence.
                                                                      (COLL-) COLLATERAL THERAPEUTICS.
                                                                                           25-APR-1997;
                                                                                           97US-0842984.
                                                                                                                 98WO-US07801.
                                                                                                                                                                                                     skin; vascular permeability.
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New truncated vascular endothelial growth factor-related protein subunits - lack part of the N-terminal sequence, used to stimulate

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RESULT
AAW17837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to truncated VRP (vascular endothelial growth CC factor (VEGF)-related protein) subunits that have at least one amino CC acid N-terminal to the first Cys of the core sequence deleted. Host CC calls transformed or transfected with expression vectors containing CC nucleic acids encoding the truncated VRP subunits are used to produce CC the truncated proteins recombinantly. The truncated VRP subunits, CC optionally expressed from gene therapy vectors, have in vivo and in vitro CC angiogenic activity and are used to stimulate angiogenesis, particularly CC coronary collateral vessel development in cases of cardiac ischaemia; to CC stimulate endothelial cell growth and migration in vitro; to treat heart CC lower limb ischaemia; stroke and peripheral vascular disease; to treat ischaemia (e.g.cardiac, chronic coronary or chronic CC lower limb ischaemia; stroke and peripheral vascular disease); to promote healing of wounds (of skin or intestines), and to increase vascular CC permeability. Sequences AAW86234 to AAW86239 represent full length VRP cc sequences from which the truncated fragments are created.
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Lyman SD
                                                   (IMMV ) IMMUNEX CORP
                                                                                                 08-NOV-1995;
                                                                                                                                                  05-NOV-1996;
                                                                                                                                                                                                      15-MAY-1997
                                                                                                                                                                                                                                                    W09717442-A1
                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Foetal liver kinase 1 binding protein; human; flk-lbp; receptor tyrosine kinase; vasculogenesis; angiogenesis; wound healing; tumour; therapy; antagonist; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW17837 standard; Protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiogenesis, e.g. for treating heart disease and ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             liver kinase A binding protein flk-1bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                     96WO-US17584
                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
21..419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 1..20
                                                                                                                                                                                                                                                                                                                                                    /label= Mat_protein
/note= "(Claim 10)"
21..35
                                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                   "(Claim 9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 375; DB 20;
Pred. No. 7.4e-40;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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AAW00932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein (fik-lbp) (see AAWI1837) that binds to the receptor tyrosine kinase fik-l expressed on vascular endothelial and other cells. The mature fiki-bp can be secreted from host cells transformed with an expression vector including an isolated fik-bp cDNA clone (see AAT68811). Fik-lbp can be used to isolate cells to which it binds, for use in studying the roles of such cells and of fik-l in vasculogenesis and angiogenesis. Angiogenesis inhibition or increased vascularisation may be clinically desirable (e.g. to suppress solid tumour growth or in wound healing, respectively). The fik-lbp can be administered to treat conditions with defective or insufficient fik-l. Polypeptides may also act as carriers to deliver diagnostic/therapeutic agents to cells to which fiki-bp binds, to generate antibodies, and to identify fik-lbp antagonists useful for treating fik-lbp mediated conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 71
                                                                                                                                                                                                                                                                             vascular endothelial growth factor receptor-3; ligand;
angiogenesis; wound healing; lymph vessel; lymphangioma;
cancer; metastasis; therapy; diagnosis; antibody; inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                 Peptide
                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                VEGF-C; Flt4;
                                                                                                                                                                                                                                                                                                                                                             Human Flt4 receptor tyrosine kinase ligand VEGF-C.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW00932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW00932 standard; Protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 30-32; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding a human foetal liver kinase 1 binding protein - used to treat conditions with insufficient protein, deliver agents to cells and identify antagonists to treat protein-mediated conditions
                                                                Peptide
                                                                                                                Peptide
                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 HNREQANLNSR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 100.0%;
Local Similarity 100.0%;
les 71; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hnreganlnsr 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fesgldlsdaepdageatayaskdleeqlrsvssvdelmtvlypeywkmykcqlrkggwq 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide comprises a human foetal liver kinase 1 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 AA;
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                receptor tyrosine kinase; VEGFR-3; human;
                 103..227
                                                                  103..225
                                                                                                                  103..217
                                                                                                                              /note= "preferred active fragment of VEGF-C,
    retaining Flt4 ligand activity (Claim 15)"
                                               /note=
                                                                                                 /note=
                                                                                                                                                                               /label= Prepro_peptide
                                                                                                                                                                                                               Location/Qualifiers
                              "preferred retaining
                                                                              retaining
"preferred active fragment of VEGF-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 375; DB 18;
Pred. No. 7.9e-40;
0; Mismatches 0;
                                                                              active fragment of VEGF-C, Flt4 ligand activity (Claim
                              active fragment of VEGF-C Flt4 ligand activity (Cla
                              activity (Claim
                                                                                activity (Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                12) "
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                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 28-JUN-1996;
01-AUG-1995;
12-JAN-1996;
14-FEB-1996;
                                                                                                                                                                                                                                                                                                  library. The polypeptide, or its active fragments, can be expressed in transformed or transfected host cells for use in claimed methods for detecting endothelial cells (e.g. to image lymphatic vessels, endothelial venules, Fil4 receptor in histochemical tissue) and also to modulate the growth of mammalian histochemical tissue) and also to modulate the growth of mammalian
                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                            endothelial cells (e.g. to accelerate angiogenesis and to promote endothelial function of lymphatic vessels). Inhibitors of
                                                                                                                                                                                                                                                                                                                                                                             This polypeptide comprises the pre-pro sequence of human VEGF-C, a novel ligand that binds specifically to human Flt4 receptor tyrosine kinase (VEGER-3), stimulating phosphorylation of the receptor. Its sequence was deduced from a cDNA clone (AAT84276) obtd. from a PC-3 prostatic adenocarcinoma cell (AFCC CRL 1435)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 112-113; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flt4 receptor tyrosine kinase ligand and related nucleic acid to modulate growth of endothelial cells and for diagnosis of endothelial cell diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYHE-) UNIV HELSINKI LICENSING
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92
                             61
                                                          32
                                                                                                                                Local Similarity
                                                                   1 FESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQ 60
                           HNREQANLNSR 71
                                                                                                                                                                                                                                 proliferation, e.g. lymphangioma or metastatic cancer.
e and quail VEGF-C sequences (see AAW00934-35) have also been
                                                     fesgldlsdaepdageatayaskdleeqlrsvssvdelmtvlypeywkmykcqlrkggwq 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1997-145688/13.
hnreganlnsr 102
                                                                                                                                                                                                                                                              such as antibodies, can be used to control endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT84276
                                                                                                                                                                                           419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Joukov V;
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0671573.
95US-0510133.
96US-0585895.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "preferred
                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retaining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                retaining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preferred active fragment of VEGF-C,
retaining Flt4 ligand activity (Claim 8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        retaining Flt4 ligand activity (Claim 14)"
                                                                                                                   0
                                                                                                              Score 375; DB 18; Pred. No. 7.9e-40; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTD OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        active fragment of VEGF-C, Flt4 ligand activity (Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   active fragment of VEGF-C, Flt4 ligand activity (Clai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              active fragment of VEGF-C, Flt4 ligand activity (Clai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity (Claim 9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity (Claim 11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity (Claim 10)"
                                                                                                                                             Length 419;
                                                                                                                 Indels
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                                                                                                              Gaps
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RESULT AAW13833

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                                                                                                          Matches
                                                                                                                                          Query Match
                                                                                                                            Best
                                                                                                                                                                                                                                                                                                                                                  A human vascular endothelial growth factor (VEGF)-related protein (VPR) (AAW1383) has been identified that binds to, and stimulates the phosphorylation of the receptor tyrosine kinase Flt4. It is postulated to be a third member of the VEGF protein family. Its amino acid sequence was deduced from a cDNA clone (AAT59929) obtd. from a glioma 661 library. Recombinant VRF can be produced in transformed host cells and used: to promote growth of vascular and
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                             with excessive neovascularisation or vascular permeability. may make it possible to avoid coronary by-pass surgery by stimulating growth of the collateral circulation.
                                                                                                                                                                                                                                                                                lymph endothelial cells; to stimulate phosphorylation of the tyrosine kinase domain of a F14 receptor; as a diagnostic; as additive to cell cultures; to screen for (ant)agonists: and to raise monoclonal antibodies used to treat conditions associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Fig 1A-D; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sarcoma etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein similar to vascular endothelial growth factor - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT59929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-192902/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vascular endothelial growth factor-releated protein; VRP; VEGF; receptor protein tyrosine kinase; Flt4; signal transduction; wound healing; vulnerary; rheumatoid arthritis; Kaposi's sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to treat e.g. wounds, tumours, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee J, Wood W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9709427-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy; diagnosis; angiogenesis; monoclonal antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human vascular endothelial growth factor-related protein VRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW13833 standard; Protein; 419
61 HNREQANLNSR 71
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                                                                                                                        Local Similarity
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                                                   FESGIDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQ 60
                                fesgldlsdaepdageatayaskdleeqlrsvssvdelmtvlypeywkmykcqlrkggwq 91
                                                                                                                                                                                              419 AA;
                                                                                                        Conservative
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   is tyrosine"
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                                                                                                      Score 375; DB 18;
Pred. No. 7.9e-40;
); Mismatches 0;
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AAW11478
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                                                                                                                       Query Match
                                                                                               Matches
                                                                                                                                                                                  mitogen for vascular endothelial cells, stimulating their growth and angiogenesis. The amino acid sequence of VEGF2 was deduced from a cDNA clone (AAT51371) obtd. from an early stage human (week embryo cDNA library. VEGF2 polypeptides can be produced in transformed host cells and used to promote angiogenesis e.g., to stimulate the growth of transplanted tissue following coronary bypass surgery, or to promote endothelialisation in vascular graft surgery. It can also be used to screen for antagonists (useful e.g. for tumour therapy) and agonists of VEGF2 activity.
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                 Human vascular endothelial growth factor 2 (VEGF2) (AAW11478) is structurally related to the VEGF/PDGF family and is a potent
                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 2; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                             DNA encoding human vascular endothelial growth factor 2 - used to promote angiogenesis or endothelialisation in vascular graft surgery
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-043137/04.
N-PSDB; AAT51371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vascular endothelial growth factor 2; VEGF2; endothelialisation; coronary bypass surgery; agonist; antagonist; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human vascular endothelial growth factor
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                       HNREQANLNSR 71
                                                          FESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQ 60
                                             fesgldlsdaepdageatayaskdleeqlrsvssvdelmtvlypeywkmykcqlrkggwq 91
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hu J,
                                                                                                                                                             419 AA;
                                                                                               Conservative
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                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         CA;
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                                                                                              Score 375; DB 18;
Pred. No. 7.9e-40;
; Mismatches 0;
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vascular graf
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                                                                                                                     Length
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92 hnreganlnsr 102

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                                                                                                                           Query Match
Best Local :
                                                                                                            Matches
                                                                                                                                                                                                                                 angiogenesis, for stimulating lymphangiogenesis, treatment or prevention of inflammation, oedema, elephantiasis, or Milroy's disease. They can also be used to modulate myelopolesis, e.g. treating granulocytopenia. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating the growth of endothelial cells. They can also be used to stimulate lymphocyte production and maturation, and to promote or inhibit trafficking of leucocytes between tissues and lymphatic vessels or to affect migration in and out of the thymus.
                                                                                                                                                                                                                                                                                                                                                       The vascular endothelial growth factor C (VEGF-C) polypeptides have activities affecting growth and migration of vascular endothelial cells, promoting growth of lymphatic endothelial cells and lymphatic The increasing vascular permeability, and affecting myelopoiesis. The products can be used for stimulating angiogeneses, for inhibiting
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated vascular endothelial growth factor polypeptide(s) - used to develop products for treating, e.g. cancers, inflammation, oedema, granulocytopenia or for wound healing or tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 35; Page 143-145; 177pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-437470/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flt4; vascular endothelial growth factor C; vascular endothelial cell; lymphatic endothelial cell; myelopoiesis; angiogeneses; inflammation; lymphangiogenesis; oedema; elephantiasis; Milroy's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                     32
   61 HNREQANLNSR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                 Similarity
                                                                                                         100.0%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419
                                                                                                          0;
                                                                                                         Score 375; DB 19; Pred. No. 7.9e-40; ; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         products can be used for stimulating angiogeneses, for inhibiting angiogenesis, treatment or prevention of inflammation, oedema, elephantiasis, or Milroy's disease. They can also be used to modulate myelopoiesis, e.g. treating granulocytopenia. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating the growth of endothelial cells. They can also be used to stimulate lymphocyte production and maturation, and to promote or inhibit trafficking of leucocytes between tissues and lymphatic vessels or to affect migration in and out of the thymus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The vascular endothelial growth factor C (VEGF-C) polypeptides have activities affecting growth and migration of vascular endothelial cells, promoting growth of lymphatic endothelial cells and lymphatic vessels, increasing vascular permeability, and affecting myelopoiesis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oedema,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-FEB-1998;
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.ymphangiogenesis; oedema; elephantiasis; Milroy's disease.
                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity tes 71; Conserv
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                                                                                                                                                                                                                                                                   FESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQ 60
                                                                                                                                                                                 HNREQANLNSR 71
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                                                                                                                     hnreganlnsr 102
                                                                                                                                                                                                                                      fesgldlsdaepdageatayaskdleeqlrsvssvdelmtvlypeywkmykcqlrkggwq 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 112-115; 177pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419
                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                           Score 375; DB 19; Pred. No. 7.9e-40; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    healing or tissue
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 419;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammation,
                                                                                                                                                                                                                                                                                                                                                               0;
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AAY30518 standard; Protein;

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FESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQ 60 fesgldlsdaepdageatayaskdleeqlrsvssvdelmtvlypeywkmykcqlrkggwq 91

32 Н Matches Query Match

Local

Similarity 100 71; Conservative

100.0%;

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Score 375; DB 20; Pred. No. 7.9e-40; ; Mismatches 0;

419;

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents vascular endothelial growth factor-2 (VEGF-2). The VEGF-2 polypeptides have activities similar to VEGF. The VEGF-2 polypeptides stimulate the growth of vascular endothelial cells, stimulate endothelial cell migration, stimulate angiogenesis, decrease blood pressure, and increase blood flow. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating a medical condition. The VEGF-2 polypeptides or polynucleotides may be useful in treating deficiencies or disorders of the immune system, by
                                                                                                                                                                                                   useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. Examples of immunologic deficiency syndromes include blood protein disorders, ataxia telangiectasia, common variable immunodeficiency, Digeorge syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vascular endothelial cell growth; endothelial cell migration; angiogenesis; blood pressure; blood flow; immune system disorder; immune cell; cancer; autoimmune disorder; blood protein disorder; ataxia telangiectasia; common variable immunodeficiency; Digeorge syndrome; HIV infection; HTLV-BLV infection; leukocyte adhesion deficiency syndrome; lymphopenia; phagocyte bacterioldal dysfunction; severe combined immunodeficients; blagocyte bacterioldal dysfunction; severe combined immunodeficients; blood protein disorder; blood protein disord
Sequence
                                                              Similarly allergic allergic asthma) or
                                                                                               Wiskott-Aldrich disorder, anemia, thrombocytopenia, or hemoglobinuria. They can also be used to modulate emostatic or thrombolytic activity. Similarly allergic reactions and conditions such as asthma (particular
                                                                                                                                                                         Wiskott-Aldrich disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Fig 1A-E; 222pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human vascular endothelial growth factor-2, used for treating, e.g. immune disorders and cancers \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human vascular endothelial growth factor-2; VEGF-2; vascular endothelial cell growth; endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-551399/46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9946364-A1.
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allergy; asthma; allergic asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ10523
                                                              asthma) or other respiratory problems, may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cao
419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                  also be treated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                 Human vascular endothelial growth factor (VEGF)-C sequence
                                                                    16-FEB-1999
                                                                                                                                                               AAW86203 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the invention. The isolated polypeptide is useful for stimulating angiogenesis, by promoting the proliferation of endothelial cells, fithe treatment of a wound, or for the treatment of tissue or bone dam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                    AAW86203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor 2 for wound healing and vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-1995;
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08-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEGF2; vascular endothelial growth factor 2; angiogenesis; bone damage; endothelial cell proliferation; tissue damage; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Full length human VEGF2 protein sequence
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                                                                                                                                                                                                                                                                                                 92
                                                                                                                                                                                                                                                                                                                                            61 HNREQANLNSR 71
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                                                                                                                                                                                                                                                                                                                                                                                     92
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DB; AAX84837.
                                                                                                                                                                                                                                                                                            hnreqanlnsr 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence is the vascular endothelial growth factor 2 (VEGF2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HNREQANLNSR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hnreganlnsr 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 1; 49pp;
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                                                                    (first entry)
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94US-0207550.
95US-0465968.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 375; DB 20;
Pred. No. 7.9e-40;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or bone damage.
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RESULT 1
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Matches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This represents the amino acid sequence of human vascular endothelial growth factor (VEGF)-C protein. The invention provides truncated VRP (VEGF-related protein) submits that have at least one amino acid N-terminal to the first Cys of the core sequence deleted. Host cells transformed or transfected with expression vectors containing nucleic acids encoding the truncated VRP submits are used to produce the truncated proteins recombinantly. The truncated VRP submits, optionally expressed from gene therapy vectors, have in vivo and in vitro anglogenic activity and are used to stimulate anglogenesis, particularly coronary collateral vessel development in cases of cardiac ischaemia; to stimulate endothelial cell growth and migration in vitro; to treat heart disease; to treat inchesis (or activity and are used to stimulate anglogenesis).
                                                                                                                                                                                      AAB10648 standard; Protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGF; VRP; vascular endothelial growth factor; VEGF-related protein; recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia; coronary; collateral vessel development; cell growth; migration; heart; lower limb ischaemia; stroke; peripheral vascular disease; intestine; wound healing; skin; vascular permeability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to treat ischaemia (e.g.cardiac, chronic coronary or chronic lower limbischaemia; stroke and peripheral vascular disease); to promote healing wounds (of skin or intestines), and to increase vascular permeability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiogenesis, e.g. for treating heart disease and ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New truncated vascular endothelial growth factor-related protein subunits - lack part of the N-terminal sequence, used to stimulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-009426/01.
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                                                                                                                                                                                                                                                                                                61 HNREQANLNSR
                                                                                                                                                                                                                                                                                                                                             hnreganlnsr 102
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                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity 100
71; Conservative
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                                                                                                                                                                                                                                                                                                            71
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 375; DB 20; 100.0%; Pred. No. 7.9e-40; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; anglogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;

Human VEGC

protein

19-JAN-2001

(first entry)

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AAB29048
ID AAB2
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18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful
Human; Flt4; fms-like tyrosine kinase 4; lymphoedema;
vascular endothelial growth factor receptor 3; VEGFR-3;
                                               Human VEGF-C protein sequence
                                                                                                                                           AAB29048 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting anglogenic activity c vascularization. This sequence represents the human VEGC protein used to illustrate the method of the invention.
                                                                                31-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 11; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth; VEGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUN-2000
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                                                                                                                                                                                                                                                                                HNREQANLNSR 71
                                                                                                                                                                                                                        hnreqanlnsr 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                419
                                                                                                                                                                                                                                                                                                                                                   Conservative
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, Xu J;
                                                                              (first entry)
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99US-0124967.
99US-0164131.
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                                                                                                                                           Protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                Score 375; DB 21;
Pred. No. 7.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JR,
                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                               Gaps
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΧX
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the protein sequence for the human vascular endothelial growth factor ( (PEGF-C). It was used to demonstrate the methods of the invention, which involve the screening of individuals to determine which vascular endothelial growth factor receptor 3 (VEGFR-3, also known as Fit4 or fms-like tyrosine kinase 4) alleles they possess and thus their likelihood of developing hereditary lymphoedema. Conditions associated with lymphoedema include Milroy Nonne syndrome, which is early onset lymphoedema and lymphoedema praecox, which is late
                                                     treatment; injury; degeneration; photoreceptors; eye; angioid streaks; retinitis; pigmentosa; human; age-related macular degeneration; diabetic retinopath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorder, comprises assaying a nucleic acid to determine a mu altering the sequence of a vascular endothelial growth factor receptor-3 -
                            Homo sapiens.
                                                                                                 Vascular endothelial growth factor 2; VEGF-2; retina; angiogenesis;
                                                                                                                            Vascular endothelial growth
                                                                                                                                                          22-DEC-2000
                                                                                                                                                                                                                 AAY97144 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 60-61; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening a human subject for increased risk of developing a lymphatic disorder, comprises assaying a nucleic acid to determine a mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Milroy-Nonne syndrome; lymphoedema praecox; VEGF-C; vascular endothelial growth factor C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAC62406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYPI-) UNIV PITTSBURGH
                                                                                                                                                                                                                                                                                       92
                                                                                                                                                                                                                                                                                                                  61 HNREQANLNSR 71
                                                                                                                                                                                                                                                                                                                                                32
                                                                                                                                                                                                                                                                                                                                                                          1 FESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                 Protein;
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                                                                                                                            factor-2 (VEGF-2).
                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 375; DB 21;
Pred. No. 7.9e-40;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTD OY
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                      0,
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WO200045835-A1

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RESULT 1
AAY70749
ID AAY77
XX AAY7
XX AAY7
XX Huma
DE Huma
XX Huma
XX VEGE
KW VEGE
KW VEGE
KW SAIC
XX Homc
XX Homc
XX Pept
FT Pept
FT Pept
FT Pro1
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                       VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35; cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis; neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma; sarcoma; malignancy; VEGF-C; vascular endothelial growth factor C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-1999;
12-FEB-1999;
03-JUN-1999;
22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Administration of vascular endothelial growth factor 2 (VEGF-2) to a patient can be used for treating injury or degeneration of photoreceptors associated with e.g. angioid streaks, retinitis pigmentosa, age-related macular degeneration, diabetic retinopathy, etc. VEGF-2 promotes angiogenesis, the formation of new blood vessels in the retina.
    Protein
                                                                  Peptide
                                                                                            Peptide
                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                     Human prepro-vascular endothelial growth factor C
                                                                                                                                                                                                                                                                   17-AUG-2000
                                                                                                                                                                                                                                                                                                                    AAY70749 standard; Protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 administering
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                    hnreqanlnsr 102
                                                                                                                                                                                                                                                                                                                                                                                                              HNREQANLNSR 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                      fesgldlsdaepdageatayaskdleeqlrsvssvdelmtvlypeywkmykcqlrkggwq 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA52080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                injury or degeneration of photoreceptors comprises 
ering to a subject vascular endothelial growth fact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 AA;
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                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0119179.
99US-0119926.
99US-0137796.
99US-0171505.
/label= N-terminal_peptide
/note= "cleavage of this peptide from partially processed
VEGF-C produces a fully processed mature form of VEGF-C
of 21-23 kD which has high affinity to VEGFR-2"
104..227
                                                                               /label= Signal_peptide
                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 375; DB 21; Pred. No. 7.9e-40; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor 2
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AAY70982

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                                                                                                                                                                                                                                                The patent discloses a method to treat neoplastic disease characterised CC by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also CC referred as vascular endothelial growth factor receptor-3, VEGFR-3) in CC endothelial cells of blood vessels adjacent to malignant neoplasm. The CC method involves administering a compound that inhibits binding of a CC ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular cc endothelial cells. The compound is useful for treating neoplastic disease CC such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used CC for manufacturing medicament useful for diagnostic screening, imaging and CC treatment of malignancies characterised by Flt4-expressing blood cells. CT file Flt4 gene maps to chromosomal region 595 and is expressed as 5.8 kb CC and 4.5 kb mRNAs which differ in their 3, sequences and are CC differentially expressed in HEL and DAMI cell lines. Flt4 CC used as a target for tumour imaging and anti-tumour therapy. CC The present sequence is a human prepro-vascular endothelial growth CC factor C (VEGF-C), a specific example of Flt4 binding compound.
                                                                                                                                     Matches
                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating neoplastic diseases such as lymphoma, carcinomas, melanomas and sarcomas, involves administering a compound capable of inhibiting binding of ligand proteins to fms-like tyrosine kinase-4 receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 15-17; Page 140-142; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-317850/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING LTD OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200021560-A1
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                                61 HNREQANLNSR
                                                                   32
                                                                                                                                                     Local Similarity
92 hnreganlnsr 102
                                                            419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaipainen A,
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0169079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "binds and stimulates VEGF-C recep
at position 156 is essential for VEGFR-2
165 is essential for VEGFR-2 and VEGFR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Has a pattern of spaced cysteine residenceminiscent of a Balbiani ring 3 protein (BR3) cleavage of signal peptide and the C-terminal peptide produces a partially processed form of about 29 kD which has high affinity to Flt4 (V
                                 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113..213
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228..419
                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "important for VEGF-C activity"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valltola R, Jussila
                                                                                                                                  0;
                                                                                                                                Score 375; DB 21; Pred. No. 7.9e-40; Mismatches 0;
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3 protein (BR3P) sequence;
                                                                                                                                                                  Length 419;
                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptors; Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              form of VEGF-C (Flt4 (VEGFR-3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binding and
binding"
                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of VEGF-C of
                                                                                                                                Gaps
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AAY70982 standard;

Protein; 419

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The present amino acid sequence is the complete human prepro-vascular endothelial growth factor (VEGF)-C. VEGF-C has the ability to stimulate re-endothelialisation of an injured blood vessel, without significant stimulate of smooth muscle cell proliferation. It can bind to and stimulate VEGFR-2 (vascular endothelial growth factor receptor) and/or VEGFR-3 phosphorylation in cells that express such receptors. An anti-restenosis agent comprising either a VEGF-C gene or protein is used in a method to reduce or prevent restenosis and stenosis of a blood
                                                                                                                                Claim 5;
                                                                                                                                                       Preventing stenosis and restenosis endothelial growth factor proteins
                                                                                                                                                                                                                                                                                                                                                                    04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding-site
                                                                                                                                                                                                                                     Yla-herttuala S, Alitalo K,
                                                                                                                                                                                                                                                              (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING (YLAH/) YLA-HERTTUALA S.
                                                                                                                                                                                                                                                                                                                 26-OCT-1998;
                                                                                                                                                                                                                                                                                                                                          26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                              WO200024412-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vascular endothelial growth factor-C; VEGF; human; re-endothelialisation; vascular endothelial growth factor receptor; VEGFR; vascular trauma; blood vessel; cardiovascular surgery; anti-restenosis agent; prevention; restenosis; stenosis; percutaneous transluminal coronary angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human vascular endothelial growth factor (VEGF)-C protein
                                                                                                                                                                                                           2000-350584/30
following vascular trauma
                                                                                                                                                                                               AAD00339,
                                                                                                                             Page 51-53; 61pp; English.
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/note= "Cleavage results in partially-processed VEGF-C
protein (29 kD)"
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137
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/note= "Cleavage results in fully-processed mature
VEGF-C protein (21-23 kD)"
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/note= "Processed vascular epithelial growth factor-C"
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Search completed: October 17, Job time: 127 sec
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Perfect score:
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12,	Sequence 5, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	2	Sequence 9, Appli	Sequence 30, Appl	Sequence 2, Appli	Sequence 10, Appl	æ	Sequence 12, Appl	•	Sequence 8, Appli	Sequence 45, Appl	Sequence 81, Appl

ALIGNMENTS

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TOPOLOGY: linear; MOLECULE TYPE: protein US-08-999-811-2
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Patent No. 5932540
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM.PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/99,811
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                               TELEFAX: (202)371-254
INFORMATION FOR SEQ ID NO:
                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
REGISTRATION NUMBER: 36,351
REFERENCE / JOONETY NUMBER: 36,351
                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 1488.1000004
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HU, JING-SHAN APPLICANT: ROSEN, CRAIG A. APPLICANT: CAO, LIANG
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Length 419

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997
                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Kerk
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC comp
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APPLICANT: ROSEN, CRAIG A
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCUL
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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    32
                                                                             Local Similarity
                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                 TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
DRMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US FILING DATE: 8-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 20005
                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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STREET: 11
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                    419 amino acids
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                                                               Conservative
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                                                         100.0%; Score 375; DB 3; 100.0%; Pred. No. 2.2e-42; O: Mismatches 0;
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US-09-042-105-18
; Sequence 18, Application US/09042105
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-042-105-18
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Best Local Similarity 100.0%;
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: TO
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                  61 HNREQANLNSR 71
                                                                                                                            FILING DATE: 0
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STREET: 1100 NEW YORK AVENUE
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HNREQANLNSR 102
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                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                Mismatches
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RESULT 4 US-08-795-430-8

Sequence 8, Appli Patent No. 613007

Application US/08795430

GENERAL INFORMATION:

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Best Local :
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APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 57
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PRIOR APPLICATION DATA:

08/585,895
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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92
                  61 HNREQANLNSR 71
                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 312/474-0448
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                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                            REFERENCE/DOCKET NUMBER:
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                                                                                                                           100.0%; Score 375; DB 4; 100.0%; Pred. No. 2.2e-42; ... Mismatches 0;
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US-08-510-133A-35
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GENERAL INFORMATION:
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Best Local
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INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                        TITLE OF INVENTION: Human Vascular EndothelialGrowth Factor NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                APPLICANT: HU, ET AL. TITLE OF INVENTION: H
COMPUTER READABLE FORM:
                       COUNTRY: UZIP: 07068
                                                            STATE:
                                                                           CITY: ROSELAND
                                                                                                  STREET:
                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                             92 HNREQANLNSR 102
                                                                                                                                                                                                                                                                                                                                                                                                   61 HNREQANLNSR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                             32
                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300 TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,133A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL INFUNE...Alitalo, Karı
APPLICANT: Alitalo, Karı
Tonkov, Vladomir
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                                                                                                                                                                                                                                                                                                                                                                                                                                           FESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                           Application PC/TUS9609001
                                                          NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-Aug-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States of America
                                                                                                E: CECCHI, STEWART
6 BECKER FARM ROAD
                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 375; DB 4; llarity 100.0%; Pred. No. 2.2e-42; Conservative 0; Mismatches 0;
                                                                                                                   CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 01
FILING DATE: 6 JUN 95
APPLICATION NUMBER: 01

08/465,968

08/207,550

CLASSIFICATION: FILING DATE: APPLICATION NUMBER:

CURRENT APPLICATION DATA:

WORD PERFECT 5.1

PCT/US96/09001

MS-DOS

3.5 INCH DISKETTE

OPERATING SYSTEM: MEDIUM TYPE:

APPLICATION NUMBER:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6130071
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NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,114
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/FI96/00427
FILING DATE: 01-AUG-1996
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular
TITLE OF INVENTION: Protein
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                          FILING DATE:
                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
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TOPOLOGY: LI
                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                    60606-6402
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                                                                                                                                                                                                                                                                                       6300 Sears Tower,
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                                                                                                                                                                                                                                     United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.4%;
98.6%;
                                                                                                                                                                                                                                                                                                                                       Vascular Endothelial Growth Factor C (VEGF-C)
Protein and Gene, Mutants Thereof, and Uses T
                                                                                         US/08/795,430
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ower, 233 South Wacker Drive
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Pred. No. 1.4e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 613007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION NIMBER: 08/585,895
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                      FILING DATE:
                                                                                                                                                                                                                    COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                          STATE:
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TELEPHONE: 312/474-0448
APPLICATION NUMBER: PCT/
FILING DATE: 01-AUG-1996
                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 HNREQANLNSR 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                        Illinois
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01-AUG-1995
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74.6%;
                  PCT/F196/00427
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                                                                                         US/08/795,430
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4e-30;
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FILING DATE: 14-FEB-1996

APPLICATION NUMBER:

08/601,132

APPLICATION NUMBER: 08/6 FILING DATE: 28-JUN-1996

08/671,573

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US-08-999-811-4
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SEQUENCE CHARACTERISTICS:
LENGTH: 415 amin - Type:
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08999811 Patent No. 5932540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ADPLICATION UMMREP. US/OR/000 811
                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                               APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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APPLICATION NUMBER: 08/51

FILING DATE:
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                                 APPLICATION NUMBER: FILING DATE: HEREW CLASSIFICATION:
                                                                                                                                                                                                                                             STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 73.6%;
Local Similarity 74.6%;
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 APPLICATION NUMBER:
                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                  ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX STREET: 1100 NEW YORK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 ---- QPTLNTR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 HNREQANLNSR 71
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REGISTRATION NUMBER: 38,153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQ 60
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Pred. No. 4.8e-29;
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                                                                                                                   Patent No. 6040157
                                                                                                                                     Sequence 4, Application US/09042105
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: 08/207,550
EARLIER FILING DATE: 1994-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen, Craig A.
APPLICANT: Cao, Liang A.
TITLE OF INVENTION: Polynucelotides Encoding Vascular Endothelial Growth
TITLE OF INVENTION: Factor 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PF112D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hu, Jing-Shan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 1488.1000004
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                    39 MTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                          50.9%; Score 191; DB 2;
100.0%; Pred. No. 1.1e-17;
tive 0; Mismatches 0;
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CORRESPONDENCE ADDRESS

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RESULT 12
US-08-510-133A-33
; Sequence 33, Application US/08510133A
; Patent No. 6221839
; GENERAL INFORMATION:
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CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
APPLICATION NUMBER: US 08/465,968
APPLICATION NUMBER: US 08/465,968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/09/042,105
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-POS/MS-DOS

SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
CORRESPONDENCE Marshall, O'Toole, Gerstein, Murray &
CORRESPONDENCE MARSHALL, O'Toole, Gerstein, Marshall, O'To
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Alitalo, Kari
Joukov, Vladomir
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Joukov, Vladomir
TITLE OF INVENTION: Receptor Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                     CITY: Chicago
                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                              COUNTRY: United States of America
                                                                                                                                                                                                                                                   STATE: Illinois
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(202)371-2540
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PatentIn Release #1.0, Version #1.25
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Pred. No. 1.1e-17;
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; MOLECULE TYPE: protein US-08-585-895-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                   CLASSIFICATION: 514
-ATTORIEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acid
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAFING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Joukov, Vladimir TITLE OF INVENTION: Recepton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Alitalo, APPLICANT: Joukov,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 St
CITY: Chicago
STATE: Illinoi:
                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/32863
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
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5. 6245530
                                                                                                                                                                                                                                                                                                                                                                                                                                                              60606-6402
                                                     : 350 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Illinois
: United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6300 Sears Tower,
                                                                                                                                                   312/474-0448
                                       linear
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US-08-915-795-5
; Sequence 5, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
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Best Local Similarity
Matches 13; Conserv
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Best Local
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NAME: EVANS, JOSEPh D.
REGISTRATION UNMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: pr
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HM PC compatible
COMPUTER: HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                   12 EQQIRAASSLEELLRITHSEDWKLWRCRLR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (2
TELEX: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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33; Conservative
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                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
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Steven A. STACKER
                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                             23.2%; Score 87; DB 4; 43.3%; Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/915,795
                                                                                                                                                                                                            12; Mismatches
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Search completed: October 17, 2001, 14:47:11 Job time: 197 sec
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amin
                                                                                                                                                              Query Match
Best Local :
                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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                                                                                                                                        Local Similarity 43.3%; Score 87; I tocal Similarity 43.3%; Pred. No. 0. es 13; Conservative 10. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/915,795 FILING DATE: CLASSIFICATION: 536
                                                                               41 EQQIRAASSLEELLRITHSEDWKLWRCRLR 70
                                                                                                             26 EEQLRSVSSVDELMTVLYPEYWKMYKCQLR 55
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1200 G Street, NW, Suite 700
                                                                                                                                                                                                                                                                                                                                                      354 amino acids
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'Kari ALITALO
                                                                                                                                                                                                                                                                                                                                                                                                                      (202) 628-8844
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                                                                                                                                                                                                                                            Human Lung
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match Length DB
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2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
58	58.5	58.5	59	59	59	59	59	59	59	59	59	59	59	59	59
15.5	15.6	15.6	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7
. 312	2488	491	1289	1005	843	804	377	377	374	330	255	246	243	234	234
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S35295	T42739	S24354	B72354	T31333	D96495	T37821	A23511	A60764	S69339	GHHU	S31866	T35934	F81536	E86622	E72001
rfbB protein - Yer	guanine nucleotide	p53-binding protei	conserved hypothet	beta-galactosidase	unknown protein [i	probable dna repai	Ig gamma-3 chain C	Ig gamma-3 chain C	Ig heavy chain V r	 Ig gamma-1 chain C 	Ig gamma-1 chain C	probable NAD(P)H o	hypothetical prote	hypothetical prote	hypothetical prote

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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; l ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; l A;Title: Complete genome sequence of Neisseria meningitidis serogroup B & A;Reference number: A81000; MUID:20175755
 Q
                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-453 <TET>
                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
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                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                      polyA polymerase NMB0843 [imported] - Neisseria meningitidis (strain MC58 serogroup
C; Species: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-786 < NHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: The sequence
A;Reference number: Z18526
A;Accession: T16509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid F59A6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;103-419/Product: vascular endothelial growth factor C #status
                                                                                                                                                   A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                   ;Cross-references: GB:AE002437; GB:AE002098; NID:g7226072; PIDN:AAF41254.1; PID:g72260:
;Experimental source: serogroup B, strain MC58
                                                                                                                                        Genetics:
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;Accession: T16509
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                                                                  Query Match
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Best Local Similarity
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   SGLDLSD
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                                                    17.9%;
27.5%;
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-AEPDAGEATAYASKDLEEQLRSVSSVD---ELMTVLYPEYWK 48
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                                                  Score 67;
Pred. No.
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Pred. No.
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Pred. No. 1.9e-35;
; Mismatches 0;
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                                    Mismatches
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                                   14;
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                                                                                                                                                                                                                                                                                                                    , K.E.; Eisen, J.;
; Dougherty, B.A.
; Pizza, M.
                                                                                                                                                                                                                                                                      Rappuoli, R.; strain MC58.
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C; Genetics:
A; Gene: VC1855
A; Map position:
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Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change
C;Accession: B82148
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B82148
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D81870
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A;Molecule type: DNA
A;Residues: 1-453 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-dependent helicase, DinG family VC1855 [imported] - Vibrio cholerae (strain N1696
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C; Keywords: nucleotidyltransferase
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A;Experimental source: serogroup A, strain 22491
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Best Local
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EMEPQAEGYTAYLAKKVLCYLQA---
                                                                                            DAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKM-----YKCQLRKGGW 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis
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31.6%;
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27.5%;
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Pred. No.
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Pred. No.
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Mungall, K.; Quail, M.A.;
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                                                                                                                                                                                                                                   Length 703
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El Tor
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I.; Sellers
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Rajandre
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DKANLVLFASYWQMREVAESLKVEFTKRGW

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G4HU
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C;Keywords: carbon-oxygen lyase; phosphoprotein; pyridoxal phosphate
F;17/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
      Ig gamma-4
C; Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome strua;Reference number: A75001
A;Accession: A75152
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A;Introns: 817/1; 1320/2; 1598/1; 1879/3
C;Superfamily: Caenorhabditis elegans hypothetical protein ZK228
                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-284 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cysteine synthase (EC 4.2.99.8) PAB0250 [similarity] - Pyrococcus abyssi (strain C; Species: Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, December 1995
A;Reference number: Z19897
A;Accession: T24483
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2408 <WIL>
A;Cross-references: EMBL:Z68219; PIDN:CAA92477.1; GSPDB:GN00022; CESP:T05A1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein T05A1.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C;Accession: T24483
                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: PAB0250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;anonymous,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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                                                                                                                             DKALNLNQFENDANFEAHYYGTARELEEQLRSIDKIPEII 148
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    chain C region - h
Homo sapiens (man)
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40.0%;
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Pred. No.
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72;
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Query Match 17.1%;
Best Local Similarity 32.1%;
Matches 25; Conservative
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RESULT
T49093
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A; Cross references: GDB:119340; OMIM:147130
A; Map position: 14q32.33-14q32.33
A; Map position: 14q32.33-14q32.33
A; Introns: 99/1; 111/1; 221/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists
                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-1403 <ALC>
A; Cross-references: EMBL: AL049711; GSPDB: GN00061; ATSP: F4F15.250
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F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status exper F;27-83,141-201,247-305/Disulfide bonds: #status predicted F;106,109/Disulfide bonds: interchain (to heavy chain) #status F;177/Binding site: carbohydrate (Asn) (covalent) #status predi
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                                                                                     A; Gene: ATSP: F4F15.250
                                                                                                                                                                  A; Experimental source:
                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                  R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; I
submitted to the Protein Sequence Database,
A;Reference number: Z25015
A;Accession: T49093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F4F15.250 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #t.C;Accession: T49093
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                                              A; Map position:
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A; Residues: 1-327 <ELL>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 RKGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 LDLSDAEP--
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    123/3;
                                                                                                                                                                  cultivar Columbia;
187/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.1%;
29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -DAGEATAYASKDLEEQLRSVSSVDELMTVLYPEY--WKMYKCQL 54
234/1; 286/2; 351/1; 385/1; 430/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64; I
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-Jun-2000 #text_change 02-Jun-2000
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                                                                                                                                                                  BAC
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9.9;
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.; Milstein, C
                                                                                                                                                                  clone
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                                                                                                                                                                  F4F15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mewes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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485/2;
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606/3;
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Score 64; DB Pred. No. 51; 11; Mismatches

30,

Indels

12;

Gaps

4.

DB 51;

Length 1403;

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A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; ABriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, Docena, C.; El-Oorry, H.; Facincani, A.P.; Ferreira, A.J.S.; submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, W.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu Chado, M.A.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Madeira, H.M.F.; Marrino, C.L.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Genlineri, D.P. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6-phosphofructokinase XF0274 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Species: Xylella fastidiosa (c;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: G82827
                                                                                                                                                                                                                                                                                                                       A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557
A;Accession: E71980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: E71980
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, ; Ives, C.; Gibson, R.; Merberg, D.; Mills, 9
Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein jhp0051 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb_1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE003880; GB:AE003849; NID:g9105080; PIDN:AAF83087.1; GSPDB:GN00:
                                                                                                                                                                                                                                                                                                A; Residues: 1-427 <SIM>
                                                                                                                                                                                                                                                                                                                                                                         A; Note: for a complete list A; Accession: G82827
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: The genome sequence of the plant pathogen Xy lella fastidiosa. A; Reference number: A82515; MUID: 20365717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE001444; GB:AE001439; NID:g4154549; PIDN:AAD05635.1; PID:g41545:
A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-120 <ARN>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QASQELGDKRSDKGEKLAELFDLLFEYIKDSKFERLKEPSAYDYSCKKLYPEQNTSQKMR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESGLDLSDAEPDAGEATA-----YASKDLEEQLRSVSSVDELMTVLYPEY---WKMY 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELLLRNKDGETHHLEDYN 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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                                                                                                                                                                                                                                                                                                                                                                                               of authors
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Pred. No. 3.7;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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Q.; Taylor, D.E.; \
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
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                                                                                                                                                                      A; Experimental source: C; Genetics: A; Note: DKFZp566I174.1
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A;Reference number: Z20555
A;Accession: T29030
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A; Residues: 1-246 <BLO>
                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                             A; Accession: T14772
                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z18182
                                                                                                                                                                                                                                                                                                                                                                                          submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                R; Bloecker, H.; Boecher, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: CESP:F53G12.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-493 <WUX>
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                                                    Matches
                                                                        Query Match
Best Local Similarity
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Best Local
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Matches 15; Conserv
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       5 LDLSDAEPDAGEATAYASKD----
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                                                                          16.8%;
24.4%;
                                                    18;
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C:Species: Homo sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision
C:Accession: T14772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 1
A;Introns: 15/1; 148/3; 258/3; 338/3; 384/2; 458/3
C;Superfamily: protein-tyrosine kinase src; protein kinase homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Wu, X.; Graves, T.
submitted to the EMBL Data Library, May 19
submitted to the sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F53G12.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
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M.; Tsuhako, M.H.; Vallada, 1
A; Reference number: A59328
                        Cross-references: EMBL:AL110241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 DNDLAITDASPGFGSAAKYTAVSICEAALDVAAMAETSTKVF----IYEAMGRHAGW
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                                                                                                                                                                                                                                                                                                                                                                                  YAFKSICELIAYHKRNHKPIYEGMTLI-
                                                                                                                                                                                                                                                                protein DKFZp566I174.1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL:AF003139; PIDN:AAB54162.1; GSPDB:GN00019; CESP:F53G12.6 ce: strain Bristol N2; clone F53G12
fetal kidney; clone DKFZp566I174
                                                                                                                                                        M.; Brandt, P.; Mer
Sequence Database,
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32.1%;
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25.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63.5; DB Pred. No. 18; 8; Mismatches
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Pred. No. 15;
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                                                                                                                                                                                                                                                                  human (fragment)
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                                                                                                                                                          Mewes, H.W.; Gassenhuber, J.; Wiemann,
se, August 1999
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----LEEQLRSVSSVDELMTVLYPEYWKMY---

Score 63; Pred. No.

DΒ

2;

Length

246;

Mismatches

26;

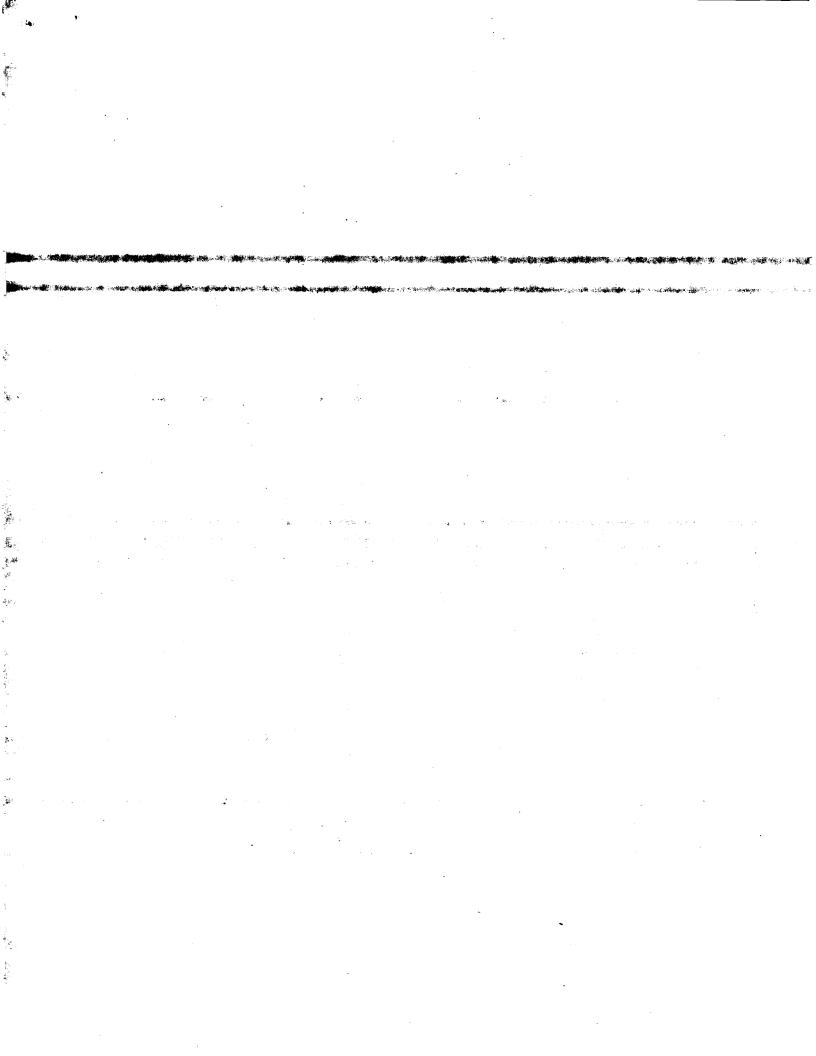
Indels

18;

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Search completed: October 17, 2001, 14:48:41 Job time: 287 sec
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C;Datc: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T42649
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, November 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qγ
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A;Molecule type: mRNA
A;Residues; 1-614 <AAAA>
A;Cross-references: EMBL:AL133046
A;Experimental source: adult testis; clone DKFZp434C0515
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C:Superfamily: herpesvirus ribonucleoside-diphosphate reductase small chain
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A;Residues: 1-366 <AAAA>
A;Cross-references: EMBL:AL137348
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A;Accession: T46249
A;Status: preliminary
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R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
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C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z22230
A; Accession: T42649
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Matches 20; Conserv
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nes 17; Conservative
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31.5%; Pred. No. 30;
ative 10; Mismatches
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
  hits satisfying chosen parameters:
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Gapop 10.0 , Gapext 0.
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375
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MTDH_UROFA
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-!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH!- SUBBURIT: HOMODIMER, DISULFIDE-LINKED!- SUBBURIT: HOMODIMER, DISULFIDE-LINKED!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS	cific activator of the tyrosine kinase receptor Flt4 c. Natl. Acad. Sci. U.S.A. 93:1988-1992(1996). UENCE FROM N.A. 2 L., Morris J.C., Towler P.S., Long A.J., Greco R., 2 L., Morris J.C., Towler P.S., Long A.J., Greco R., 2 L., Morris J.C., Towler P.S., Long A.J., Greco R., 2 L., Morris J.C., Towler P.S., Long A.J., Greco R., 2 L., Morris J.C., Towler P.S., Long A.J., Greco R., 2 L., Morris J.C., Towler P.S., Long A.J., Scaltreto H., Weich N., Neben S., Finner K. 1 L., Wang J., Nickbarg E., Gassaway R., Turner K. d.C.R., 2 L., Morris J., Nickbarg E., Gassaway R., Turner K. d.C.R., 2 L., Morris J., Nickbarg E., Gassaway R., Turner K. d.C.R., 2 L., Morris J., Nickbarg E., Gassaway R., Turner K. d.C.R., 2 L., Morris J., Nickbarg E., Gassaway R., Turner K. d.C.R., 2 L., Morris J., Nickbarg E., Gassaway R., Turner K. d.C.R., 2 L., Morris J., Nickbarg E., Gassaway R., Turner K. d.C.R., 2 L., Morris J., Nickbarg E., Gassaway R., Turner K. d.C.R., 2 L., Morris J., Nickbarg E., Gassaway R., Turner K. d.C.R., 2 L., Morris J., Nickbarg E., Gassaway R., Turner K. d.C.R., 2 L., Morris J., Nickbarg E., Gassaway R., Turner K. d.C.R., 2 L., Morris J., Nickbarg E., Gassaway R., Turner K. d.C.R., 2 L., Morris J., Nickbarg E., Gassaway R., Turner K. d.C.R., 2 L., Morris J.,	ERRATUM. MEDLINE-96203094; PubMed-8612600; MEDLINE-96203094; PubMed-8612600; Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E., Saksela O., Kaikkinen N., Alitaio K.; EMBO J. 15:1751-1751(1996). [3] [3] [3] [3] [3] [8] MEDLINE-96312526; PubMed-8700872; Lee J., Gray A., Yuan J., Luoh SM., Avraham H., Wood W.I.; "Vascular endothelial growth factor-related protein: a ligand and	NCHI_TAXID=9606; [1] SEQUENCE FROM N.A., AND SEQUENCE OF 103-120. SEQUENCE FROM N.A., AND SEQUENCE OF 103-120. MEDLINE=96178224; PubMed=8617204; JOUKOV V., Pajlssola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E., Saksela O., Kaikkinen N., Alitalo K.; "A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases."; EMBO J. 15:290-298(1996).	VEGC_HUMAN VEGC_HUMAN STANDARD; PRT; 419 AA. PRT; 419 A

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Matches 71
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EMBL; U43142; AAA852
EMBL; U58111; AAB029
HSSP; P15692; 1VPF.
                                                      MEDLINE=97388482; PubMed=9247316; Fitz L.J., Morris J.C., Towler P., Wang J., Gassaway R., Nickbarg E.,
                    Giannotti J., Finr
Turner K.J., Wood
                                                                                                                                                                                                                                                   MEDLINE=97164697; PubMed=9012504; Kukk E., Lymboussaki A., Taira S.,
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BALB/C;
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Mammalia; Eutheria;
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    "Characterization
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15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR
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PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
Mitogen; Growth factor; Glyco
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InterPro; IPR002400; -.
Pfam; PF00341; PDGF; 1.
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21-JUL-1986
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P01861;
                  Ellison J.W., Buxbaum "Nucleotide sequence of DNA 1:11-18(1981).
                                              SEQUENCE FROM N.A. MEDLINE=83157104; PubMed=6299662;
                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                              IG GAMMA-4 CHAIN C
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                     IGHG4
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InterPro; IPR000072; -.
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CELL GROWTH.
- SUBUNIT: HOMODIMER, D
- SIMILARITY: BELONGS T
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PS50278; PDGF_2; 1.
Growth factor; Glycoprotein;
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1 - 30
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TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
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Pred. No. 1.7e-24;
5; Mismatches 9
                                                                                     Craniata; Vertebrata; Catarrhini; Hominidae,
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D9D3DD3CECC659D6 CRC64;
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immunoglobulin
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COVALENTLY LINKED COMPLEX WITH THE C-JUN/AP-1 TRANSCRIPTION
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                         NCBI_TaxID=7962;
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; Cypriniformes; Cyprinidae; Cyp
                                                                                                                                                                                                                                                                   Cyprinus carpio (Common carp)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constant region of a gamma 4 chain."; Biochem. J. 117:33-47(1970).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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and this statement is not removed.
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4.1;
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BOI2_YEAST
                                       the
                                                                                         Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GeoBank/DDBJ databases. I- FUNCTION: BINDS TO THE BEM1 PROFEIN. INVOLVED IN BUD IN SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
-!- SIMILARITY: CONTAINS 1 SAM DOMAIN.
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Eukaryota; Fungi; Ascomycota; Saccharomyc
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                modified
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                                                                                                                                                                                  Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
                                                                                                                                                                                                  Chung E., Duncan M., Guzman E., Hartzell G.,
Hyman R., Kayser A., Komp C., Lashkari D., Le
                                                                                                                                                                                                                           Aviles E.,
                                                                                                                                                                                                                                       STRAIN-S288C / AB972;
Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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InterPro; IPR001871; -.
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                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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Pred. No. 5;
7; Mismatches
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; A8F8781044AB8CE1 CRC64;
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                                                                                                                                                                                                             Carpenter J., Chen E., Cherry Hartzell G., Hunicke-Smith S.,
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                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- FUNCTION: PROBABLY PLAYS A ROLE IN ANCHORING
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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SEQUENCE
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MEDLINE-94155465; PubMed-8111972;

MEDLINE-94155465; PubMed-8111972;

Milner-Lorillon O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00169; PH; 1.
Pfam; PF00536; SAM; 1.
Pfam; PF00018; SH3; 1.
  Elongation
                                             Pfam; PF00647; EF1G_domain; Pfam; PF00043; GST; 1.
                                                                                                                                              EMBL; S69726; AAB29958.1;
                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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InterPro; IPR001452; -.
InterPro; IPR001660; -.
InterPro; IPR001849; -.
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                                                                                               InterPro; IPR001662;
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                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO OTHER SPECIES' GAMMA SUBUNIT AS WELL AS TO N-TERMINAL OF SOME EUKARYOTIC AMINO ACID-TRNA SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELLULAR COMPONENTS.
SUBUNIT: EF-1 IS COMPOSED OF FOUR SUBUNITS: ALPHA,
                                                                                                                                                                                                                                                                                                                                                                                                                                    DELTA, AND GAMMA
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U18916;
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PS50003;
                           PS50040; EF1G; 1.
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AAC03212.1;
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                                                                                                                                                                                                               EMBL; M95789; AAA29732.1; -. PIR; A48455; A48455.
                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-IP-PC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium chabaudi.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACIDIC PHOSPHOPROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deleersnijder W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93116806;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5825;
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                                                                                                                                                                                      Signal; Antigen; Membrane; Repeat; OR 24 (POTENTIAL).
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Pred. No. 32;
l3; Mismatches
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Pred. No. 11;
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P01859;
                                                                                                                                                                                   MEDLINE=69064124; PubMed=5782707; Frangione B., Milstein C., Pink J.R.L.; "Structural studies of immunoglobulin G. Nature 221:145-148(1969).
                                                                                                                                                                                                                                                                                                          Milstein C., Frangione B.; "Disulphide bridges of the heavy Biochem. J. 121:217-225(1971).
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                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                             This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinf the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-121 (DOT).
MEDLINE-95255298; PubMed-7737190;
Stoppini M., Bellotti V., Negri A.,
"Characterization of the two unique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang A.-C., Tung E., Fudenberg H.H.;
"The primary structure of a human IgC2 hee
evolutionary, and functional implications.
J. Immunol. 125:1048-1054(1980).
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MEDLINE=82197621; PubMed=6804948;
Ellison J.W., Hood L.E.;
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21-JUL-1986 (Rel.
01-OCT-2000 (Rel.
EMBL; V00554;
                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=72033500;
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Mammalia; Eutheria; Primates;
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Hofmann T., Parr D.M.;
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"A note of the amino acid sequence
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amino acid sequences of the three heavy
ins of a human IgG2 myeloma protein.";
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Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
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  CAB58438.1;
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Bioinformatics and the EMBL
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InterPro; IPR000495; -. InterPro; IPR003006; -.

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RESULT EFFICALT ID EXTENDED IN EXEMPT 15 EXEMPT 15 DT 011 DT 011 DT 011 DT 01 DT 01 DT 01 TO CO Xeles OC Amino CO Amino 
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Best Local
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Nucleic
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                               "Expression of elongation factor 1 alpha (EF-1 alpha) and 1 beta gamma (EF-1 beta gamma) are uncoupled in early Xenopus embryos.";
Dev. Genet. 14:440-448(1993).
-i- FUNCTION: PROBABLY PLAYS A ROLE IN ANCHORING THE COMPLEX TO OTHER
                                                                                                                             TISSUE=Oocyte;
MEDLINE=94155465; PubMed=8111972;
                                                                                                                                                                                                                                              Cormier P., Osborne H.B., Morales J., Bassez T., Poulhe Mazabraud A., Mulner-Lorillon O., Belle R.; "Molecular cloning of Xenopus alongation factor 1 gamma, M-phase promoting factor substrate.";
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GC1_HUMAN
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21-JUL-1986 (Rel. C
21-JUL-1986 (Rel. C
15-JUL-1999 (Rel. 3
                 Edelman G.M. 
"The covalen
                                                                                                 "The covalent structure of a human gamma G-immunoglobulin. VII. acid sequence of heavy-chain cyanogen bromide fragments H1-H4." Eiochemistry 9:3161-3170(1970).
                                                                                                                                           MEDLINE-71064024; PubMed-5489771;
Cunningham B.A., Rutishauser U., Gall W.E.,
Waxdal M.J., Edelman G.M.;
                                                        SEQUENCE OF 136-329 (EU).
MEDLINE=71064025; PubMed=5530842;
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Ellison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human im
Nucleic Acids Res. 10:4071-4079(1982).
                                              Rutishauser
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                    SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
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                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
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CONFLICT 134 134 G -> E (IN REF.
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PIR; S20060; S20060.
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                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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SIMILARITY: TO OT
                 covalent structure of a
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    of heavy-chain
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human gamma G-immunoglobulin. 8. Amino cyanogen bromide fragments H5-H7.";
                                           .A., Bennett
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                                           Konigsberg W.H.,
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Biochemistry

9:3171-3181(1970).

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and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";
Biochemistry 20:2361-2370(1981).

-i- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. ROL & EU SEQUENCES HAVE THE GIM(3)

MARKER & THE GIM (NON-1) MARKERS.
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                                                                                                                                                                                                   between the Swiss Institute of Bioinformat. the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                    InterPro; IPR000495; -.
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Pfam; PF00047; ig; 3.
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"Three-dimensional structure determination of antibodies. Printer of crystallized monoclonal immunoglobulin IgGl KOL, Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
                          Immunoglobulin
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-i- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCII GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
-i- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES
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Khosravi R., Maya R., Gottlieb T., On

"Rapid ATM-dependent phosphorylation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taubert H.W., Kappler M., Meye A., Bartel F., Schlott T Schmidt H., Wuerl P.;
"A Mbo II polymorphism in exon 11 of the human MDM2 gene normal blood donors and in soft tissue sarcoma patients Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                    Lohrum M.A.E., Ashcroft M., Kubbutat M.H.G., Vousder "Identification of a cryptic nucleolar-localization Nat. Cell Biol. 2:179-181(2000).
                                                                                                          NUCLEOLAR LOCALIZATION SIGNAL. MEDLINE=20173879; PubMed=10707090;
                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                           Fang S., Jensen
"Mdm2 is a RING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Translational enhancement of mdm2 oncogene cells containing a stabilized wild-type p53 Cancer Res. 57:3562-3568(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [3]
SEQUENCE FROM N.A. (ISOFORM MDM2-ALPHA).
MEDLINE-20065171; PubMed-10597303;
                                                                                                                                                                                              MUTAGENESIS OF CYS-441 AND CYS-478.
MEDLINE=20076498; PubMed=10608892;
                                                                                                                                                                                                                                                                                                                         "Activity of MDM2, a ubiquitin ligase, dependent on the RING finger domain of Oncogene 19:1473-1476(2000).
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20190101;
                                                                                                                                                                                                                                                                                                                                                                                                           Honda R., Tanaka H., Yasuda H.; "Oncoprotein MDM2 is a ubiquitin FEBS Lett. 420:25-27(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESQUENCE OF 6-491 FROM N.A. (ISOFORM MDM2-A1).
Liang H., Atkins H., Abdel-Fattah R., Suaeyun R.,
"Genomic Organisation of the Human MDM2 Oncogene its Alternatively Spliced mRNA's.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ dat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncogene
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                                                                                                                                                                                                                                                                                      MEDLINE=20187618;
                                                                                                                                                                                                                                                                                                   MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                               Honda R., Yasuda H.;
                                                                                                                                                                                                                                                                                                                                                                                       MUTAGENESIS OF CYS-449
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98111004; PubMed=9450543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGENESIS OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95380270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-24 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Veldhoen N., Metcalfe S., Milner J.
"A novel exon within the mdm2 gene
vitro and disrupts the p53-binding
Oncogene 18:7026-7033(1999).
                                                                                                                                                                                                                                                                                                                 01
                                                                                                                                                                                                                                     Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF 301-481 FROM N.A.
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DNA
                                                                                                                                                                                                                                   275:8945-8951(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                           J.P., Ludwig R.L., Vousden finger-dependent ubiquitin
                                                                                                                                                                                                                                                                                                                                                                          PubMed=10723139;
                                                                                                                                                                                                                                                                                     PubMed=10722742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=7651818;
damage.";
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ve intronic
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          Oren M., on of MDM2
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domain of mdm2 protein.";
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         Shiloh Y.,
12 precedes p
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protein ligase
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                                                                                              Vousden
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and Relationship
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                                                                                              K.H.;
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EMBL; M92424; AAA60568.1; --
EMBL; 212020; CAA78055.1; --
EMBL; 23199; AAA75514.1; --
EMBL; U33200; AAA75515.1; --
EMBL; U33201; AAA75516.1; --
EMBL; U33202; AAA75517.1; --
EMBL; U33203; AAA75518.1; --
EMBL; U33203; AAA75518.1; --
EMBL; U33203; CAB64448.1; --
EMBL; U33203; CAB64448.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97081050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure of the MDM2 oncoprotein bound to the transactivation domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Levine A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISEASE: SEEMS TO BE AMPLIFIED IN CERTAIN TUMORS (INCLUDING SOFT TISSUE SARCOMAS, OSTEOSARCOMAS AND GLICOMAS). A HIGHER FREQUENCY OF SPLICE VARIANTS LACKING P53 BINDING DOMAIN SEQUENCES WAS FOUND IN LATE-STAGE AND HIGH-GRADE OVARIAN AND BLADDER CARCINOMAS. FOUR OF THE SPLICE VARIANTS SHOW LOSS OF P53 BINDING. THAT FAILED TO MISCELLANGOUS: MUND RINGER MUTATIONS THAT FAILED TO UBIQUITINATE P53 IN VITRO DID NOT TARGET P53 FOR DEGRADATION WHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: REGION I IS SUFFICIENT FOR BINDING P53 AND INHIBITING ITS G1 ARREST AND APOPTOSIS FUNCTIONS. IT ALSO BINDS P73 AND E2F1.
REGION II CONTAINS MOST OF A CENTRAL ACIDIC REGION REQUIRED FOR INTERACTION WITH RIBOSOMAL PROTEIN L5 AND A PUTATIVE C4-TYPE ZINC FINGER. THE RING FINGER DOMAIN WHICH COORDINATES TWO MOLECULES OF ZINC INTERACTS SPECIFICALLY WITH A WHETHER OR NOT ZINC IS PRESENT AND MEDIATES THE HETERO-OLIGOMERIZATION WITH MIMM4. IT IS ALSO ESSENTIAL FOR ITS UBIQUITIN LIGASE E3 ACTIVITY TOWARD P53 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE MDM2 / MDM4 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELIULAR LOCATION: NUCLEAR AND CYTOPLASMIC. EXPRESSED PREDOMINANTLY IN THE NUCLEOPLASM. INVERACTION WITH ARF(P14) RESULTS IN THE LOCALIZATION OF BOTH PROTEINS TO THE NUCLEOL NUCLEOLAR LOCALIZATION SIGNALS IN BOTH ARF(P14) AND MDMZ MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COFACTOR: ZINC IS RE
SUBUNIT: BINDS P53,
SPECIFICALLY TO RNA.
                                                                                                                                                                                                                                                                                                                                                                                  European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 RING FINGER DOMAIN
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TISSUE SPECIFICITY: UBIQUITOUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOWARD P53 AND
TARGETS IT FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: INHIBITS P53- AND P73-MEDIATED CELL CYCLE ARREST AND APOPTOSIS BY BINDING ITS TRANSCRIPTIONAL ACTIVATION DOMAIN. FUNCTIONS AS AN UBIQUITIN LIGASE E3, IN THE PRESENCE OF E1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEPENDENT MANNER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN (RB), ElA-ASSOCIATED PROTEIN P300 AND TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXPRESSED IN CELLS
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u39736;
                  U28935; AAA82237.1;
                                                                                                                                                                                                                                                                               an
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                                                                                                                                                                                                                                                                             equires a license agreement (See email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                     Swiss Institute or Broing Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IS REQUIRED FOR UBIQUITIN LIGASE E3 ACTIVITY P53, P73, ARF(P14), RIBOSOMAL PROTEIN L5 AND RNA. CAN INTERACTS ALSO WITH RETINOBLASTOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QUITOUS. ISOFORMS MDM2-A, -B, -C, -D A OF HUMAN CANCERS BUT ABSENT IN NORMAL
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                                                                                                                                                                                                                                                                                                                                                  There are no rest
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                                                                                                                                                                                                                                                                                                  http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDM2-ALPHA;
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                                                                                                                                                                                                                                                                                                                               Usage
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DOMAIN
                                                EMBL;
        Interpro; IPR002029; -
Pfam; PF00185; OTCace;
                                                                   use by non-profit institutions as lon-
modified and this statement is not remov-
entities requires a license agreement 'ss
or send an email to license@isb-sib.ch).
                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                               Gregor J., Davis N.W., Kirkpatrick H.A.,
Mau B., Shao Y.;
                                                                                                                                                                                                 Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                           EcoGene; EG13053;
                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
-!- SIMILARITY: SOME, TO ORNITHINE CARBAMOYLTRANSFERASE.
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                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
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Nuclear protein; Ligase; Ubiquitin conjugation alternative splicing; Zinc; Zinc-finger;
                                        EMBL;
                                                                                                                                                                                                                         MEDLINE=97426617; PubMed=9278503;
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                                      AE000370; AAC75908.1;
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Last sequence update)
Last annotation update)
PROTEIN IN KDUI-LYSS INTERGENIC
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Pred. No. 28;
'0; Mismatches
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NUCLEAR EXPORT SEQUENCE.
ARF BINDING.
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MDM2-D)
MDM2-C)
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                                                                            .isb-sib.ch/announce/
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                                                                                        and
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                                                                                                                       a collaboration -
MBL outstation -
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SEQUENCE

363

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    CARBOHYD
CARBOHYD
CARBOHYD
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P42702;
01-NOV-1995
                                        CARBOHYD
CARBOHYD
                                                                  DOMAIN
DISULFID
                                                                                            DOMAIN
TRANSMEM
                                                                                                                       SIGNAL CHAIN
                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                 Alternative
                                                                                                                                                           Receptor; Transmembrane; Glycoprotein; Immunoglobulin
                                                                                                                                                                        PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
                                                                                                                                                                                       Pfam; PF00041;
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                                                                                                                                                                                                                             MIM; 151443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gearing D.P., Thut C.J., Vandenbos T., Gimpel S.D., King J., Price V., Cosman D., Beckmann M.P.; "Leukemia inhibitory factor receptor is structurally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIFR.
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                               MEMBRANE-BOUND AND A SECRETED FORM.

ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND MAY ARISE BY ALTERNATIVE SPLICING.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY MITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS. SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. 10:2839-2848(1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X61615; CAA43805.1;
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16; Conserv
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1097
833
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143

    Last sequence update)
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    FACTOR RECEPTOR PRECURSOR (LIF-R).

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27.6%;
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

N-LINKED (GLCNAC...) (POTENTIAL).

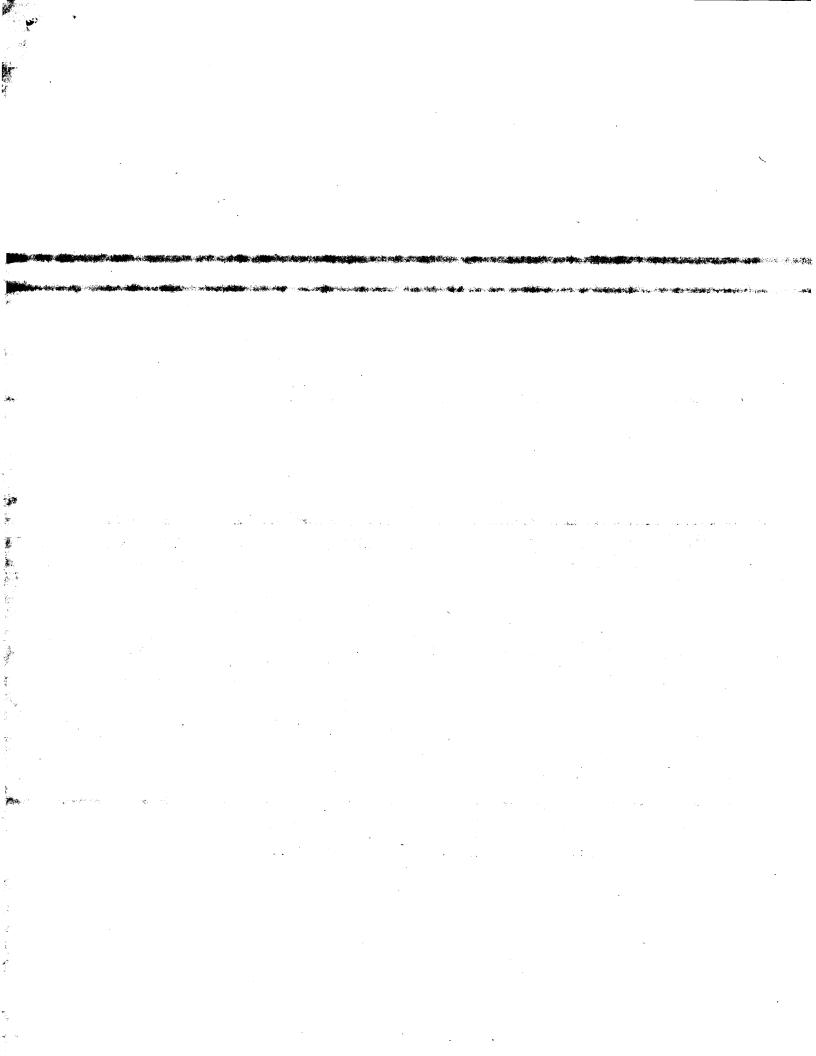
N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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Pred. No. 23;
10; Mismatches
                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                      LEUKEMIA INHIBITORY FACTOR RECEPTOR
                                                                                                                                  POTENTIAL.
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Best Local S
Matches 18
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             6 DLSDAEPDAGEATAYASKDLEEQLRSVSSVDE---LMTVLYPEYWKMYKCQLRKGGWQHN 62
                          l Similarity
18; Conser
                                                             243
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                           Conservative
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MW; C8602
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L1; Mismatches
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	O	· UT	4	ω	N	—	No.	Result
64	64	64	64	64.5	65	65	66	66	67	67	67	67.5	69	86	87	88	284	316	Score	
17.1	17.1	17.1	17.1	17.2	17.3	17.3	17.6	17.6	17.9	17.9	17.9	18.0	18.4	22.9	23.2	23.5	75.7	84.3	Match Length	% Query
1368	1367	926	284	4488	2408	1612	703	602	1299	453	453	347	786	358	354	326	418	420		
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O81809 arabidopsis			Q9v1q3 pyrococcus	Q9qzhl mus musculu	Q22184 caenorhabdi	Q9vyq2 drosophila	Q9kqz2 vibrio chol	Q9w397 drosophila	Q9steO brassica na	Q9jv08 neisseria m	Q9jzy9 neisseria m	Q9vmy5 drosophila	Q21027 caenorhabdi	P97946 mus musculu	O43915 homo sapien	O35251 rattus norv	057352 coturnix co	Q9xs50 bos taurus	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
60	60	60	60.5	61	61.5	61.5	61.5	62	62	62	62	62	62.5	62.5	62.5	63	63	63	63	63.5	63.5	63.5,	63.5	64	64
					16.4	16.4	16.4	16.5	16.5	16.5	16.5	16.5	16.7	16.7	16.7	16.8	16.8	. 16.8	16.8	16.9	16.9	16.9	16.9	17.1	17.1
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ALIGNMENTS

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33 FESGLGFSDTEPDAGENKAYAGKEMEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQ 92	B 2
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Query Match 84.3%; Score 316; DB 6; Length 420; Best Local Similarity 83.1%; Pred. No. 1.4e-27; Matches 59; Conservative 3; Mismatches 9; Indels 0; Gaps	~ = ~
CHAIN 21 420 VASCULAK ENDOTHELIAL GROWTH FACTOR C. SEQUENCE 420 AA: 46681 MW: 58BA84317A3C8E2D CRC64:	SO
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EMBL; AB004275; BAA77687.1;	DR
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nily.";	RT
Liu X., Yonekura H., Yamaqishi S., Yamamoto Y., Yamamoto H.;	RA
TISSUE-HEART;	RC
SEQUENCE FROM N.A.	RP
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NCBI_TaxID=9913;	0X
Bovidae; Bovinae; Bos.	8
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	8
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SEQUENCE
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01-JUN-1998
01-JUN-1998
01-MAR-2001
STRAIN-SPRAGUE DAWLEY;
MEDLINE=97349118; Pubm
Yamada Y., Nezu J., Sh
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                                                                 SEQUENCE FROM N.A
                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                            VEGF-D
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PRODOM; PD001629; -; 1.
PROSITE; PS00249; PDGE-1; 1.
PROSITE; PS50278; PDGF-2; 1.
SMART; SM00141; PDGF; 1.
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Alitalo K., Le Douarin N.M.;
"Avian VEGF-C: cloning, embryonic expression
of the differentiation of VEGFR2-expressing
                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2001 (TrEMBLrel. 16, VASCULAR ENDOTHELIAL GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Development 125:743-752(1998).
EMBL; Y15837; CAA75799.1; -.
HSSP; P15692; 1VPP.
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MEDLINE=98167900; PubMed=9435294;
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mes 53; Conser
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418 AA;
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                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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  PubMed=9205122;
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418
46839
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74.68;
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16,
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ta; Craniata; Vert
hae; Galliformes;
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Pred. No. 5.5e
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VASCULAR ENDOTHELIAL GROWTH FACTOR

; 099BFCC79151BF2B CRC64;
                                                                                                                       Craniata; Vertebrata; Sciurognathi; Muridae;
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    Hirata
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mes; Phasianidae; Phasianinae;
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                                                                                                                                               Euteleostomi;
                                                                                                                         Murinae;
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Best Local :
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O43915;
01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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                                                                   "Vascular endothelial growth factor D (VEGF-D) is a ligand for the tyrosine kinases VEGF receptor 2 (Fik1) and VEGF receptor 3 (Fit4)."; Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).

EMBL; V12864; CAA73371.1; -.

EMBL; V12865; CAA73371.1; JOINED.

EMBL; V12866; CAA73371.1; JOINED.

EMBL; V12867; CAA73371.1; JOINED.

EMBL; V12868; CAA73371.1; JOINED.

EMBL; V12869; CAA73371.1; JOINED.

EMBL; V12869; CAA73371.1; JOINED.

EMBL; V12869; CAA73371.1; JOINED.

EMBL; V12879; CAA73371.1; JOINED.
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MEDITINE=98140120; PubMed=9479493;

Rocchigiani M., Lestingi M., Luddi A., Orlandini M.,

Rossi E., Ballabio A., Zuffardi O., Oliviero S.;

"Human FIGF: cloning, gene structure, and mapping to

between the PIGA and the GRPR genes.";
                                                EMBL; Y12863; CAA73370.1;
HSSP; P15692; IVPP.
                                                                                                                                                                                                                                                                                                                                                                                                                     Achen M.G., Jeltsch M., K
Alitalo K., Stacker S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics
[3]
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Mammalia; Eutheria;
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Molecular cloning of a novel vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics
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HSSP; P15692; 1VPP
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Genomics 42:483-488(1997).
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  PF00341; PDGF;
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16; Conservative
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                             IPR000072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9435229;
ch M., Kukk E.,
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Primates;
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Best Local Similarity
                                                                                                                                                                                                                    Matches
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HSSP, B1562: 1VPP.
MGD; MGI:108037; Figf.
InterPro; IPR000072; -.
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; -; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
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01-MAY-1997
01-MAY-1997
01-MAR-2001
Q21027;
01-NOV-1996
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PROSITE; PS00249; PDGF_1;
PROSITE; PS50278; PDGF_2;
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97349118; PubMed=9205122;
Yamada Y., Nezu J., Shimane M., H
"Molecular cloning of a novel vas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ordandini M., Marconcini L., Ferruzzi R., "Identification of a c-fos-induced gene t platelet-derived growth factor/vascular e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
MEDLINE=97030254; PubMed=8876195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X99572; CAA67892.1;
EMBL; D89628; BAA14002.1;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics
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                                                                                                                                                                          EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR 71
                                                                                                                                       EQQIRAASSLEELLQIAHSEDWKLWRCRLKL-----KSLASMDSR
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                                                                                                                                                                                                                                                                                                                     SM00141; PDGF;
CE 358 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR FIGF
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7 (TrEMBLrel.
1 (TrEMBLrel.
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(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acad. Sci.
                                                                                                                                                                                                                    Conservative
                                       PRELIMINARY;
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Rodentia;
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Created)
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                                       PRT;
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Sciurognathi; Muridae;
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0.095;
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                                                                                                                                                                                                                                                       Length 358;
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; Murinae; Mus
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Best Local S
Matches 18
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Q9VMY5;
Q1-MAY-2000
Q1-MAY-2000
Q1-MAY-2000
           Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Mahril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                  Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyo
                                                                                                                                                                                                                                                                           CG12582 PROTEIN CG12582.
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"2.2 M
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson
Craxton M., Dear S., Du Z., Durbin R., Favel I.O A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                                                               STRAIN-BERKELEY;
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U41994; AAA83456.1; -.
Interpro; IPRO00436; -.
SMART; SM00032; CCP; 1.
SEQUENCE 786 AA; 79211 MW;
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Eukaryota; Metazoa; Nemat.
Rhabditidae; Peloderinae;
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                                                                                                                            MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
18; Conser
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rinae; Caenorhabditis.
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RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Carry N.S., Gelbart W.M., Glasser K.,

RA Dodson K., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Mount S.M., Mattei B., McIntosh T.C., McLeod M.P., McPherson D. L.,

RA Mount S.M., Welson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Menszolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Wang A.H., Wang X.,

RA Yelson K.H., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Yeh R.-, Shori B., Walley R., Shon W., Zhon W., Shith H.O.,

"The genome sequence of Drosophila melanogaster.";

DR MILL Shit M. S
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Best Local Similarity
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Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E. Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B stra
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01-OCT-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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01-OCT-2000
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STRAIN-MC58 / SEROGROUP B;
MEDLINE-20175755; PubMed-10710307;
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Bacteria; Proteobacteria;
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347 AA; 39271 MW;
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Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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ia; beta subdivision;
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      serogroup B strain
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Best Local
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Q9JV08;
01-OCT-2000
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01-MAR-2001
                                                                                                                                                                                                                                                                                               Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.";
                                                                                                                                                                               PROSITE; PS00036; BZIP_BASIC; UNKNOWN_1.
Transferase; Nucleotidyltransferase.
SEQUENCE 453 AA; 51719 MW; FCBB4E93F
                                                                                                                                                                                                                                                  menigitidis Z2491.";
Nature 404:502-506(2000).
EMBL; AL162755; CAB84318.1;
Interpro; IPR001871; -.
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; PubMed=10761919;
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InterPro; IPR002646; -.
Pfam; PF01743; Po174, Po1; 1.
PROSITE; PS00036; BZIP_BASIC;
SEQUENCE 453 AA; 51654 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=65699;
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EMBL; AE002437; AAF41254.1;
                                                                                                                                                                                                                                        InterPro;
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312 HWKSNLQQG 320
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                          49
                                                                                                                         Local
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                          MYKCQLRKG
                                                      NGFDIPDDIHPLLNALRVSDGIAGKMTVLALKNTDERLRADKSVSVGFVLAALMWPELER 311
                                                                                 SGLDLSD-----
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19; Conser
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19; Conser
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                                                                    ----AEPDAGEATAYASKDLEEQLRSVSSVD---ELMTVLYPEYWK 48
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                                                                                                             16;
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                                                                                                          Score 67; DB:
Pred. No. 17;
16; Mismatches
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Last annotation update)
(EC 2.7.7.19).
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Pred. No. 1
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RESULT Q9STE0

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RESULT
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Best Local Similarity 41.9
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Interpro; IPRO01245; -.
Interpro; IPRO01245; -.
Interpro; IPRO01299; -.
Interpro; IPRO02299; -.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00118; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                          Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wahl J.F., Agbayani A., An H.-J., Andrews-Pfeinkoch C., Baldwin D., Rallow B. W. Bazun B. Barndon R. Andrews-Pfeinkoch C., Baldwin D., Rallow B. W. Bazun B. Bazun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1117
                       Ballew R.M.,
Beeson K.Y.,
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TremBLrel.
01-MAR-2001 (TremBLrel.
CG7246 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9W397;
                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9W397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES. EMBL; AJZ38845; CAB54520.1; -. HSSP; Q00534; 1BI7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica napus (Rape).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sg
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AtMAP3Kepsilon1 gene.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAP3K EPSILON 1 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jouannic S., Tregear J.W., Kreis "Characterisation of a B. napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AHASRNSREQLRSHGGLDVYLSLLDDEYWSV 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYASKDLEEQLRSVSSVDELMTVLYPEYWKM 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPAS; TISSUE=MICROSPORE-DERIVED EMBRYOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
Basu A., Baxendale J., Bayraktaroglu L., Beasley
Benos P.V., Berman B.P., Bhandari D., Bolshakov S
Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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41.9%;
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16,
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13, Last sequence update)
16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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highly similar to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602
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61;
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                                                                                                                                                                                                                                                                                                                                                            Hexapoda; Insecta;
a; Brachycera; Musco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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e; eurosids II;
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                                            E.M.,
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
A Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.";
EMBL; AE003446; AAF46437.1; -.
EMBL; AE003446; AAF46437.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
                                                                                                         SEQUENCE FROM N.A.

SEROTYPE 01;
STRAIN-EL TOR N19961 / SEROTYPE 01;
STRAIN-EL TOR N19961 / SEROTYPE 01;
MEDLINE-20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwir Heidelberg J.F., Lisen J.A., Nelson W.C., Peterson J.D., Umayam. Dodson R.J., Nelson K.E., Read T.D., Tettelin H., Richardson Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Wekalanos J.J., Ve
                                                                                                                                                                                                                                                                                                                                                                09KQZ2;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
ATP-DEPENDENT HELICASE, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Li X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
                                                                                                McDonald L., Utterback T., Salzberg S.L., Smith H.O., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischma Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                             Nature 406:477-483(2000).
EMBL; AE004261; AAF95003.1;
                                                                   cholerae
                                                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                               Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9KQZ2
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InterPro;
                                                                                  "DNA sequence of both
                                                                                                                                                                                                                                                                                              NCBI_TaxID=666;
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Cherry J.M., Cawley
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17; Conser
IPR001989;
                                                                                                                                                                                                                                                                                                              Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAT;
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31.5%;
                                                                                  chromosomes
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15, I
16, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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Last annotation updat
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                   of
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                                                                                   the
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                                                                                  cholera
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Dew I., Dietz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 602;
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                                                                                  pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                    Umayam L.A.,
hardson D.,
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                                                                                                                    Venter J.C.,
                                                                                  Vibrio
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RX MEDILINE-20195005; pubMed=10731132;
RX MEDILINE-20195005; pubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.G., Champe M., Pfeiffer B.D., RA Man H. J., Zhang Q., Chen L.X., RA Man H. J., Zhang Q., Chen L.X., RA Man H. J., Andrews-Pfannkoch C., Baidwin D., RA Man H. J., Andrews-Pfannkoch C., Baidwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Bolchan M.A., Butler H., Cadieu E., Center A., Chandra I., Chertis R.C., Benos P.V., Berman B.P., Bhandari D., Bolshakov S. M., Poulle J. B., Davies P., Bhandari D., Bolshakov S. G., Dunn P., Ra Gerbal S., Davies P., Barris R., Chandra I., Dev I., Dietz S.M., Poulle J. B., Davies P., Bhandari D., Bolshakov S. G., Dunn P., Ra Gerbal S., Davies P., Barris R., Chandra I., Partiera S., Davies P., Man Gerbal S., Pan S., Gebart M.M., Harris M., Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang D., Li Z., Liang D., Li Z., Liang D., Li Z., Liang D., Man Gerbal S., Pan S., 
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Q9VYQ2
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Best Local
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01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD004758; -; Helicase. SEQUENCE 703 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG2779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VYQ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       514 EMEPQAEGYTAYLAKKVLCYLQA----DKANLVLFASYWQMREVAESLKVEFTKRGW 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 DAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKM-----YKCQLRKGGW 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN
 FBgn0030371;
1612 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78488 MW;
CG2779.
149407 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.6%;
31.6%;
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16,
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
D73877D13EF5F24C CRC64;
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38;
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Q9QZH1 Q9QZH1; 01-MAY-2000 01-MAY-2000

(TrEMBLrel. PRELIMINARY;

13, 13,

Created)
Last sequence update)

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RESULT
Q9QZH1
ID Q9Q
AC Q9Q
DT 01-
DT 01-
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Best Local
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Q22184;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-OCT-2000 (TrEMBLrel. 1
                                                                                                       1590
                                                                                                                                                        1530
                                                                                                                                                                                                                                                                                                                                                                                                 Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., D. Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen i
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                       InterPro; IPR002106; -.

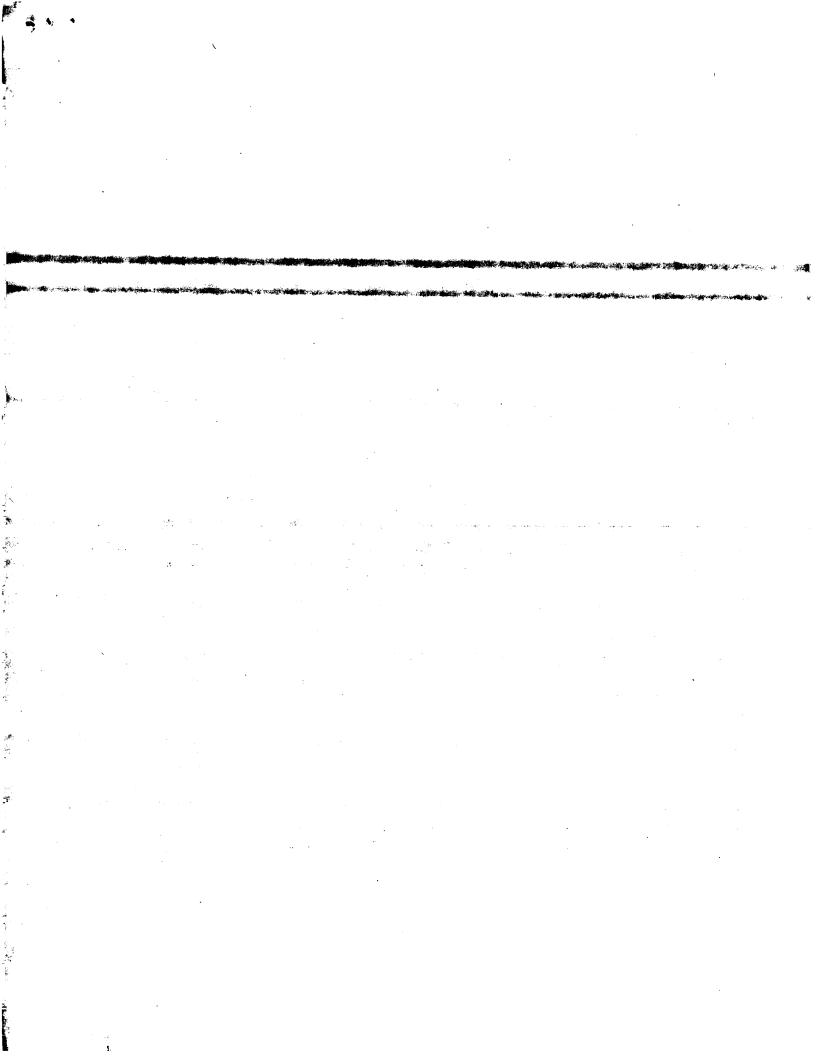
Pfam; PF00665; rve; 1.

PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.

PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.

SEQUIENCE 2408 AA; 269763 MW; 6C9542F1FA80AC09
                                                                                                                                                                                                                                                                                                                                       Nature 368:32-38(1994).
EMBL; 268219; CAA92477.1;
InterPro; IPR001584; -.
InterPro; IPR001969; -.
                                                                                                                                                                                                                                                                                                                                                                                            elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lloyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1530 DDEPSSKEKKQYV-KDLIKKLKKGDECDE--DDVYPDVRDCRKYYRCEVKKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID≗6239;
                                                                                                                    47 WKMYKCQLRKG--GWQHNR-EQANLN
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                                                                                                     QKSFACRSRKNKRAWVHNRVEQYNEN
                                                                                                                                                      TDASQDIYAAAAYAHFKYESWAPVTRLIASKNKIKETSVTNYTIPKLELLGILRTSRPTF 1589
                                                                                                                                                                               SDAEPDAGEATAYASKDLE------EQLRSVSSVD-----ELMTVL---YPEY
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                                                                                                                                                                                                          25; Conserv
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                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peloderinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
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                                                                                                                                                                                                                      17.38;
29.18;
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01,
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Pred.
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Pred.
                                                                                                     1615
                                                                                                                                                                                                                                                                      UNKNOWN_1.
6C9542F1FA80AC09 CRC64;
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nes 27;
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Search completed: October 17, 2001, ^{\cdot} 14:50:55 Job time: 421 sec
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Best Local Similarity 26.7%; Pr
Matches 24; Conservative 11;
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InterPro: IPR001680; -.
InterPro: IPR001993; -.
InterPro: IPR001993; -.
InterPro: IPR001993; -.
InterPro: IPR001993; -.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
PROSITE; PS00639; THIOL_PROTEASE,HIS; UNKNOWN_1.
PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
SMART; SM00302; AAA; 1.
SMART; SM00302; AAA; 1.
SMART; SM00302; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SUPP D.M., Brueckner M., Kuehn M.R., Witte D.P., Lowe L.A.,
McGrath J., Corrales J.M., Potter S.S.;
"Targeted deletion of the ATP binding domain of left-right dynein confirms its role in specifying development of left-right
                                                                                        1313 VIIYVRRSIDNWTETQWRQINVEQMDLELR 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asymmetries.";
Development 0:0-0(1999).
EMBL; AF183144; AAF07922.1; -.
MGD; MGI:1100864; Dnahc11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                             1263 LDKANQELEA------LEEEMEQMQNSARLFEVALPEYKQMKQCRQEIRLLKGLWD 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Last annotation update) LEFT-RIGHT DYNEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNAHC11 OR LRD.
                                                                                                             60 -----QHNREQANLNSR 71
                                                                                                                                                                                  5 LDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKC----QLRKGGW- 59
                                                                                                                                                                                                                                  Score 64.5; DB 11;
Pred. No. 5.1e+02;
1; Mismatches 22;
                                                                                                                                                                                                                                                                                                                             1C5E0050928D949A CRC64;
                                                                                                                                                                                                                                                                       Length 4488;
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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                         Score
                                        seq length: 0 seq length: 2000000000
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1: /SIDS8/gcgdata,
2: /SIDS8/gcgdata,
3: /SIDS8/gcgdata,
4: /SIDS8/gcgdata,
5: /SIDS8/gcgdata,
6: /SIDS8/gcgdata
6: /SIDS8/gcgdata
7: /SIDS8/gcgdata
8: /SIDS8/gcgdata
11: /SIDS8/gcgdata
11: /SIDS8/gcgdat
11: /SIDSB/gcgdat
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1218
1 CMSKLDVYROVHOTTON--
                                                                                                                                                                                                                                                                                                                                                                                                                                         1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT: *
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT: *
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT: *
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT: *
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT: *
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7: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT: *
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Listing first 45 summaries
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                                                                                                                                                                                                                                                         Length DB
                      292
297
302
307
318
318
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ALIGNMENTS

RESULT AAW86225

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AAW86225 standard; protein;

292 AA

Human VEGF-C truncated fragment 4.

16-FEB-1999 AAW86225;

(first entry)

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VEGF; VRP; vascular endothelial growth factor; VEGF-related protein; recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia; coronary; collateral vessel development; cell growth; migration; heart; lower limb ischaemia; stroke; peripheral vascular disease; intestine; wound healing; skin; vascular permeability.
WPI; 1999-009426/01.
                                                                                            20-APR-1998;
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                                                                                                                                            W09849300-A2
                                                                                                                                                                   Homo sapiens.
                                              (COLL-) COLLATERAL THERAPEUTICS.
                                                                     25-APR-1997;
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AAW75740

New truncated vascular endothelial growth factor-related protein subunits - lack part of the N-terminal sequence, used to stimulate

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                                      25-APR-1997;
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                                                       98WO-US07801
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                                                                                                                                                                                                                                                                                  VEGF; VRP; vascular endothelial growth factor; VEGF-related protein; recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia; coronary; collateral vessel development; cell growth; migration; heart; lower limb ischaemia; stroke; peripheral vascular disease; intestine; wound healing; skin; vascular permeability.
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20-APR-1998; 05-NOV-1998

98WO-US07801.

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                                                    sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rqkacepgfsyseevcrcvpsywkrpqms 302
                                                                                                               healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209;
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                                                                                                         nt; truncated; gene therapy; angiogenesis; cardiac ischa collateral vessel development; cell growth; migration; b ischaemia; stroke; peribheral vascular disease; intest ling; skin; vascular permeability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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Pred. No. 4.4e-90;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209
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                                                                                                                                                                                                   protein;
ischaemia;
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WO9849300-A2

Homo sapiens

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Best Local
                                                 Growth factor; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acids encoding the truncated VRP subunits are used to produce the truncated proteins recombinantly. The truncated VRP subunits, optionally expressed from gene therapy vectors, have in vivo and in vitro angiogenic activity and are used to stimulate angiogenesis, particularly coronary collateral vessel development in cases of cardiac ischaemia; to stimulate endothelial cell growth and migration in vitro; to treat teart disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic lower limb ischaemia; stroke and peripheral vascular disease); to promote healing of wounds (of skin or intestines), and to increase vascular permeability. Sequences AAW86222 to AAW86225 represent truncated
                                 pharmaceutical
                                                                                                                  14-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor (VEGF)-related protein) subunits that have at least one amino acid N-terminal to the first Cys of the core sequence deleted. Host cells transformed or transfected with expression vectors containing
                                                                                                                                                                                   AAY08284 standard; Protein; 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New truncated vascular endothelial growth factor-related protein subunits - lack part of the N-terminal sequence, used to stimulate anglogenesis, e.g. for treating heart disease and ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 permeability. Sequences fragments of VEGF-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Fig 2D; 113pp; English.
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                                                                                                                                                                                                                                                                                        RQKACEPGFSYSEEVCRCVPSYWKRPQMS 209
                                                                                                                                                                                                                                                                                                                                                         NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN
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                                                                                                                                                                                                                                                                                                                                                                                                        dstdgfhdicgpnkeldeetcqcvcraglrpascgphkeldrnscqcvcknklfpsqcga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cmskldvyrqvhsiirrslpatlpqcqaanktcptnymwnnhicrclaqedfmfssdagd
                                                                               growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1218; DB 20; Length 307; ilarity 100.0%; Pred. No. 4.5e-90; Conservative 0; Mismatches 0; Indels 0;
                                                                               factor protein
                                                                                                                (first entry)
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                                                 dimer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to truncated VRP (vascular endothelial
                                                                               fragment VEGF-C
                                               cysteine knot; cellular inclusion
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                                               body;
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                                                                      VEGF; VRP; vascular endothelial growth factor; VEGF-related protein; recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia; coronary; collateral vessel development; cell growth; migration; heart; lower limb ischaemia; stroke; peripheral vascular disease; intestine; wound healing; skin; vascular permeability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes the novel preparation of biologically active dimers of recombinant human growth factors of the cysteine knot family starting from cellular inclusion bodies. Such dimers are are useful in pharmaceutical compositions and the method provides yields of 31-39.7%, in examples, compared with about 10% for the conventional method (see Biochemistry, 28 (1989) 2956). AAY08278-Y08301 are human growth factor
05-NOV-1998
                         WO9849300-A2
                                                 Homo sapiens
                                                                                                                                                   Human VEGF-C full length sequence
                                                                                                                                                                               16-FEB-1999
                                                                                                                                                                                                                              AAW86237 standard; protein; 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein fragments used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preparing active growth factor dimers yield
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                                                                                                                                                                                                                                                                                                                                                                                                 dstdgfhdicgpnkeldeetcqcvcraglrpascgphkeldrnscqcvcknklfpsqcga
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                                                                                                                                                                                                                                                                                               rqkacepgfsyseevcrcvpsywkrpqms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 AA;
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                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1218;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to truncated VRP (vascular endothelial growth CC factor (VEGF) related protein) subunits that have at least one amino CC acid N-terminal to the first Cys of the core sequence deleted. Host CC cells transformed or transfected with expression vectors containing CC nucleic acids encoding the truncated VRP subunits are used to produce CC the truncated proteins recombinantly. The truncated VRP subunits, CC optionally expressed from gene therapy vectors, have in vivo and in vitro CC angiogenic activity and are used to stimulate angiogenesis, particularly CC coronary collateral vessel development in cases of cardiac ischaemia; to CC simulate endothelial cell growth and migration in vitro; to treat heart CC lower limb ischaemia; stroke and peripheral vascular disease); to promote CC healing of wounds (of skin or intestines), and to increase vascular CC permeability. Sequences AAW86234 to AAW86239 represent full length VRP CC sequences from which the truncated fragments are created.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 209; Conser
                                                                                                                                                        13-JAN-1998
                                                                                                                                                                                           AAW17837;
                                                                                Foetal liver kinase 1 binding protein; human; flk-lbp;
                                                                                                                                                                                                                               AAW17837 standard; Protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                    371
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                                                                                                                                                                                                                                                                                                                                                                                                          healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                 foetal liver kinase A binding protein
                                                                   tyrosine kinase; vasculogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 2D; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 AA;
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                                                                                                                                                      (first entry)
                                                 tumour; therapy;
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                                                 antagonist;
                                                                  angiogenesis;
                                                                                                                   flk-1bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                             180
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Homo sapiens

AAW00932 standard; Protein;

419

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                                                                                                                                                                                                                                                                                                                  This polypeptide comprises a human foetal liver kinase 1 binding protein (flk lbp) (see AAW1837) that binds to the receptor tyrosine kinase flk1 expressed on vascular endothelial and other cells. The mature flk1-bp can be secreted from host cells transformed with an expression vector including an isolated flk-lbp cDNA clone (see AAT68811). Flk-lbp can be used to isolate cells to which it binds, for use in studying the roles of such cells and of flk-l in vasculogenesis and angiogenesis. Angiogenesis inhibition or increased vascularisation may be clinically desirable (e.g. to suppress solid tumour growth or in wound healing, respectively). The flk-lbp can be administered to treat conditions with defective or insufficient flk-l. Polypeptides may also act as carriers to deliver diagnostic/therapeutic agents to cells to which flk1-bp binds, to generate antibodies, and to identify flk-lbp antagonists
                                                                                                                                                                                                               Query Match
Best Local S
Matches 209
                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding a human foetal liver kinase 1 binding protein to treat conditions with insufficient protein, deliver agen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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  391
                           181
                                                      331
                                                                              121
                                                                                                          271
                                                                                                                                                                                                               hes 209;
                                                                                                                                                             211
                                                                                                                                   61
                                                nrefdentcqcvckrtcprnqplnpgkcacectespqkcllkgkkfhhqtcscyrrpctn
                                                                                                                                                                       CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1997-281031/25
DB; AAT68811.
                                                                 NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN
                                                                                                                                DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGA 120
rqkacepgfsyseevcrcvpsywkrpqms
            RQKACEPGFSYSEEVCRCVPSYWKRPQMS
                                                                                                       dstdgfhdicgpnkeldeetcqcvcraglrpascgphkel
                                                                                                                                                          cmskldvyrqvhsiirrslpatlpqcqaanktcptnymwnnhicrclaqedfmfssdagd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1,
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 30-32; 43pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identify antagonists to treat protein-mediated conditions
                                                                                                                                                                                                                                                                                  419
                                                                                                                                                                                                                                                                                                          treating
                                                                                                                                                                                                                  Conservative
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/note= "(Claim 10)"
21..35
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21..419
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                                                                                                                                                                                                                                                                                                         flk-1bp mediated conditions.
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RESULT AAW00932

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The polypeptide, or

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28-JUN-1996;
01-AUG-1995;
12-JAN-1996;
14-FEB-1996;
     This polypeptide comprises the pre-pro sequence of human VEGF-C, a novel ligand that binds specifically to human Flt4 receptor tyrosine kinase (VEGFR-3), stimulating phosphorylation of the receptor. Its sequence was deduced from a cDNA clone (AAT84276) obtd. from a PC-3 prostatic adenocarcinoma cell (ATCC CRL 1435)
                                                                                           Flt4 receptor tyrosine kinase ligand and related nucleic acid to modulate growth of endothelial cells and for diagnosis of endothelial cell diseases
                                                                       Claim 7;
                                                                                                                                                                                                                                                                     01-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vascular endothelial growth factor receptor-3; ligand;
anglogenesis; wound healing; lymph vessel; lymphangioma;
cancer; metastasis; therapy; diagnosis; antibody; inhibi
                                                                                                                                      N-PSDB; AAT84276
                                                                                                                                                                      Alitalo
                                                                                                                                                                                           (UYHE-) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGF-C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Flt4 receptor tyrosine kinase ligand VEGF-C.
                                      nis polypeptide
novel ligand ++
                                                                                                                                                 1997-145688/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F1t4;
                                                                      Page 112-113; 183pp; English.
                                                                                                                                                                      Joukov V;
                                                                                                                                                                                           HELSINKI LICENSING
                                                                                                                                                                                                              96US-0671573.
95US-0510133.
96US-0585895.
96US-0601132.
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                                                                                                                                                                                                                                                                     96WO-FI00427
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32..227
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retaining Flt4 ligand activity (Claim
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Flt4 ligand activity (Claim
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Flt4 ligand
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RESULT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed in transformed or transfected host cells for use in claimed methods for detecting endothelial cells (e.g. to image lymphatic vessels, endothelial venules, Flt4 receptor in histochemical tissue) and also to modulate the growth of mammalian endothelial cells (e.g. to accelerate angiogenesis and to promote endothelial function of lymphatic vessels). Inhibitors of VEGF-C, such as antibodies, can be used to control endothelial cell proliferation, e.g. lymphangioma or metastatic cancer. Mouse and quail VEGF-C sequences (see AAM00934-35) have also been
                                                                                                                                                                                                                                                                                       Vascular endothelial growth factor-releated protein; VRP; VEGF; receptor protein tyrosine kinase; Flt4; signal transduction; wound healing; vulnerary; rheumatoid arthritis; Kaposi's sarcoma;
          Lee J,
                                 (GETH ) GENENTECH INC
                                                        08-SEP-1995;
                                                                              30-AUG-1996;
                                                                                                      13-MAR-1997.
                                                                                                                             WO9709427-A1
                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                               therapy;
                                                                                                                                                                                                                                                                                                                                      Human vascular endothelial growth factor-related protein VRP
                                                                                                                                                                                                                                                                                                                                                            05-JUN-1997 · (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             AAW13833 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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         Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                               diagnosis; angiogenesis; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 AA;
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                                                        95US-0003491
                                                                              96WO-US14075
                                                                                                                                                                                                      1..20
/label Sig_peptide
                                                                                                                                                                                                 20..419
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                               /note=
                                                                                                                                                                                    /label= Mat_protein
                                                                                                                                                              "deduced residue from
                                                                                                                                                   tyrosine"
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6e-90;
                                                                                                                                                             nucleotide sequence
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AAW75751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A human vascular endothelial growth factor (VEGF)-related protein (VRP) (ARMI383) has been identified that binds to, and stimulates the phosphorylation of, the receptor tyrosine kinase FI14. It is postulated to be a third member of the VEGF protein family. Its amino acid sequence was deduced from a cDNA clone (ART59229) obtd. from a glioma G61 library. Recombinant VRF can be produced in transformed host cells and used: to promote growth of vascular and lymph endothelial cells; to stimulate phosphorylation of the tyrosine kinase domain of a FI14 receptor; as a diagnostic; as an additive to cell cultures; to screen for (ant)agonists: and to raise monoclonal antibodies used to treat conditions associated with excessive neovascularisation or vascular permeability. VRP may make it possible to avoid coronary by-pass surgery by stimulating growth of the collateral circulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 209;
                                                                                                                                        Synthetic
                                                                                                                                                                              Flt4; vascular endothelial growth factor C; vascular endothelial cell; pymphatic endothelial cell; myelopoiesis; angiogeneses; inflammation;
                                                                                                                                                                                                                                                     14-DEC-1998 (first entry)
                                         W09833917-A1
                                                                                               Modified-site
                                                                                                                                                                                                                         Vascular endothelial growth factor C protein analogue.
                                                                                                                                                                                                                                                                                  AAW75751;
                                                                                                                                                                                                                                                                                                              AAW75751 standard; Protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sarcoma etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein similar to vascular endothelial growth to treat e.g. wounds, tumours, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-192902/17
N-PSDB; AAT59929.
                                                                                                                                                                    lymphangiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                   391
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                                                                                               Location/Qualifiers 156
                                                                                  /note=
                                                                                                                                                                     oedema;
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                                                                               "Xaa
                                                                                                                                                                    ; myelopoiesis; angiogeneses; inf
elephantiasis; Milroy's disease.
                                                                  can be anything be nothing"
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                                                                                cysteine,
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06-AUG-1998

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AC AAW7
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DT 20-N
DT U0-N
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DE Huma
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KW F1t4
KW Lymp
KW Lymp
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The vascular endothelial growth factor C (VEGF-C) polypeptides have activities affecting growth and migration of vascular endothelial cells, promoting growth of lymphatic endothelial cells and lymphatic vessels, increasing vascular permeability, and affecting myelopoissis. The products can be used for stimulating angiogenesis, for inhibiting angiogenesis, for stimulating lymphangiogenesis, treatment or prevention of inflammation, oedemma, elephantiasis, or Milroy's disease. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating the growth of endothelial cells. They can also be used for middlate lymphocyte production and maturation, and to promote or inhibit trafficking of leucocytes between tissues and lymphatic vessels or to affect migration in and out of the thymus.
                                                                                                                                                              Human vascular
                                                                                                                                                                                                                                                                      AAW75740 standard;
                                                    Homo sapiens
                                                                                                         Flt4; vascular endothelial growth factor C; vascular endothelial cell;
lymphatic endothelial cell; myelopoiesis; angiogeneses; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                     lymphatic endothel
lymphangiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 35; Page 143-145; 177pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING
                                                                                                                                                                                                                                                                                                                                                                 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 100.0%;
Similarity 100.0%;
109; Conservative 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Joukov V;
                                                                                                                                                                                                (first entry)
                                                                                                                                                            endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US01973
                                                                                        oedema;
                                                                                                                                                                                                                                                                          Protein;
                                                                                      ; myelopoiesis;
elephantiasis;
                                                                                                                                                          growth factor C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTD.
                                                                                     angiogeneses;
Milroy's dise
                                                                                                                                                            protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                       inflammation;
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      AAW86203
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The vascular endothelial growth factor C (VEGF-C) polypeptides have activities affecting growth and migration of vascular endothelial cells, promoting growth of lymphatic endothelial cells and lymphatic vessels, increasing vascular permeability, and affecting myelopoiesis. The products can be used for stimulating angiogeneses, for inhibiting angiogenesis, for stimulating lymphangiogenesis, treatment or prevention of inflammation, oedema, elephantiasis, or Milroy's disease. They can also be used to modulate myelopoiesis, e.g. treating granulocytopenia.
VEGF; VRP; vascular endothelial growth factor; VEGF-related protein; recombinant; truncated; gene therapy; anglogenesis; cardiac ischaemia; coronary; collateral vessel development; cell growth; migration; heart; lower limb ischaemia; stroke; peripheral vascular disease; intestine; wound healing; skin; vascular permeability.
                                                                                                                                                                                                 AAW86203 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                               Human vascular endothelial growth factor (VEGF)-C sequence
                                                                                                                                   16-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated vascular endothelial growth factor polypeptide(s) used to develop products for treating, e.g. cancers, inflammatioedema, granulocytopenia or for wound healing or tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING LTD
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                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y can also be used for modulating the growth of endothelial cells.
y can also be used to stimulate lymphocyte production and maturation,
to promote or inhibit trafficking of leucocytes between tissues and
phatic vessels or to affect migration in and out of the thymus.
                                                                                                                                                                                                                                                                                                             RQKACEPGFSYSEEVCRCVPSYWKRPQMS 209
                                                                                                                                                                                                                                                                                                                                                          /NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN 180
                                                                                                                                                                                                                                                                             rqkacepgfsyseevcrcvpsywkrpqms 419
                                                                                                                                                                                                                                                                                                                                           nrefdentcqcvckrtcprnqplnpgkcacectespqkcllkgkkfhhqtcscyrrpctn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 112-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1218; ilarity 100.0%; Pred. No. 6e Conservative 0; Mismatches
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                                                                                                                               (first entry)
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                                                                                                                                                                                               protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6e-90;
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Best Local Sim
Matches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transformed or transfected with expression vectors containing nucleic acids encoding the truncated VRP subunits are used to produce the truncated proteins recombinantly. The truncated VRP subunits, optionally expressed from gene therapy vectors, have in vivo and in vitro angiogenic activity and are used to stimulate angiogenesis, particularly coronary collateral vessel development in cases of cardiac ischaemia; to stimulate endothelial cell growth and migration in vitro; to treat heart disease; to treat ischaemia (e.g.cardiac, chronic coronary or chronic lower limb ischaemia; stroke and peripheral vascular disease); to promote healing of wounds (of skin or intestines), and to increase vascular permeability.
Human VEGC protein.
                               19-JAN-2001
                                                                                              AAB10648 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This represents the amino acid sequence of human vascular endothelial growth factor (VEGF)-C protein. The invention provides truncated VRF (VEGF-related protein) subunits that have at least one amino acid N-terminal to the first Cys of the core sequence deleted. Host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiogenesis, e.g. for treating heart disease and ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New truncated vascular endothelial growth factor-related protein subunits - lack part of the N-terminal sequence, used to stimulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-009426/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                       CMSKLDYYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD 60
                                                                                                                                                                         RQKACEPGFSYSEEVCRCVPSYWKRPQMS 209
                                                                                                                                                                                                                                                                                                                                                                      cmskldvyrqvhsiirrslpatlpqcqaanktcptnymwnnhicrclaqedfmfssdagd 270
                                                                                                                                                                                                                                         nrefdentcqcvckrtcprnqplnpgkcacectespqkcllkgkkfhhqtcscyrrpctn
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                         (first entry)
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Pred. No. 6e-90;
Mismatches 0;
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vascular endothelial growth factor; human; vulnerary; cytostatic;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel vascular endothelial growth factor X CC (PEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has CC vulnerary, cytostatic, antirheumatic, antiatritritic, antipsoriatic and CC antidiabetic activity and acts as an angiogenesis and vascularization CC regulator. An antisense molecule of the invention is useful for treating CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic certinopathy by inhibiting angiogenic activity or inappropriate CC vascularization including formation and proliferation of new blood concerts, growth and development of tissues, tissue regeneration and organ CC and tissue repair in a subject. The products of the invention are useful CC for preparing medicaments for treating wounds such as dermal ulcers, comparing treating treating wounds such as dermal ulcers, comparing treating treat
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 209
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18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gordon RD, :
Dhanaraj SN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue repeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth; VEGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 11; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-442669/38.
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                                                                                                                                                                                     DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGA 120
                                                                                        RQKACEPGFSYSEEVCRCVPSYWKRPQMS 209
rqkacepgfsyseevcrcvpsywkrpqms 419
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, Xu J;
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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99US-0124967.
99US-0164131.
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100.0%; Pred. No. 6e
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                      6e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Length 419;
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                                                                                                                                                                                                                                                                                                           The present sequence is the protein sequence for the human vascular endothelial growth factor C (PEGF-C). It was used to demonstrate the methods of the invention, which involve the screening of individuals to determine which vascular endothelial growth factor receptor 3 (VEGFR-3, also known as Flt4 or fms-like tyrosine kinase 4) alleles they possess and thus their likelihood of developing hareditary lymphoedema. Conditions associated with lymphoedema include Milroy-Nonne syndrome, which is early onset lymphoedema and lymphoedema praecox, which is late
                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening a human subject for increased risk of developing a lymphatic disorder, comprises assaying a nucleic acid to determine a mutation altering the sequence of a vascular endothelial growth factor receptor-3 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LUDW-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vascular endothelial growth factor receptor 3; VEGF Milroy-Nonne syndrome; lymphoedema praecox; VEGF-C; vascular endothelial growth factor C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYPI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Flt4;
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  391
                           181
                                                    331
                                                                             121
                                                                                                       271
                                                                                                                                                         211
                                                                                                                               61
                                                                                                                                                                    1 CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD 60
                                                                                                                   DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGA 120
rqkacepgfsyseevcrcvpsywkrpqms
                         RQKACEPGFSYSEEVCRCVPSYWKRPQMS
                                                                         NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN
                                                                                                    \tt dstdgfhdlcgpnkeldeetcqcvcraglrpascgphkeldrnscqcvcknklfpsqcga
                                                                                                                                                       cmskldvyrqvhsiirrslpatlpqcqaanktcptnymwnnhicrclaqedfmfssdagd 270
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UNIV HELSINKI LICENSING
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                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                           Conservative
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Pred. No. 66
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ΧX

such as breast care and sarcomas. Flt4

carcinomas,

squamous cell carcinomas,

lymphomas, melanomas

receptor

tyrosine

kinase

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RESULT 1
AAY70749
ID AAY7
The patent discloses a method to treat neoplastic disease characterised by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also referred as vascular endothelial growth factor receptor-3, VEGFR-3) in endothelial cells of blood vessels adjacent to malignant neoplasm. The method involves administering a compound that inhibits binding of a ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular endothelial cells. The compound is useful for treating neoplastic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4; VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35; cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis; neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma; sarcoma; malignancy; VEGF-C; vascular endothelial growth factor C.
                                                                                                                                                                                                                                                                                                                  Treating neoplastic diseases such as lymphoma, carcinomas, melanomas and sarcomas, involves administering a compound capable of inhibiting binding of ligand proteins to fms-like tyrosine kinase-4 receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-317850/27
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                                                                                                                                                                                                                                                        15-17; Page 140-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaipainen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HELSINKI LICENSING LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= C-terminal_peptide.
/note= "Has a pattern of spaced cysteine residues
/note= "Has a pattern of spaced cysteine (BR3P) sequence;
reminiscent of a Balbiani ring 3 protein (BR3P) sequence;
cleavage of signal peptide and the C-terminal
peptide produces a partially processed form of VEGF-C of
about 29 kD which has high affinity to Flt4 (VEGFR-3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at position 156 i
165 is essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- "cleavage of this peptide from partially processed VEGF-C produces a fully processed mature form of VEGF-C of 21-23 kD which has high affinity to VEGFR-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "binds and stimulates VEGF-C ition 156 is essential for VEGER-2 and VEGER-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "important for VEGF-C
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VEGFR-3 binding"
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                                                                                                                                                                                                                                                                                                                                                                        for manufacturing medicament useful for diagnostic screening, imaging and treatment of malignancies characterised by Flt4-expressing blood cells. The Flt4 gene maps to chromosomal region 5q35 and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in their 3' sequences and are differentially expressed in HEL and DAMI cell lines. Flt4 belongs to a subfamily of class III receptor tyrosine kinases (RTKs). It is used as a target for tumour imaging and anti-tumour therapy: The present sequence is a human prepro-vascular endothelial growth factor C (VEGF-C), a specific example of Flt4 binding compound.
                                                                                                                                                                                                                                                                                                                                               Sequence
121 NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN 180
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Search completed: October 17, 2001, 14:46:00 Job time: 126 sec

Title: Perfect score:

Run on:

Scoring table: Sequence:

Sequence Sequence Sequence Sequence

Sequence Sequence

6, Appli 2, Appli 2, Appli 2, Appli 20, Appl 20, Appl 25, Appl 25, Appl 25, Appl 25, Appl 27, Appl 28, Appl 29, Appl 20, Appl 21, Appl 22, Appl 23, Appl 24, Appl 25, Appl 26, Appl 27, Appl 28, Appl 29, Appl 20, Appl 20, Appl 21, Appl 22, Appl 23, Appl 24, Appl 25, Appl 26, Appl 27, Appl 28, Appl 29, Appl 20, Appl 20, Appl 21, Appl 22, Appl 23, Appl 24, Appl 25, Appl 26, Appl 27, Appl 28, Appl 29, Appl 20, Appl 20, Appl 21, Appl 21, Appl 22, Appl 23, Appl 24, Appl 25, Appl 26, Appl 27, Appl 28, Appl 29, Appl 20, Appl 20, Appl 20, Appl 20, Appl 21, Appl 21, Appl 22, Appl 23, Appl 24, Appl 26, Appl 27, Appl 28, Appl 29, Appl 20, Appl 20, Appl 20, Appl 21, Appl 22, Appl 23, Appl 24, Appl 26, Appl 27, Appl 28, Appl 29, Appl 20, Appl 20, Appl 20, Appl 20, Appl 21, Appl 21, Appl 22, Appl 24, Appl 26, Appl 27, Appl 28, Appl 29, Appl 20, Appl 20,

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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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Listing first 45 summaries
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US-09-042-105-1
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; Sequence 33, Application
; Patent No. 6221839
; GENERAL INFORMATION:
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Best Local Similarity
Matches 209; Conserv
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INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Alitalo, Karı
Joukov, Vladomir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Receptor Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                            LENGTH: 350 amino acids
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                                                                                        100.0%; ilarity 100.0%; Conservative 0
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US-08-185-432-19
US-08-185-432-19
US-08-532-384-20
US-08-820-170A-25
US-09-25-699-25
US-09-273-565-25
US-09-185-432-17
US-08-480-309-19
US-08-480-309-19
US-08-347-594A-2
US-08-440-159-10
US-08-400-159-10
US-08-400-159-10
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                                                                                        Score 1218; DB 4;
Pred. No. 1.4e-104;
; Mismatches 0;
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Best Local Similarity
                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
TYPE: amino acid
TOPOLOGY: lin-
WOLECUT
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
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APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor
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     181
                                     262
                                                                        121
                                                                                                      202 DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGA 261
                                                                                                                                                                         142 CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD 201
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CLASSIFICATION: 514
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SOFTWARE: PatentIn Release #1.0, Version #1
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
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                                                       NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN 180
                                                                                                                                                                                             CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD 60
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RQKACEPGFSYSEEVCRCVPSYWKRPQMS 209
                                    NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN
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                                                                                                                                                                                                                                              100.0%; Score 1218; DB 4; Length 350; llarity 100.0%; Pred. No. 1.4e-104; Conservative 0; Mismatches 0; Indels 0
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SYSTEM: PC-DOS/MS-DOS
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00 Sears Tower, 233 South Wacker Drive
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Best Local Similarity
Matches 209; Conserv
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                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS: LENGTH: 419 amino acids
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FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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APPLICATION NUMBER: PCT/F
FILING DATE: 01-AUG-1996
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 01-AUG-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                    TELEFAX: 25-3856
211 CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/60 FILING DATE: 14-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/795,430 FILING DATE:
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CITY: Chicago
STATE: Illino:
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                                                                                                                                                                                                                                                                                                                                                                                        NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
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                 1 CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD 60
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                                                                                                                                                                                                                      amino acid
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: United States of America
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                                                                           Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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00 Sears Tower, 233
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                                                                                          100.0%;
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                                                                                          Score 1218; DB 4;
Pred. No. 1.7e-104;
                                                                         Mismatches
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                                                                                                            Length 419;
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                                                                                                                                                                                                                                                        Matches 209;
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INFORMATION FOR SEQ ID NO: 35:
                                    331
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181 RQKACEPGFSYSEEVCRCVPSYWKRPQMS 209
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                                                                                                                          61 DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGA 120
                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                   1 CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alitalo, Kari
Joukov, Vladomir
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                  NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN 180
                                                                                                                                                                                CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RQKACEPGFSYSEEVCRCVPSYWKRPQMS 419
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                                                                                                         DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGA 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 419 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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STREET: 6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08510133A
                                                                                                                                                                                                                                                        Conservative
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Tower, 233
                                                                                                                                                                                                                                                       Score 1218; DB 4;
Pred. No. 1.7e-104;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                         DB 4; Length 419;
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; Sequence 4, Application US/08999811
; Patent No. 5932540
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Best Local Similarity
Matches 208; Conserv
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APPLICANT: HU, JIN
APPLICANT: ROSEN,
APPLICANT: CAO, LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202)371-2540 INFORMATION FOR SEQ ID NO: 4:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
PRIOR APPLICATION NUMBER: US 08/465,968
APPLICATION NUMBER: US 08/465,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/999,811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                   181 RQKACEPGFSYSEEVCRCVPSYWKRPQMS 209
                                                                                        121 NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN 180
                                                                                                                                             202 DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGA 261
                                                                                                                                                                                                                    142 CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: WASHINGTON
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                                                                      NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN 321
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                                                                                                                                                                                                                                                                                           Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                        99.7%;
99.5%;
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                                                                                                                                                                                                                                                                                       Score 1214; DB 2;
Pred. No. 3.3e-104;
1; Mismatches 0;
350
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                                                                                                                                                                                                                                                                                                                           Length 350;
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SEQ ID NO 2
LENGTH: 350
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Patent No. 6040157
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Best Local
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FILE REFERENCE: PF112D1
CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: 08/207,550
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1994-03-08 NUMBER OF SEQ ID NOS: 9
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APPLICANT: Rosen, Craig
APPLICANT: Cao, Liang
                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CUBRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2 NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HU, JING-SI
APPLICANT: ROSEN, CRAI
APPLICANT: CAO, LIANG
                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGA 261
                                                   APPLICATION NUMBER: FILING DATE: HEREWI
                                                                                                                                                                                                                                          STREET: 1100 NEW CITY: WASHINGTON
APPLICATION NUMBER:
                                    CLASSIFICATION:
                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGA 120
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ROSEN, CRAIG A.
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                                                   HEREWITH
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99.5%;
                                                                   US/09/042,105
US 08/207,550
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RESULT 8
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                          APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN 180
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                                                                                                                                                             COUNTRY: U
ZIP: 20005
                                                                                                                                                                                               STREET: 1100 NEW CITY: WASHINGTON STATE: DC
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                 APPLICATION NUMBER: FILING DATE: HEREW
                                                                                                                                                                                                                                 ADDRESSEE: STERNE, KESSLER, OSTREET: 1100 NEW YORK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGA 120
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: ERIC K. STEFFE REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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(202)371-NO: 4:
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                                                                                                                         Floppy disk
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                 HEREWITH
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                                                                                                                                                                                                                                                                                                           VASCULAR ENDOTHELIAL GROWTH FACTOR
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                                                                                                                                                                                                                                                      KESSLER, GOLDSTEIN & FOX
                                US/08/999,811
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:

US 08/207,550

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GENERAL INFORMATION:
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Best Local S
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SEQUENCE CHARACTERISTICS:
LENGTH: 419 amin
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                  CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ADDITIONALIMEDED: 15 (2000) 105
                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HU, CAPPLICANT: ROSEI APPLICANT: CAO,
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ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R
                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2 NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US FILING DATE: 8-MAR-1994
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nes 208; Conserv
                                                                     APPLICATION NUMBER: FILING DATE: HEREW
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ROSEN, CRAIG A.
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                    US 08/207,550
                                                                                      US/09/042,105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/09042105 Patent No. 6040157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 208; Conserv
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                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOR COMPATIBLE
COMPUTER: IBM FOR COMPATIBLE
COMPUTER: FOR COMPATIBLE
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HU, JING-SHAN APPLICANT: ROSEN, CRAIG A. APPLICANT: CAO, LIANG
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LENGTH: 419 amino acid
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REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CAO, LIANG TITLE OF INVENTION: V
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                       CLASSIFICATION
                                                         FILING DATE:
                                                                                                                                                                                                           ZIP: 20005
                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                   CITY: WASHINGTON
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                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/465,968
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                                                         HEREWITH
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                                                                                                                                                                                                                                                                                                                                                                VASCULAR ENDOTHELIAL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                        KESSLER, GOLDSTEIN & FOX
 US 08/207,550
                                                                           US/09/042,105
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Pred. No. 46
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:

CLASSIFICATION:

8-MAR-1994

FILING DATE: 0
CLASSIFICATION:

06-JUN-1995

US 08/465,968

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PCT-US96-09001-2
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
                               OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/USS
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION DATA:
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                   APPLICANT: HU, ET AL.
TITLE OF INVENTION: H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997
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                                                                                                                      COMPUTER:
                                                                                                                                                                                                              CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                           ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                  CLASSIFICATION
                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD 60
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                                                  PCT/US96/09001
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    Mismatches

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US-08-795-430-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Applicat Patent No. 6130071
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 208;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F196/00427
FILING DATE: 01-AUG-1996
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladdimir
TITLE OF: INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 6 JUN 95
APPLICATION NUMBER: 08/20
FILING DATE: 8 MAR 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                    FILING DATE: CLASSIFICATION:
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CITY: Chicago
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                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                              ZIP:
                                                                                                                                                                                                                                                                                                                                       STATE:
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REFERENCE/DOCKET NUMBER: 32
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                 COUNTRY:
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TELEFAX: 201-994-1744
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: United States of America
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99.5%;
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08/671,573
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 01-AUG-

PRIOR APPLICATION DATA:

01-AUG-1995

08/510,133

APPLICATION NUMBER: FILING DATE: 14-NOV

14-NOV-1994

08/340,011

ATTORNEY/AGENT INFORMATION:

NAME: Gass, David A.
REGISTRATION NUMBER: 38,153

REFERENCE/DOCKET NUMBER:

28967/33691

FILING DATE: 14-FEB-PRIOR APPLICATION DATA:

14-FEB-1996

08/601,132

APPLICATION NUMBER: 08/51 FILING DATE: 12-JAN-1996

08/585,895

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

28-JUN-1996

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RESULT 13
US-08-795-430-13
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                                                                                                                                                                                                                                                                             Patent No. 61300...
GENERAL INFORMATION:
GENERAL INFORMATION:
Alitalo, Kari
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INFORMATION FOR SEQ ID NO:
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Protein
TITLE OF INVENTION: Protein
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LENGTH: 415 amino acid
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                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                            COUNTRY: United States of America ZIP: 60606-6402
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                                                                                                                                STATE:
                                                                                                                                                                 STREET:
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TOPOLOGY: linear
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                                                                                                                            Chicago
: Illinois
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                                                                                                                                                               6300 Sears Tower,
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                 Marshall, O'Toole,
300 Sears Tower, 233
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                                                                                                                                                                                                                       Vascular Endothelial Growth Factor C (VEGF-C)
Protein and Gene, Mutants Thereof, and Uses Thereof
57
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85.6%; Pred. No. 2.2e-92;
tive 18; Mismatches 12;
                                                                                                                                                                 Gerstein, Murray & Borun
South Wacker Drive
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NUMBER OF SEQUENCES: TITLE OF INVENTION:

GROWTH FACTOR

Evenson, McKeown, Edwards & Lenahan P.L.L.C.

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                                                                                                                                      US-08-915-795-3
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                                                                             Sequence 3, Application US/08915795 Patent No. 6235713 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 158; Conserv
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Best Local 9
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APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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TELEFAX: 25-3856
                                                                                                                                                                                                               389 VRTKRCDAGFLLAEEVCRCVRTSWKRPLMN 418
                                                                                                                                                                                                                                                                                              329
                                                                                                                                                                                                                                                   180 NROKACEPGFSYSEEVCRCVPSYWKRPOMS 209
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NAME: NAME: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/60 FILING DATE: 14-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD 60
                                                                                                                                                                                                                                                                                        PNKEFDEEKCQCVCKKTCPKHHPLNPAKCICECTESPNKCFLKGKRFHHQTCSCYRPPCT
                                                                                                                                                                                                                                                                                                                                                                     SDTSEGFH-ICGPNKELDEETCQCVCKGGVRPISCGPHKELDRASCQCMCKNKLLPSSCG
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amino acid
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75.28;
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Pred. No. 8.5e-78;
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STREET: CITY: W STATE:

Washington

1200 G Street, NW, Suite 700

COUNTRY:

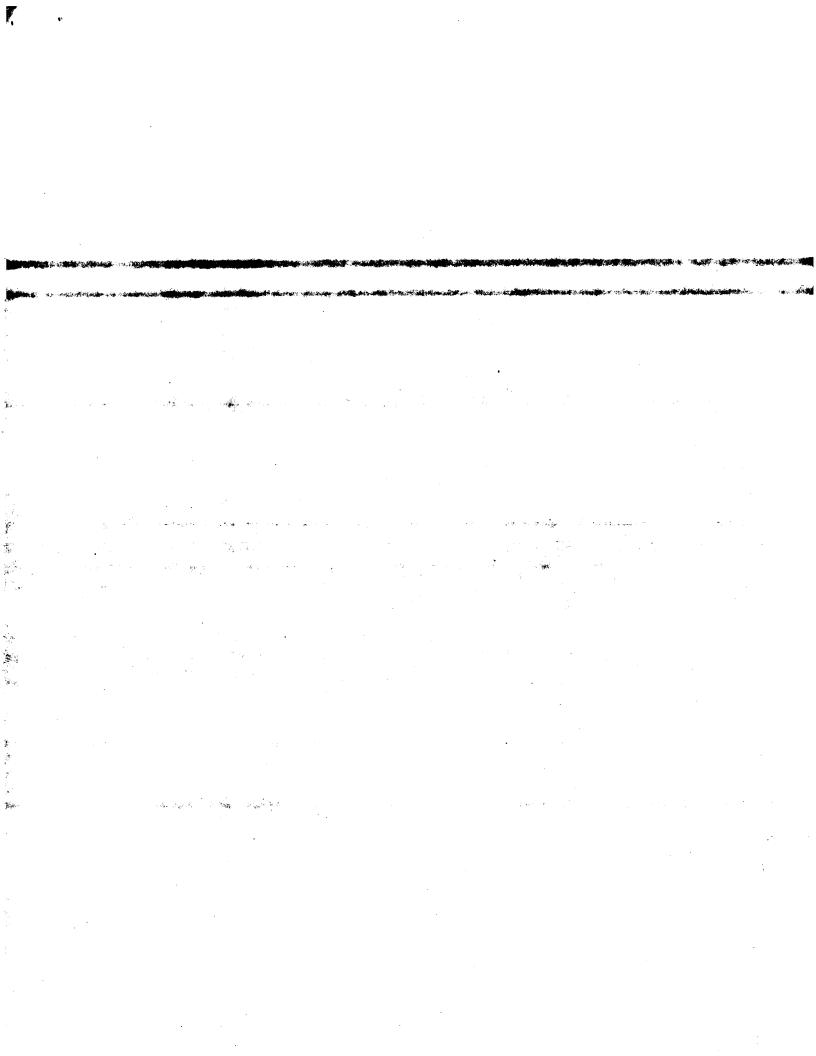
United States of America

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Sequence 5, Application US/08915795;
Patent No. 6235713;
GENERAL INFORMATION:
APPLICANT: MARC G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: KARI ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                RESULT 15
US-08-915-795-5
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Best Local S
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: NO
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Relicurrent Application Data: Application NUMBER: US
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126
                                                                                                                                                                                                                                                                                                                                                                                           179 TNRQKACEPGFSYSEE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                  237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 TED----HSHLQE------PALCGPH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 RHPYSIIRRSI--QIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQE-----ENPŁAG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 FHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
 COUNTRY:
                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 RQVHSIIRRSLPATLPQ---CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENTCQCVCKRTCPRNQPLNPGKCAC-ECTESPQKCLLKGKKFHHQTCSC-----YRRPC 178
                                                                                                                                                                                                                                                                                                                                                                                                                              EDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPC 296
                                   Washington
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                                                  E: Evenson, McF
1200 G Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 628-8844
United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .20.8%; score 253.5; DB 4; Length 325; 30.1%; Pred. No. 4.1e-16;
                                                    McKeown, Edwards & Lenahan P.L.L.C. et, NW, Suite 700
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; TISSUE TYPE: Human Lung
US-08-915-795-5
                                                                                                                                                                                                                                                                                                      Query Match 20.8
Best Local Similarity 30.1
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 628-884
TELEX: N/A
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: p:
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION
TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
326 ASGKTACAKHCRFPKE 341
                                  179 TNROKACEPGFSYSEE 194
                                                                      266 EDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPC
                                                                                                          126 ENTCOCVCKRTCPRNQPLNPGKCAC-ECTESPOKCLLKGKKFHHQTCSC-----YRRPC 178
                                                                                                                                                   246 TED----HSHLQE------PALCGPH----
                                                                                                                                                                                                                             197 RHPYSIIRRSI--QIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQE-----ENPLAG 245
                                                                                                                                                                                     66 FHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                            9 RQVHSIIRRSLPATLPQ----CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                      20.8%;
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                                                                                                                                                                                                                                                                                                      ; Score 253.5; DB 4
; Pred. No. 4.5e-16;
27; Mismatches 49
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                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                        49; Indels 61;
                                                                                                                                                   ----- MMFD 265
                                                                                                                                                                                                                                                                                                                                          Length 354;
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8

Search completed: October 17, 2001, 14:47:10 Job time: 196 sec



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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq
Maximum DB seq
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
238
180.5
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length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Match Length DB
BLOSUM62
Gapop 10.0 ,
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1218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              October 17, 2001, 14:48:36; Search time 78.16 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CMSKLDVYRQVHSIIRRSLP.....SYSEEVCRCVPSYWKRPQMS
Gapext 0.5
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A56175
A49175
S19694
T34264
A49128
A449128
A449128
A45612
A35844
A61625
A61625
A61625
A57170
T27283
A56136
T30201
T29764
T16408
J01322
A55624
A47221
A32160
T25933
T27319
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                                                                                                                                                                                                                                                                                           SUMMARIES
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                     fibrillin 1 precur
tenascin-C - human
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transmembrane prot
Xotch protein - Af
tenascin-like prot
fibrillin-2 precur
hypothetical prote
probable tenascin
fibrillin-2 precur
hypothetical prote
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185K secretory pro
tenascin precursor
adhesive plaque pr
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hypothetical prote
cell-fate determin
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fibrillin-1 precur
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slit-1 protein
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123	123.5	124	124	125.5	125.5	125.5	125.5	125.5	126	126.5	127	127	127.5	127.5	128
10.1	10.1	10.2	10.2	10.3	10.3	10.3	10.3	10.3	10.3	10.4	10.4	10.4	10.5	10.5	10.5
1106	220	3712	570	3020	2531	2531	1111	346	2555	497	4135	2871	3635	2321	2703
N	N	N	N	Ŋ	N	N	N	N	N	N	N	2	N	N	Н
T13938	S29195	S18253	A48836	A43932	A46019	T31070	T26972	T46914	A40043	T27827	T42629	A55567	T10053	S78549	A24420
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C;Genetics: A;Gene: GDB:VEGFC; VRP A;Cross-references: GDB:3890883; OMIM:601528 A;Cross-references: GDB:3890883; OMIM:601528 F;1-12/Domain: signal sequence #status predicted <sig> F;13-102/Domain: propeptide #status predicted <pro></pro></sig>	nslated f	A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and A;Reference number: S69208 A;Reference number: S69208 A;Accession: S69208 A;Molecule type: mRNA A;Residues: 1-419 <lee> A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989 R;Morris, J.C. submitted to the EMBL Data Library, May 1996</lee>	A; Residues: '70-419 < JOUI> A; Residues: '70-419 < JOUI> A; Note: this sequence has been revised in reference \$69207 A; Accession: \$71443 A; Molecule type: protein A; Residues: 'X',104-120 < JOUI> R; Lee, J; Gray, A.; Yuan, J; Luoh, S.M.; Avraham, H.; Wood, W.I. submitted to the EMBL Data Library, December 1995	RESULT 1 S59207 Vascular endothelial growth factor C precursor - human N;Alternate names: FLT4 ligand DHM C;Species: Homo sapiens.(man) C;Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 08-Oct-1999 C;Accession: S69207; S61795; S71443; S69208; G02559 R;Joukov, V; Pajusola, K; Kaipainen, A; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel EMBO J. 15, 1751, 1996 A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand A;Reference number: S69207; MUID:96203094 A;Accession: S69207 A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-419 <jou> A;Cross-references: EMBL:394216; NID:g1177488; PIDN:CAA63907.1; PID:e221096; PID:g118 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995 A;Cross-references: EMBL:394216; NID:g1177488; PIDN:CAA63907.1; PID:e221096; PID:g118 A;Note: this is a revision to the sequence from reference S61795 A;Note: this is a revision to the sequence from reference S61795 R;Joukov, V; Pajusola, K; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel EMBO J. 15, 290-298, 1996 A;Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the F1t4 A;Accession: S61795 A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA</jou>	ארום ארום איני איני איני איני איני איני איני אינ

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RESULT 3
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A:Title: The balbiani ring 3 gene in Chironomus A:Reference number: S08167; MUID:90172404
A:Accession: S08167
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Best Local Similarity
"~+~hes 62; Conserv?
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C;Superfamily: unassigned Balbiani ring proteins
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R; Paulsson, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Chironomus tentans
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: x52263; NID: g7057; PIDN: CAA36506.1; PID: g7058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-1700 < PAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Balbiani ring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;103-419/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                    1260
                                                                                                                                                                                                                                                                                                                                                                      1204
                                                                                       1429 DATC 1432
                                                                                                                                                          1372 GKCTGAQVWCSKACKCVCPAQKKCDSPKTWDENSCSCQCPKNMRPPTG---GCNAGRTWD 1428
                                                                                                                                                                                                                              1312 KSWNDDSCSCQCKSKMPCGGCPPNQQWNEKDCECKCSATGNCPAGQTWNSQTCQCSCPAT 1371
                                                                                                                         193 EEVC
                                                                                                                                                                                              146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGA 120
                                                                                                                                                                                                                                                                                                                                    TDGFHDICGPNKELDEETCQCVCRAG---
                                                                                                                                                                                                                                                                                                                                                                      PTPAPTCSNNQKYSNVSCSCGCNPGKPKNGCPGNQIWCDNTCRCVCPKNMEKPADN---- 1259
                                                                                                                                                                                                                                                                                                                                                                                                        PATLPQCQAANK - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RQKACEPGFSYSEEVCRCVPSYWKRPQMS
                                                                                                                                                                                               GKC-----
                                                                                                                                                                                                                                                                KELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRT--CPRNQPLN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD
                                                                                                                                                                                                                                                                                                  -----C-KTKWWNDEMCQCVCKPGCPEGGCKGVMKWNANTCSCECPADKAKPASCGDK 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RQKACEPGFSYSEEVCRCVPSYWKRPQMS 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S08167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 protein - midge (Chironomus tentans)
   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lendahl, U.; Galli, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vascular endothelial growth factor C #status experimental <MAT>
                                                                                                                                                                                          ACECTESPOKCLLKGKKFHHOTCSCY----RRPCTNRQKACEPGFSYS 192

    midge (Chironomus tentans) (fragment)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.5%;
                                                                                                                                                                                                                                                                                                                                                                                                      ------TCPTNYMWNNHICRCLAQEDFMFSSDAGDDS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 238;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1218;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ericsson, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .8; DB 2;
1.2e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tentans has a diverged
                                                                                                                                                                                                                                                                                                                                                                                                                                       74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wieslander,
                                                                                                                                                                                                                                                                                                                                -----LRPASCGPH 97
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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N;Contains: Lewacca. C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A32230; B32230; A33379; B33379; C33379; S01292; A30903
C;Accession: A32230; B32230; A33379; B33379; C3379; S01292; A30903
C;Accession: A32230; B32230; A33379; B33379; C3379; S01292; A30903
C;Accession: A32230; B32230; A33379; B33379; B242888, B242888, B24288, B24288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:J04519
R;Spring, J.; Beck, K.; Chiquet-Ehrismann,
Cell 59, 325-334, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: A detailed structural model of cytotactin: protein homologies, alternative A;Reference number: A32230; MUID:89184536
A;Accession: A32230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M24160
A;Experimental source: salivary gland
C;Superfamily: unassigned Balbiani ring proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Balbiani ring 3 in A; Reference number: JQ0542; A; Accession: JQ0542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Chironomus tentans
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 17-Mar-2000
C;Accession: JQ0542
A;Molecule type: mRNA
A;Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',45
A;Accession: C33379
                                                                                                                            A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',45
A;Cross-references: GB:M23121; NID:g212746; PIDN:AAA49086.1; PID:g212749
A;Accession: B33379
                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A33379; MUID:90030407
A; Accession: A33379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Two contrary functions of tenascin: dissection of the active sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-1044,1318-1810 <JO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:J04519; NID:g211717; PIDN:AAA48745.1; A;Accession: B32230
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A; Residues: 1-1810 < JON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N; Alternate names: cytotactin; hexabrachion N; Contains: tenascin 190K; tenascin 200K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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A; Residues: 1-160 < DIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tenascin precursor - chicken
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVCSCGCPVPRPDC-TNGQIYNINTCAC---GCGIDKPSCPKQQIYNWKTCDCECPNGMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCGNKKFFDKPSCECKCKNN--PST--SPQVWDADDCECKCPKDKQKPQGGCDGGQKWND 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRT------CPRNQPLNP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
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Pred. No. 2.1e-07;
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F;592-673/Domain: fibronectin type III repeat homology <FN3A>
F;681-765/Domain: fibronectin type III repeat homology <FN3B>
F;773-857/Domain: fibronectin type III repeat homology <FN3B>
F;773-857/Domain: fibronectin type III repeat homology <FN3C>
F;865-949/Domain: fibronectin type III repeat homology <FN3E>
F;957-1037/Domain: fibronectin type III repeat homology <FN3E>
F;1046-1128/Domain: fibronectin type III repeat homology <FN3E>
F;1137-1219/Domain: fibronectin type III repeat homology <FN3H>
F;1138-1310/Domain: fibronectin type III repeat homology <FN3H>
F;1318-1399/Domain: fibronectin type III repeat homology <FN3I>
F;1407-1487/Domain: fibronectin type III repeat homology <FN3X>
F;1590-1798/Domain: fibronectin type III repeat homology <FN3X>
                                   J. Biol. Chem. 270, 6698-6701, 1995
A;Title: Mussel adhesive plaque protein gene
A;Reference number: A56175; MUID:95204464
A;Accession: A56175
                                                                                                                                                                                                                                        adhesive plaque protein Mgfp2 precursor - Mediterranean mussel C;Species: Mytilus galloprovincialis (Mediterranean mussel) C;Date: 27-Apr-1995 #sequence_revision 03-Oct-1995 #text_change
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A56175
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F;34-1810/Product: tenascin 230K #status predicted <MAT>
F;223-249/Domain: EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 27-181, 'R',183-204, 'G',206-221, 'A',223-380,'D',382-386,'H',388-444,'HN',
A;Residues: EMBL:X08030
A;Cross-references: EMBL:X08030
A;Note: part of this sequence was confirmed by protein sequencing
A;Note: part of this sequence fibrings beta/gamma homology; fibronectin 'A
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A;Molecule type: mRNA
A;Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',452-5
A;Cross-references: GB:M23121
                                                                                                                                                                        C; Accession: A56175
R; Inoue, K.; Takeuchi, Y.; Miki, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibroneconservation; alternative splicing; calcium binding; cell adhesion; duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S01292; A; Accession: S01292
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A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVCKNKLFPSQCG----ANREFDENTC---QCVCKR-----TCPRNQPLN----P 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGYTGP--DCGEELCPHGCGIHGRCVGGRCVCHEGFTGEDCNEPLCPNNCHNRGRCVDNE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNC--SEPACPRNCL-NRGLCVRAKCICEEGFTGEDCSQARCPSDCNDQGKCVDGVCVCF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQCQAANKTCPTNYMWNNHIC---RCLAQEDF-----MFSSDAGDDS--TDG----F 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HDICGPNKELDEETC------QCVCRAGLRPASCG----PHKELDRNSC---Q 106
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                                                                                                       epidermal
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                                                                                                       growth facto
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F;560-591/Domain: 1
F;674-705/Domain: 1
F;712-743/Domain: 1
F;836-867/Domain: 1
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A;Cross-references: GB:D43794; NID:g602767; PIDN:BAA07852.1; PID:d1008438; PID:g6
C;Superfamily: unassigned EGF-related proteins; EGF homology
C;Keywords: duplication
F;1-17/Domain: signal sequence *status predicted <SIG>
F;387-419/Domain: EGF homology <EGF1>
F;429-660/Domain: EGF homology <EGF>
F;23,36,43,56,75,382,424,455,468,473/Modified site: 3',4'-dihydroxyphenylalanine
                                                                                                                                                                                                                                                             A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:126158)
C;Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision be C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol F;143-174/Domain: EGF homology <EGX1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: Notch homolog
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 20-Sep-1999
C;Accession: A49157 #11570; S32113
QУ
                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-1203 <LAR>
A;Cross-references: EMBL:X68279; NID:g287989; PIDN:CAA48340.1; PID:g287990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues
A;Reference number: A49175; MUID:93178563
A;Accession: A49175
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Matches 67
                                             Matches
                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 NVCKPTPCKNSGRCVNKGSSYNCICKGGYSGPTCGENVCKPNPCQNRGRCYPDNSDDGFK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 SADKFGDYSCECRPGYFGPECERYVCAPNPCKNGGICSSDGSGGYRCRCKGGYSGPTCKV 267
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    33 CPTNYMWNNHICRCL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEEVCRCVPSY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLPQCQAANKTCPTNYMWN------NHICRCL------AQEDFMF---SSDAGDD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVSKPCKNRGKCIWNGKAYRCKCAYGYGGRHCTKKSYKKNPCASRPCKNRGKCTDKGNGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ESPQKCLLKGKKF------HHQTCSCYR-----RPCTNRQKACEPGFSY 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CQCV-----CK---RTCPRNQPLNPGKC-----ACECT---
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                                             Similarity 62; Conser
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                      EGF
EGF
EGF
                                                                                                                                                    homology <EGX1>
homology <EGF1>
homology <EGF>
homology <EGX2>
homology <EGX3>
homology <EGX3>
                                                               11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.0%;
21.5%;
                                             16;
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    ----AQEDFMFSSDAGDD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 146.5; DB 2
Pred. No. 0.00019;
6; Mismatches .83
                                           Score 139.5; DB 2;
Pred. No. 0.0013;
5; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICGPNKELDEETC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .83;
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    STDG-FHDIC----
                                                                                    Length 1203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 135;
                                             Indels 115;
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                                           Gaps
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F;802-884/Domain: fibronectin type III repeat homology <FN3C>
F;892-976/Domain: fibronectin type III repeat homology <FN3C>
F;892-976/Domain: fibronectin type III repeat homology <FN3C>
F;984-1064/Domain: fibronectin type III repeat homology <FN3C>
F;1073-1155/Domain: fibronectin type III repeat homology <FN3C>
F;1164-1246/Domain: fibronectin type III repeat homology <FN3C>
F;1254-1335/Domain: fibronectin type III repeat homology <FN3H>
F;1254-1335/Domain: fibronectin type III repeat homology <FN3I>
F;1343-1423/Domain: fibronectin type III repeat homology <FN3I>
F;1431-1511/Domain: fibronectin type III repeat homology <FN3I>
F;1526-1734/Domain: fibrinogen beta/gamma homology <FBG>
F;38,166,184,327,788,1034,1079,1121,1354/Binding site: carbohydr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Nishi, T.; Weinstein, J.; Gillespie, W.M.; Paulson, J.C. Eur. J. Biochem. 202, 643-648, 1991
A;Title: Complete primary structure of porcine tenascin. D A;Reference number: S19694; MUID:92104189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: contactin; hexabrachion
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F; 346-372/Domain:
F; 377-403/Domain:
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A; Residues: 1-1746 <NIS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
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Matches
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                                175
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                             RRP-----
                                                                          EGQCVCDEGFAGADCSERRCP-SDCHNRGRCLDGRCECDDG--
                                                                                                                                                                        VCDEGFTGEDCGELICPKDCFDRGRCINGTCYCDEGFEGEDCG
                                                                                                                                                                                                                  VCRAGLRPASCG----PHKELDRNSC---QCVCKNKLFPSQCGANREFDENTC-----
                                                                                                                                                                                                                                                                   SRETCPVPCSEEHGRCVDGRCVCQEGF----AGEDCNEPLCLHNCHGRGRCVENE---C
                                                                                                                                                                                                                                                                                                                ANKTCPTNYMWNNHIC----RCLAQEDFMFSSDAGDDSTDG--FHDICGPNKELDEETCQC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDGRCIDLVNGYQCNCQPGTS 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDTNPLNGQYICTCPQGYKGADCTEDVDECAMANSNPCEHAGKCVNTDGAFHCECLKGYA
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
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EGF homology <EGF2>
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                                                                                                                      -KRTCPRNQPLNPGKC---ACECTESPQKCLLKGKKFHHQTCSCY 174
                                                                                                                                                                                                                                                                                                                                                               11.5%; Score 139.5; DB 1; 26.2%; Pred. No. 0.0017; tive 17; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190
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                                                                                                                                                                        -RLACPHGCRGRGRCE
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                                                                          ----FEGEDCGEL 406
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                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell-fate determining gene Notch2 protein - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1: C;Accession: A49128 R;Weinmaster, G.; Roberts, V.J.; Lemke, G.
                      F;1909-1941/Domain:
F;1943-1975/Domain:
                                                                     F;1191-1222/Domain:
F;1876-1908/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Weinmaster, G.; Roberts
Development 116, 931-941,
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                                                                                                                      F;1153-1184/Domain:
                                                                                                                                             F;1067-1098/Domain:
                                                                                                                                                                   F; 1029-1060/Domain:
                                                                                                                                                                                         F;877-908/Domain:
                                                                                                                                                                                                                    F;799-830/Domain:
                                                                                                                                                                                                                                        F; 264-295/Domain:
                                                                                                                                                                                                                                           C;Superfamily: unassigned ankyrin repeat
F;264-295/Domain: EGF homology <EGX1>
                                                                                                                                                                                                                                                                                       A; Note:
                                                                                                                                                                                                                                                                                                                A; Experimental source: Schwann cell
                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-2471 <WEI>
                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; not
                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A49128; MUID:93202015 A; Accession: A49128
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Notch2: a second mammalian Notch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: U41624; PIDN: AAA83316.1; CESP: F46C8.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-2195 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: T34264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Wilcox,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: T34264
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DЪ
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Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1736 NCVQHVVPDMGNCQRQCGNNQVCIQDQCQCRNGYYAQTE 1774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1676 YLVLQETCISDRCNCVQPSVDAISGGCMNQCGNNQVCIQDQCLCRNGYYAQPETCTGDRC 1735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 CQAANKTCPTNYMWNNHICRCLAQEDFMFS--SDAGDDSTDGFHDICGPNKELDEETCQC 83
                                                                                                                                                                                                                                                                                       sequence extracted from NCBI backbone (NCBIP:127811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCRAGL--RPASCGPHKELDRNSCQCV-----CKNKLFPSQCGANREFDENTCQC--- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDLTNTICTGNSQCIDGICKCPNNQGAINGRCSNMGNANCGNIQ--CGTNQICIQDSCQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-----NRQKACEPGESYSEEVCRCVPSYWKRPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- VCKRTC--PRNQPLNP-----GKCACECTES----PQKCLLK-GKKFHHQTCSCYRR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -CRPGYYQQPGSC-----LQDRCNCIQEVESDSCLNR----QCGMNQVCIQDQCQCRSG 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCPGGCSGHGRCVNGQCVCDEG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                            EGF homology <EGX2>
                                                                                         : EGF homology <EGF>
: EGF homology <EGX3>
: EGF homology <EGF3>
: EGF homology <EGX4>
                                                                                                                                                                                                                    EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <WIL>
                                          ankyrin repeat homology ankyrin repeat homology
                      ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80/1; 159/1; 182/1; 208/2; 246/1; 308/1; 367/1; 1811/1; 1874/1; 1920/1; 2011/2; 2068/3; 2117/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1992
                                                                                                                                                                                                                                                                                                                                                                                   compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 139.5; DB Pred. No. 0.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-Nov-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                              proteins;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                      <AN2>
<AN4>
                                                                       <AN1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F46C8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207
                                                                                                                                                                                                                                                              ankyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                              repeat homology; EGF homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1626
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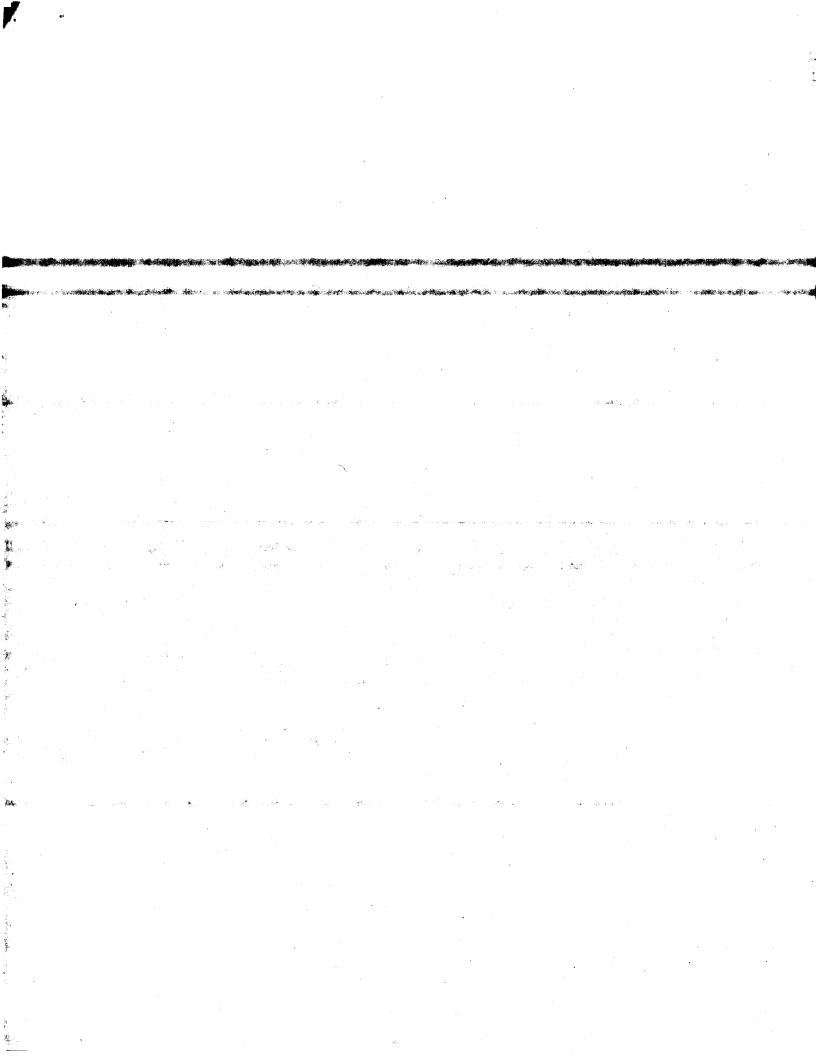
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RESULT
S42612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: sequence extracted from NCBI backbone (NCBIN:64543, NCBIP:64547)
C;Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type C;Keywords: extracellular matrix; glycoprotein; tandem repeat E;287-313,Domain: EGF homology CEGF>
E;287-313,Domain: EGF homology CEGF>
F;346-427/Domain: fibronectin type III repeat homology <FN1>
F;435-517/Domain: fibronectin type III repeat homology <FN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-647 < OND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A43902; MUID:92038434
A;Accession: A43902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Onda, H.; Poulin, M.L.; Tassava, R.A.; Chiu, I.M. Dev. Biol. 148, 219-232, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tenascin - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Feb-1999
C;Accession: A43902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:M76615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A43902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;2009-2041/Domain: ankyrin repeat homology <AN5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Characterization of a newt tenascin cDNA and localization
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                     201 RGRCVNGQCVCDEGF 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450 GPRCEMDINECHSDPCQNDATCLDKIGGFTCLCMPGFK----GVHCELEVNECQSNPCVN 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 CDTNPLNGQYICTCPQAYKGADCTEDVDECAMANSNPCEHAGKCVNTDGAFHCECLKGYA 449
                                                                                                                                                                                                                                                                                                                                   39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 CPTNYMWNNHICRCL-------AQEDFMFSSDAGDD-----STDG-FHDIC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
                                                                                                                                                                                                                                                                                                                                                           CPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC----QCVCRAGL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFMGEDCADLRCP-NDCNNRGRCVNGQCVCDEG---
                                                                                                                                                                                                                                                  TGEDCGELTCPNNCNNRGRCVNGLCVCDDGFQGDDCSELRCPNDCNDRGRCVNGKCVCKE 151
                                                                                                                                                                                                                                                                                         RPASCG----PHKELDRNSC---QCVCKNKLFPSQCG----ANREFDENTC---QCVCKR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-----RQKACEPGFS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLCDENIDNCDPDPC------HHGQCQDGIDSYTCICNPGYMGAICSDQIDECYSSPCL 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGQCVDKVNRFQCLCPPGFTGPVCQ-IDIDDCSSTPCLNGAKCIDHPNGYECQCATGFTG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---CKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKC----ACECTE---- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------SPQKCLLKGKKFHHQTC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDGRCIDLYNGYQCNCQPGTS 638
                                                                                                                                                                                                          -----TCPRNQPLNPGKCA---CECTESPQKCLLKGKKFHHQTCSCYRRP---- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
                                                                                                                             -CTNRQKACEPGF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                 -NNRGRCVEDECVCDEGFTGDDCSE---LIC-PNDCFDRGRCINGVCFCDEGF 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   11.3%; Score 138; DB 2; Length 647 28.2%; Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 139.5; DB 2;
Pred. No. 0.0022;
                                                                                                                                                                   --FMGEDCSDLRCPGDCNN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --SCYRRPCT 179
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                                                           F;184-215/Domain: I
F;222-254/Domain: I
F;456-487/Domain: I
F;757-788/Domain: I
                     F;1025-1056/Domain: EGF homo
F;1924-1956/Domain: ankyrin
                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-2524 <COF>
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F;1957-1989/Domain: ankyrin
                                                                                                                                              F;146-177/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 EVCRCVPSY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 KCLLKG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 CVCK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97
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R;COIIMAN, C.; Harris, W.; Kintner, C. Science 249, 1438-1441, 1990
A;Title: Xotch, the Xenopus homolog of Drosophila notch. A;Reference number: A35844; MUID:90385285
A;Accession: A35844
A;Status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmembrane protein precursor - zebra fish C;Species: Brachydanio rerio (zebra fish) C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_cha C;Accession: $42612 R;Bierkamp, C; Campos-Ortega, J.A. Mech. Dev. 43, 87-100, 1993 A;Title: A zebrafish homologue of the Drosophila neurogenic A;Reference number: $42612; MUID:94128602 A;Accession: $42612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1023-1054/Domain: EGF homology <EGF2>
F;1185-1216/Domain: EGF homology <EGF2>
F;1185-1947/Domain: BGF homology <EGF2>
F;1915-1947/Domain: ankyrin repeat homology F;1948-1980/Domain: ankyrin repeat homology F;1982-2014/Domain: ankyrin repeat homology F;2015-2047/Domain: ankyrin repeat homology F;2015-2048-2080/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-2437 <BIE>
A; Cross-references: EMBL:X69088; NID:g433866; PIDN:CAAA8831.1; PID:g433867
C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
F;755-786/Domain: EGF homology <EGF1>
                                                                                                                                                                                                                                  C; Superfamily: unassigned ankyrin repeat C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xotch protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     715 HNECSSNPCIHGSCLDQINSYRCVCEAGWMGRNCDININECLSNPCVNGGTCKDMTSGYL 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    655 DKINGYECVCEPGYSGSMCNINIDDCALNPCHNGGTCIDGVNSFTCLCPDGFRDATCLSQ 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DSTDGFHDICGP-----NKELDE-----ETC------QCVCRAGLRPASC-GP 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCRAGFSGPNCQMNINECASNPCLNQGSCIDDVAGFKCNCMLPYTGEVCENVLAPCSPR 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCKNGGVCRESEDFQSFSCNCPAGWQGQTCEVDINECVRNPCTN-GGVCENLRGGFQ---
                                                                                    EGF homology <EGX1>
EGF homology <EGF1>
EGF homology <EGF>
EGF homology <EGX2>
EGF homology <EGX3>
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EGF homology <EGX3>
ankyrin repeat homology
ankyrin repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.3%;
22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---- QCVCKNKLFPSQCGAN-REFDENTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --KKFHHQTC----SCYRRPCTNRQKACE---PGFSYSE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 137.5; DB Pred. No. 0.0031;
                                                                                                                                                                                                                                                                                                                                                    sequence not shown; not compared
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                                                                                                                                                                                                                                                                proteins; ankyrin repeat homology; EGF homo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <AN1><AN2><AN3><AN4>
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A;Gene: ten-a
A;Cross references: FlyBase:FBgn0004446
A;Cross references: FlyBase:FBgn0004446
C;Superfamily: unassigned EGF-related proteins; E
C;Keywords: tandem repeat
F;1-62/Domain: signal sequence #status predicted
F;63-782/Product: tenascin-like protein #status p
F;497-524/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-782 <BAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A61625; A; Accession: A61625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Baumgartner, S.; Chiquet-Ehrismann, Mech. Dev. 40, 165-176, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tenascin-like protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jan-2000
C;Accession: A61625; S28463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: X68794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Ten(a), a Drosophila gene related A; Reference number: A61625; MUID:93264270
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Best Local S
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Best Local
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                                                                                                                                                                      79
                                                                                                                                                                                                                                          23 LPQCQAANK----TCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDE 78
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HWTGPDCSQAVCSLDCGRNGVCESGKCRCNSGWTGNLCDQLPCDSRCSEHG-QCKNGTCV 646
                                                                                                                             GTCVAGQCYCKAGWQGEDCG---TIDQQVYQCL----PGCSEHGTYDLETGQCVCER
                                                                                                                                                                  ETC---QCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKR 135
                                                                                                                                                                                                       --YSEEVCRCVPSY 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGPNKELDE-ETCQCVCRAGLRPASCGPHKELDRNSC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GRCKESEDFETFSCECPPGWQGQTC----EIDMNECVNRPCRNGATCQNTNGSYKCNCK 896
                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                              11.2%; Score 136; DB 2; 1
23.4%; Pred. No. 0.0018;
tive 19; Mismatches 75;
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21.7%;
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Pred. No. 0.00
Pred. No. 0.00
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77;
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                                                                                          -CTESP--QKCLLKGKKFHHQTCS 172
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A;Title: An amplifiable DNA region from the Mycoplasma A;Reference number: Z18888; MUID:95014025 A;Accession: T18355
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J. Bacteriol. 176, 5929-5937, 1994
                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mycoplasma hyorhinis
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T18355
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A;Residues: 1-2907 <ZHA>
A;Cross-references: GB:L39790; NID:g762830; PIDN:AAA74908.1;
A;Cross-references: GB:L39790; NID:g762830; PIDN:AAA74908.1;
C;Superfamily: unassigned ECF-related proteins; EGF homology
F;1239-1274/Domain: EGF homology <EGF1>
F;2488-2523/Domain: EGF homology <EGF>
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R;Zhang, H.; Hu, W.; Ramirez, F.
J. Cell Biol. 129, 1165-1176, 1995
A;Title: Developmental expression of fibrillin
A;Reference number: A57278; MUID:95263670
A;Accession: A57278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibrillin-2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1996 #sequence_revision
                                                                                                                                                                   C;Genetics:
A;Genetic code:
                                                                                                                                                                                                          A; Cross-references: EMBL:L11447; NID:g150156;
                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-1187 <
                                                                                                                                                                                                                                                                     A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein P3 - Mycoplasma hyorhinis C;Species: Mycoplasma hyorhinis
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                                                            Query Match
Best Local S
Matches 47
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2543 TLGGFTCKCPPGFTQHHTACIDNNECGSQPSLCGAKGICQNTPGSFSCECQRGFSLDASG 2602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2485 LDECSQSPKPC--NFICKNTKGSYQCSCPRGYVLQEDGKTCKDLDECQTKQHNCQFLCVN 2542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 EVCRCVPSYWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 QPLNPGKC---ACECTESPQKCLL-KGKKFHHQTCSCYR-RPCTNRQKACEPGFSYSE-- 193
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                       43
                                                            Local Similarity les 47; Conserv
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                     ICRCLAQEDFMFSSDAG-----
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60; Conser
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                                                               Conservative
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                                                                                11.18;
24.98;
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                                                                                Score 135.5; DB Pred. No. 0.0027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 136; DB 2; Length 2907; Pred. No. 0.0046; Mismatches 83; Indels 8
                   -DDSTDGFH------DICGPNKELDEETCQC-
                                                               Mismatches
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                                                                                                 DB 2;
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                                                                                                 Length 1187
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                                                            Indels
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77;
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                                                            13;
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Result
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Maximum Match 100%
Listing first 45 summaries
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VASCULAR ENDOTHELIAL GROWTH FACTOR (FLT4-L).
Kukk E., Lymboussaki A., Taira S., Kaipainen A., Joukov V., Alitalo K.;
"VEGF-C receptor binding and pattern of expression suggests a role in lymphatic vascular development. Development 122:3829-3837(1996).
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MEDLINE=97164697;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                            NCBI_TaxID=10090;
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"Characterization of murine Flt4 ligand/VEGF-C.";
Oncogene 15:613-618(1997).
-I- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND E
                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitogen;
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Pfam; PF00341; PDGF; 1.
PRINTS; PR00438; GFCYSKNOT.
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use by non-profit institutions as long as its content is in
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STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPEP
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                                                                              387
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                                                                                                                          327
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                                                                                                                                                                                                                                                              Local Similarity
les 179; Conserv
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                                                                                                                                                                                                                           CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD
                                                                                                                                                                    RQKACEPGFSYSEEVCRCVPSYWKRPQMS
                                                                                                                          NREFDENTCQCVCKRTCPRNQPLNPGKCACECTENTQKCFLKGKKFHHQTCSCYRRPCAN
                                                                                                                                       NREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN
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                                                                              RLKHCDPGLSFSEEVCRCVPSYWKRPHLN
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PS50278; PDGF_2; 1.
Growth factor; Glycoprotein; Signal;
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AAB46707.1; -.
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                       STANDARD;
27, Created)
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TO THE PDGF/VEGF FAMILY OF GROWTH
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N-LINKED (GLCNAC...

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N-D9D3DD3CECC659D6 CI
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Pred. No. 1.2e
8; Mismatches
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Best Local
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SIGNAL
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"The Balblani ring 3 gene in Chironomus tentans has a diverged
repetitive structure split by many introns.";
J. Mol. Biol. 211:331-349(1990).
-!- FUNCTION: USED BY THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR
STRUCTURE, THE LARVAL TUBE. BALBIANI RING PROTEIN 3 COULD P
ROLE AS A TRANSPORT PROTEIN THAT BINDS TO OTHER PROTEINS
INTRACELLULARLY AND IN THE GLAND LUMEN IN ORDER TO PREVENT
FROM FORMING WATER-INSOLUBLE FIBERS TOO EARLY.
                                                                                                                                                                                                                                                                                                                                                                1312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Salivary gland; mEDLINE=90172404; PubMed=1689777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BALBIANI RING PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: SALIVARY GLAND. DOMAIN: HAS 82 APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: SECRETED.
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                                                                                                                                                              DATC
                                                                                                                                                                                                               EEVC
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                                                                                                                                                                                                                                                           GKCTGAQVWCSKACKCVCPAQKKCDSPKTWDENSCSCQCPKNMRPPTG---GCNAGRTWD 1428
                                                                                                                                                                                                                                                                                                                  GKC------
                                                                                                                                                                                                                                                                                                                                                           KSWNDDSCSCQCKSKMPCGGCPPNQQWNEKDCECKCSATGNCPAGQTWNSQTCQCSCPAT
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                                                                                                                                                                                                                                                                                                                                                                                                             X52263; CAA36506.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit institutions as long
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Neoptera; Endopterygota; Diptera; Nematocera;
Jea; Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tentans (Midge)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-KTKWWNDEMCQCVCKPGCPEGGCKGVMKWNANTCSCECPADKAKPASCGDK 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                      STANDARD;
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Last annotation update)
3 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 238; DB 1
Pred. No. 1.2e-1
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                                      1808
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A33379; B33379; C33379;

A33379

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EMBL; W23121; AAA49086.1; -.
EMBL; X08031; CAB40811.1; -.
EMBL; X08030; CAB30824.1; ALT_
EMBL; V08041; AAA48748.1; ALT_
EMBL; M20816; AAA48749.1; ALT_
EMBL; M20816; AAA48749.1; ALT_
PIR; A30903; A30903.
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TISSUE=Embryo;
MEDLINE=90030407; PubMed=2478295;
MEDLINE=90030407; PubMed=90030407;
MEDLINE=90030407; PubMed
PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF EPITHELIAL TUMORS.

SUBUNIT: HEXAMERIC. A HOMOTRIMER MAY BE FORMED IN THE TRIPLE COILED-COIL REGION AND MAY BE STABILIZED BY DISULFIDE RINGS AT BOTH ENDS. TWO OF SUCH HALF-HEXABRACHIONS MAY BE DISULFIDE LINKE WITHIN THE CENTRAL GLOBULE.

SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.

AND 190 KDA; ARE PRODUCTS: 3 ISOFORMS; 230 KDA (SHOWN HERE), 200 KDA AND 190 KDA; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ARE PRODUCED IN A TISSUE-AND TIME-SPECIFIC MANNER DURING DEVELOPMENT.

INDUCTION: BY TGF-BETA.

SIMILARITY: CONTAINS 11 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordatae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989 (Rel. 10, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN)
(GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR
MATRIX ANTIGEN) (GP 150-225).
                                                                                                                                                                                                                                                                                                                                or send
                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
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EMBO J. 7:2977-2982(1988).
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FUNCTION: SAM (SUBSTRATE-ADHESION MOLECULE) THAT APPEARS INHIBIT CELL MIGRATION. MAY PLAY A ROLE IN SUPPORTING THE
A30903;
A31930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE BETA AND GAMMA CHAINS OF FIBRINGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                            an email to license@isb-sib.ch).
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A31930
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InterPro; IPR00561; -.

InterPro; IPR001777; -.

InterPro; IPR002181; -.

InterPro; IPR002181; -.

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InterPro; IPR002181; -.

Pfam; PF00047; fibrinogen_C: 1

Pfam; PF00041; fn3; 11.

PROSITE; PS01186; EGF_1; 14.

PROSITE; PS01186; EGF_2; 14.

Glycoprotein; Cell adhesion; R
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COLLED COIL (POTENTIAL)
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EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 10.
EGF-LIKE 11.
EG
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FP2_MYTGA STANDARD;
ID FP2_AYTGA STANDARD;
AC Q25464;
DT 30-MAY-2000 (Rel. 39, Cr
DT 30-MAY-2000 (Rel. 49, La
DT 01-OCT-2000 (Rel. 40, La
DE ADHSSIVE PLAQUE MATRIX P
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Mytilus galloprovincialis (Mediterranean mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
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61; Conservative
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SIMILARITY: CONTAINS 11 EGF-LIKE DOMAINS.
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PTM: SOME TYROSINES ARE HYDROXYLATED (THUS
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pean Bioinformatics Institute. There as
non-profit institutions as long as if
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EGF_2; 10
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Q28833;
01-OCT-2000
Lavergne J.M., Piao Y.C., Ferreira V., Kerbiriou-N Bahnak B.R., Meyer D., Bahnak B.R., Meyer D., "Primary structure of the factor VIII binding doma nd rabbit von Willebrand factor.";
Biochem. Biophys. Res. Commun. 194:1019-1024(1993)
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01-OCT-2000 (Rel.
                                                                                                                                         Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                             Sus scrofa (Pig).
                                                                                          Seaman W.T., Read M.
Submitted (MAR-1998)
                                                                                                    SEQUENCE FROM N.A
Seaman W.T., Read
                                                                                                                                NCBI_TaxID=9823;
                                                                                                                                                                         F8VWF OR VWF
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                                                              MEDLINE=93356762;
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PubMed=8352759;
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Cetartiodactyla; Suina; Suidae;
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Last annotation update)
PRECURSOR (VWF) (FRAGMENT)
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the EMBL/GenBan
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                                                                                          EMBL/GenBank/DDBJ
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Pred. No. 1.8e-05;
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                                                   Kerbiriou-Nabias
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    HOMEOSTASIS,
                                                                                          databases
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Plan; PF01826; Til; Pfan; PF01826; Til; Pfan; PF01876; ENDOTHELIN.

PRINTS; PR00365; ENDOTHELIN.

PROSITE; PS00234; VWFA; 3.

R PROSITE; PS01208; VWFC; 3.

JR PROSITE; PS01185; CTCK_1; 1.

JR PROSITE; PS01125; CTCK_2; 1.

PROSITE; PS01225; CTCK_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00007; Cys_knot; 1.
Pfam; PF00092; vwa; 3.
Pfam; PF00093; vwc; 3.
Pfam; PF00094; vwd; 3.
Pfam; PF01026; TIL; 3.
PRINTS; PR00365; ENDOTHELIN.
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InterPro; IPR001007; -.
InterPro; IPR001846; -.
InterPro; IPR002035; -.
InterPro; IPR002035; -.
InterPro; IPR002919; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VASCULAR INJURY (BY SIMILARITY).
SUBUNIT: MULTIMERIC (BY SIMILARITY).
PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR
INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
SIMILARITY: CONTAINS 3 VWFC DOMAINS.
SIMILARITY: CONTAINS A C-TERMINAL CYSTINE KNOT-LIKE DOMAIN
SIMILARITY: SOME, TO SILKWORM HEMOCYTIN.
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                                 SEQUENCE FROM N.A.
Stoy S.J., Shibuya I
Johnson G.S.;
Submitted (AUG-1996)
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Canis familiaris (Dog).
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                                 (AUG-1996)
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24.7%;
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                                   the EMBL/GenBank/DDBJ databases
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                                                                  D.J., Holzhauer J., Mohammed
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Length

2482; 81;

Indels

Gaps

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2001 50

99

CRC64;

(POTENTIAL)

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RA MADOUSO D.J., Christopherson P.A., Kroner P.A., Montgomery R.R.;
RT aregion encoding the glycoprotein ID/IX binding domain.";
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
C -!- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEOSTASIS, IT
PARTICIPARES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A
C NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF
C VASCULAR INJURY (BY SIMILARITY).
C -!- SUBUNIT: MULTIMERIC (BY SIMILARITY).
C -!- TISSUE SPECIFICITY: BLOOD.
C -!- PIM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR
C -!- SIMILARITY: CONTAINS 3 WAFA DOMAINS.
C -!- SIMILARITY: CONTAINS 3 WAFA DOMAINS.
C -!- SIMILARITY: CONTAINS 4 VWED DOMAINS.
C -!- SIMILARITY: SOME, TO SILKWORM HEMOCYTIN.
C -!- SIMILARITY: SOME, TO SILKWORM HEMOCYTIN.
Plasma;
SIGNAL
PROPEP
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L76227; 
EMBL; L16903; 
EMBL; AF099154
EMBL; U66246; 
HSSP; P04275; 
HSSP; P04275;
                                                                                                                                                                             Pfam; PFO
Pfam; PFO
Pfam; PFO
PRINTS; P
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between
                                                                                                                                                                                                                                                                                             Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venta P.J., Li J., Yuzbasiyan-Gurkan V., Brewer G.J., Schall W.D.; "Complete sequence of the structural gene for canine von Willebrand factor and identification of a mutation causing Scottish terrier vor Willebrand's disease."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Montgomery R.R., Fahs S. Submitted (AUG-1996) to
                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                   nterPro; IPR000359; ...

terPro; IPR001007; ...

terPro; IPR001846; ...

terPro; IPR002035; ...

terPro; IPR002035; ...

terPro; IPR002019; ...

am; PF000007; Cys_knot; 1.

am; PF00093; vwa; 3.

m; PF00093; vwa; 3.

m; PF00094; vwd; 4.

VIS; PR00453; VWFADOMAIN.

SITE; PS0125; CTCK_2; 1.

ITE; PS0123; CTCK_2; 1.

ITE; PS0123; VWFA. 3
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L16903; AAA30903.1;
AF099154; AAD04919
                                                                                                                                                                               coagulation;
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SCGPHK -- ELDRNS 104

TCPTNYMWNN--HICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC

32

Query Match Best Local S Matches 67

ch 11.5%; l Similarity 20.5%; 67; Conservative

Score 140.5; Pred. No. 0.00 97; Mismatches

DВ

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Gaps -Q 82

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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation (OYTOTACTIN) (NEURONECTIN)
TENASCIN PRECURSOR (TN) (HEXABRACHION) (OYTOTACTIN) (NEURONECTIN)
(GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR
MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C) (P230).
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                                                                                                                                                                                                                                                                                                                                                                            outgrowth from rat cerebral cortex neurons grown on monolayer
                                                                                                                                                                                                                                                                                                                                                                                        Wakatsuki S., Ho S.H., Arioka M., Yamasaki M., Kitamoto K.; "Isolation and characterization of a 230 kDa protein (p230) specifically expressed in fetal brains: its involvement in neurite
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98158323; PubMed=9498558; Wakatsuki S., Ho S.H., Arioka M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nishi T., Weinstein J., Gillespie W.M., Paulson J. "Complete primary structure of porcine tenascin: tenascin transcript in adult submaxillary glands. Eur. J. Biochem. 202:643-648(1991).
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TISSUE=Submaxillary gland;
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Mammalia;
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aryota; Metazoa; Chordata; Craniata; Vertebrata;
malia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                  SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
ALTERNATIVE PRODUCTS: 3 ISOFORMS; MAJOR, MINOR-1 AND MINOR-2 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ARE PRODUCED IN A TISSUE-AND TIME-SPECIFIC MANNER DURING DEVELOPMENT. TISSUE SPECIFICITY: SUBMAXILLARY GLANDS AND BRAIN.
DEVELOPMENTAL STAGE: PREDOMINANTLY EXPRESSED IN THE EMBRYONIC AND EARLY POSTNATAL STAGES. LITTLE OR NO DETECTION IN ADULT BRAIN.
                                                                                                                                                                      FUNCTION: PLAYS A ROLE DURING EARLY BRAIN DEVELOPMENT PARTICUTIN GROWTH CONE GUIDANCE. INVOLVED IN NEURITE OUTGROWTH FROM CORTICAL NEURONS GROWN ON THE MONOLAYER OF ASTROCYTES. SUBUNIT: HEXAMERIC. A HOMOTRIMER MAY BE FORMED IN THE TRIPLE COILED-COIL REGION AND MAY BE STABILIZED BY DISULFIDE RINGS & BOTH ENDS. TWO OF SUCH HALF-HEXABERACHIONS MAY BE DISULFIDE LIMITAL THE CENTRAL GLOBULE.
                                                                                                                                                                                                                                                                                           FUNCTION: SAM (SUBSTRATE-ADHESION MOLECULE), THAT APPERINHIBIT CELL MIGRATION. MAY PLAY A ROLE IN SUPPORTING OF EPITHELIAL TUMORS.
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                      SIMILARITY:
                                        INDUCTION: BY TGF-BETA.
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   EGF-LIKE DOMAINS. FIBRONECTIN TYPE
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Pfam; PF00147; fibrinogen_C;
Pfam; PF00041; fn3; 10.
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EGF_2; 14.
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Cypriniformes; Cyprinidae; Rasborinae; Danio.
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                ) (Zebra danio).
; Craniata; Vertebrata; !
Teleostei; Euteleostei;
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    PRINTS; PRO0009; EGFTGF.

PRINTS; PRO0010; EGFBLOOD.

PROSITE; PS5008B; ANK_REPEAT; 4.

PROSITE; PS50297; ANK_REP_REGION; 1.

PROSITE; PS00010; ASX_HUDROXYL; 23.

PROSITE; PS00022; EGF_1; 34.

PROSITE; PS01187; EGF_CA; 22.

PROSITE; PS01187; EGF_CA; 22.
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HSSP; P00740; 11XA.

ZFIN; ZDB-GENE-990415-173; notch.

InterPro; IPR000152; -.

InterPro; IPR000561; -.

InterPro; IPR000800; -.

InterPro; IPR001336; -.

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Pfam; PF00008; ank; 6.

Pfam; PF00006; notch; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBRYO DEVELOPMENT. MAY BE INVOLVED IN THE GORMATION OF THE NEURAL PLATE, NOTOCHORD AND BRAIN VESICLES.

IN SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

DEVELOPMENTAL STAGE: EXPRESSED IN ALL CELLS IN PREGASTRULATION STAGES. DURING GASTRULATION IS DIFFERENTIALLY EXPRESSED, ACCUMULATING PREDOMINANTLY IN THE PRECHORDAL MESODERM AND NOTOCHORD. AT THE END OF GASTRULATION, EXPRESSED ALONG THE ANTERIOR POSTERIOR AXIS INCLUDING THE DEVELOPING NEURAL PLATE AND DIFFERENTIATING MESODERM. ALSO PRESENT IN THE DEVELOPING BRAIN AND HEAD REGIONS.

SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 3 LINYNOTCH REPEATS.
                                                                                                                                                                                                                                                                                      PROSITE; PS01187; EGF_CA; 22.
Differentiation; Neurogenesis; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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57; Conservative
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                       STANDARD;
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13; Mismatches
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PRINTS; PRODOID; EGFBLOOD.

PROSITE; PSS0088; ANK_REPEAT; 4.

PROSITE; PSS00297; ANK_REP_REGION; 1

PROSITE; PS00010; ASX_HYDROXYL; 23.

PROSITE; PS000022; EGF_1; 34.

PROSITE; PS01186; EGF_2; 29.

PROSITE; PS01187; EGF_CA; 21.

Differentiation; Neurogenesis; Repe
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InterPro; IPRO00561; -.
InterPro; IPRO00800; -.
InterPro; IPRO01438; -.
InterPro; IPR001881; -.
InterPro; IPR001811; -.
InterPro; IPR001010; -.
Pfam; PF00008; EGF; 36.
Pfam; PF00023; ank; 6.
Pfam; PF00023; ank; 6.
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"Xotch, the Xenopus homological Science 249:1438-1441(199)
[2]
REVISIONS TO 1759-1782.
Kintner C.;
Submitted (JUN-1996) to t
  Transmembrane;
SIGNAL 1
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01-OCT-1996
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NEUROGENIC LA
XOTCH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-90385285; PubMed-2402639;
MEDLINE-90385285; PubMed-2402639;
Coffman C., Harris W., Kintner C.;
"Xotch, the Xenopus homolog of Drosophila notch.";
Science 249:1438-1441(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN EARLY EMBRYOS.
SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.
SIMILARITY: CONTAINS 36 EGF-LIKE DOWAINS.
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 6 ANK REPEATS.
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NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN).
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CYTOPLASMIC (POEGF-LIKE 1.

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                                                              KKFHHQTCSCYRRPCTNRQK-----ACEPGFS----
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InterPro; IPR000822;
InterPro; IPR000822;
InterPro; IPR001881;
InterPro; IPR001881;
InterPro; IPR001881;
InterPro; IPR002212;
InterPro; IPR002212;
InterPro; IPR001881;
InterPro; IPR00181;
IPR000008; EGF; 46;
Pfam; PF00008; TB; 9
PR0SITE; PS00010; ASX_HYDIPR0SITE; PS00010; ASX_HYDIPR0SITE; PS001187; EGF_CA;
PR0SITE; PS01187; EGF_CA;
INTERPROSITE; PS0
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Q61555; Q63957;
15-DEC-1998 (Rel. 37, I
15-DEC-1998 (Rel. 37, I
15-DEC-1998 (Rel. 37, I
15-DEC-1998 (Rel. 37, I
FIBRILLIN 2 PRECURSOR.
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                                                                                                                                                     PROSITE; PS00010; ASX_HYDROXYL; 43.
PROSITE; PS00102; EGF_1; 2.
PROSITE; PS01186; EGF_2; 36.
PROSITE; PS01187; EGF_CA; 43.
Extracellular matrix; Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Fibrillin genes map to regions of conserved mouse/human synteny on mouse chromosomes 2 and 18.";

Genomics 18:667-672(1993).

-!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS THAT BINDS CALCIUM, FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.

-!- SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIUM BINDING EGF-LIKE DOMAINS.

-!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING-PROTEIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
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MEDLLINE=95263670; PubMed=7744963;

Zhang H., Hu W., Ramirez F.;

"Developmental expression of fibrillin

of extracellular microfibrils.";

J. Cell Biol. 129:1165-1176(1995).
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Putnam E.A., Zhang H., Ramirez F., Milewicz D.M.;
"Fibrillin-2 (FBNZ) mutations result in the Marfan-like disorder,
congenital contractural arachnodactyly.";
Nat. Genet. 11:456-458(1995).
-!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
THAT BINDS CALCIUM. FIBRILLIN-2-CONTAINING MICROFIBRILS REGULATE
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MEDLINE-94165150; PubMed-8120105;

Zhang H., Apfelroth S.D., Hu W., Davis E.C., Sanguineti C.,

Bonadio J., Mecham R.P., Ramirez F.;

"Structure and expression of fibrillin-2, a novel microfibrillar

component preferentially located in elastic matrices.";

J. Cell Biol. 124:855-863(1994).
                                   EMBL; U03272; AAA18950.1; EMBL; X62009; -; NOT_ANNO
                                                                                    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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"Linkage of Marfan Syndrome and a phenotypically related disorder to
two different fibrillin genes.";
Nature 352:330-334(1991).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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MEDLINE-91304.567; PubMed-1852206;
Lee B., Godfrey M., Vitale E., Hori H.
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Nature 352:330-334(1991).
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MEDLINE=91317849;
Sakai L.Y., Keene
"Purification and
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                                             Nature
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                                                                                                                                                                                                                                                      Corson G.M., Chai
"Fibrillin binds
                                                                                                                                                                                                                                                                SEQUENCE OF 1-932 FROM N.A.
TISSUE-placenta, and Fibroblast;
MEDLINE=94010947; PubMed=7691719;
Corson G.M., Chalberg S.C., Dietz
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MEDLINE=93372860;
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Mammalia; Eutheria;
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PRECURSOR.
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PubMed=1860873;
D.R., Glanville R.W., Bachinger H.P.;
partial characterization of fibrillin,
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Primates;
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ter D.W.;
a phenotypically
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Corson G.M., Puffenberger E.G., Hamosh A., Nanthakumar
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"mutation in the epidermal growth factor-like
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Collod-Beroud G.,
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"Software and
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genetic disorders.";
cell 85:597-605(1996).
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MEDLINE=96222301; PubMed=8653794;
Downing A.K., Knott V., Werner J.M.,
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                                                                                             MEDLINE=92235290;
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MEDLINE=96174615; PubMe
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"Calcium binding properties
pair from human fibrillin-1
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C., Soussi T., Junien
abase for the analysis
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PubMed=8568869;
Cardy C.M.,
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             r E.G., Kendzior R.J. Jr.,
Francomano C.A., Cutting G.
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pr-like motif of the fibril
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D., Peltonen
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VARIANT MFS CYS-627.
VARIANT MFS CYS-627.
MEDLINE=94272487; PubMed=8004112;
Hayward C., Rae A.L., Porteous M.E.M.,
"Two novel mutations and a neutral poly
of the fibrillin gene (FBN1): SSCP scre
of the fibrillings.";
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                                                                 MEDLINE=95174777; PubMed=7870075; Hayward C., Porteous M.E.M., Broc
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factor-like motifs of the FBN1 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT EL LYS-2447.
MEDLINE=94245249; PubMed=8188302;
Lonnqvist L., Child A., Kainulain
VARIANTS MFS G217;N1023;R1074;Y1242;R1513;E2127;W2151;K2447
MEDLINE=94184368; PubMed=8136837;
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MEDLINE=94314977; Pu
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MEDLINE=95067970; PubMed=7977366;
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Dietz H.C., McInto
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M.A., Miller D.C., Francke
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19:573-576(1994).
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Francomano C.A.;
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                                                        .M., Brock D.J.I
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plypeptide is connected to a novel
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                                                                                                                                         Sykes
lin in
                                                                                                                                                                                                                                                                                                                               .M., Logie L.J., Brock L.J.;
polymorphism in EGF-like domains
screening of exons 15-21 in Marfi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-NOV-1997 (Rel. 35, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Primary structure and developmental fibrillin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=95130561;
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                               SIMILARITY: CONTAINS 7
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                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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, Bonadio J.;
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PS00022; EGF_1; 2.
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PS01187; EGF_CA; 45.
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00008; EGF; 46.
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AC Q61549;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update),
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HO
DE (CELL SURFACE GLYCOPROTEIN F4/80).

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J. Biol. Chem. 271:486--
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MEDLINE=97312684; PubMec
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DIS
                                                                         "Molecular cloning of F4/80, a murine macrophage-restricted surface glycoprotein with homology to the G-protein-linked transmembrane 7 hormone receptor family.";

J. Biol. Chem. 271:486-489(1996).
                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Peritoneal cav
MEDLINE-96132946; PubMed-8550607;
MCKnight A.J., Macfarlane A.J., Dri
                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
[1]
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InterPro; IPR001881; -.
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: IN MACROPHAGES; BUT ABSENT FROM THOSE WHICH
ARE LOCALIZED WITHIN T-CELL AREAS OF LYMPH NODES AND SPLEEN.
LOW LEVEL OF EXPRESSION ON BLOOD MONOCYTES.
SIMILARITY: CONTAINS 7 EGF-LIKE DOMAINS.
SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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TE; PS00650; G_PROTEIN_REC
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TE; PS01187; EGF_CA; 5.
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E 7, CALCIUM-BINDING
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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                                                                                                                                                                                                                                                                                                                                   sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_unclassified:*
sp_vertebrate:*
sp_virus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	1079	88.6	420	6	Q9xs50	Q9xs50 bos taurus
2	927	76.1	418	13	057352	057352 coturnix co
ω	345	28.3	126	11	035757	035757 rattus norv
4	253.5	20.8	354	4	043915	043915 homo sapien
ហ	245.5	20.2	1704	ű	Q94446	. Q94446 chironomus
6	241.5	19.8	358	11	P97946	P97946 mus musculu
7	235.5	19.3	1698	u	Q94438	Q94438 chironomus
8	217.5	17.9	326	11	035251	035251 rattus norv
9	171.5	14.1	704	ω	074567	074567 trichoderma
10	153	12.6	122	σ	Q9GLX1	Q9glx1 bos taurus
11	151	12.4	1810	<u></u> 3	Q90824	Q90824 gallus gall
12	148	12.2	800	5	Q9VB78	Q9vb78 drosophila
13	148	12.2	1532	13	Q90994	Q90994 gallūs gall
14	148	12.2	1714	13	Q90995	Q90995 gallus gall
15	145	11.9	543	ß	Q9VJU5	Q9vju5 drosophila
16	145	11.9	620	G	Q9NKD8	Q9nkd8 drosophila
17	145	11.9	830	4	043701	043701 homo sapien
18	145	11.9	830	4	Q14162	Q14162 homo sapien
19	144	11.8	663	5	044247	

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61 DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGA 120

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45 133.5 11	44 134 11	134	. 134	134	134	134	38 134.5 11	135	135	135.5	135.5	135.5	136	136	136	138	138	139.5	139.5	139.5	139.5	139.5	139.5	139.5	140.5
0 2180	0 2906							i	.1	·	-	1	N	.2	.2	W	w	5	Մ	5	5	5	5	.5	
80 5	06 11	52 5	64 5	19 11	18 11	42 13	99 4	87 4	78 13	14 11	06 11	87 2	53 5	77 5	77 5	01 5	48 5	75 5	71 11	71 4	71 4	70 11	11 5	03 11	65 5
001768	Q9WUH9	061240	Q9TVQ2	Q63722 ·	Q9QXX0	P79941	Q9NQ36	000508	Q9IBG4	054796	035452	Q49549	Q25253	Q9VYP1	Q24550	Q9VJU4	Q9NKD7	Q9GP97	Q9QW30	Q9H240	Q04721	035516	Q9VB21	Q06008	Q9NL50
001768 caenorhabdi	Q9wuh9 rattus norv	061240 halocynthia	Q9tvq2 caenorhabdi	. Q63722 rattus norv	Q9qxx0 mus musculu	P79941 xenopus lae	Q9nq36 homo sapien	000508 homo sapien	Q9ibg4 xenopus lae	O54796 mus musculu	O35452 mus musculu		Q25253 lucilia cup	. Q9vyp1 drosophila	Q24550 drosophila	Q9vju4 drosophila	Q9nkd7 drosophila	Q9gp97 caenorhabdi	Q9qw30 rattus sp.	Q9h240 homo sapien	Q04721 homo sapien	035516 mus musculu	Q9vb21 drosophila	Q06008 mus musculu	Q9n150 sarcophaga

ALIGNMENTS

Qу Дъ	Ma Qu	SQ	D D D		무무단	R R R R	22888	os Dr Dr	RESULT Q9XS50 ID Q
1 CMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDEWFSSDAGD 60 	Query Match Best Local Similarity 85.6%; Score 1079; DB 6; Length 420; Matches 179; Conservative 14; Mismatches 16; Indels 0; Gaps	SIGNAL 1 20 POTENTIAL. SIGNAL 1 20 VASCULAR ENDOTHELIAL GROWTH FACTOR C. CHAIN 21 420 VASCULAR ENDOTHELIAL GROWTH FACTOR C. SEQUENCE 420 AA; 46681 MW; 58BA84317A3C8E2D CRC64;	PROSITE: PS50278; PDGF_1; 1: PROSITE: PS50278; PDGF_2; 1: SMART; SM00141; PDGF; 1:	; IPR000072; 00341; PDGF; 1. PS00249: PDGF	DDBJ da	UENCE FROM N.A. SUE-HEART; X., Yonekura H., Yamaqishi S., Yamamo	Mammalia: Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. NCBI_TaxID=9913;:	1999 (TrEMBLrel. 12, Created) 1999 (TrEMBLrel. 12, Last sequence update) 2001 (TrEMBLrel. 16, Last annotation update) R ENDOTHELIAL GROWTH FACTOR C PRECURSOR. 100 (Bovine)	ULT 1 S50 Q9XS50 PRELIMINARY; PRT; 420 AA.

Вþ

272

DSADGFHDICGPNKELDEETCQCVCKGGLQASSCGPHKELDRDSCQCVCKNKLFPSSCGA

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RESULT
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Best Local
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SIGNAL
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SEQUENCE
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PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
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InterPro; IPR002400; -.
Pfam; PF00341; PDGF; 1.
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EMBL; Y15837; CAA75799.1; -.
HSSP; P15692; 1VPP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-98167900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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01-JUN-1998
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                                                       NRQKACEPGFSYSEEVCRCVPSYWKRPQMS 209
                                                                                                        ANREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCT 179
                                                                                                                                                                                                        CMSKLDYYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD 60
                                              VRTKRCDAGFILAEEVCRCVRTSWKRPLMN
                                                                                                                                                        -DSTDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCG 119
                                                                                           PNKEFDEEKCQCVCKKTCPKHHPLNPAKCICECTESPNKCFLKGKRFHHQTCSCYRPPCT
                                                                                                                                           SDTSEGFH-ICGPNKELDEETCQCVCKGGVRPISCGPHKELDRASCQCMCKNKLLPSSCG
                                                                                                                                                                                          CMSKLDVYRQVHSIIRRSLPATQTQCHVANKTCPKNHVWNNQICRCLAQHDFGFSSHLGD 269
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VASCULAR ENDOTHELIAL GROV

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No. 6.7e-93;
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Best Local S
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O43915; O1-JUN-1998 (TrEMBLrel. 0
01-JUN-1998 (TrEMBLrel. 0
01-MAR-2001 (TrEMBLrel. 1
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Mandriota S.J., Pepper M.S
Submitted (JUN-1997) to th
EMBL; AF010302; AAB63248.1
HSSP; P15692; ZVPF.
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                                 SEQUENCE FROM N.A. MEDLINE=98118549; PubMed=9435229;
                                                                                                                                                                                                                                                                                Rocchigiani M., Lestingi M., Luddi A., Orlandini Rossi E., Ballabio A., Zuffardi O., Oliviero S.; "Human FIGF: cloning, gene structure, and mappin between the PIGA and the GRPR genes.";
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=98140120;
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIGF OR VEGF-D.
Homo sapiens (Human).
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01-JAN-1998 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
  Alitalo
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Pfam; PF00341; PDGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                  Achen M.
                                                                                                                                     "Molecular cloning
                                                                                                                                                            Yamada Y.,
                                                                                                                                                                                                      TISSUE-LUNG;
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 Genomics
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        i.g.,
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126 A
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Jeltsch M., K
Stacker S.A.;
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novel vascular
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16,
              Kukk E.,
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Pred. No. 4.5e-30;
0; Mismatches 4
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Sciurognathi; Muridae;
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                  Maekinen
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                  Α.,
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rt tyrosine kinases VEGF receptor 2 (Fikl) and VEGF receptor 3 (Flt4).";
L Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
R EMBL; Y12866; CAA73371.1; --
R EMBL; Y12865; CAA73371.1; JOINED.
R EMBL; Y12866; CAA73371.1; JOINED.
R EMBL; Y12866; CAA73371.1; JOINED.
R EMBL; Y12866; CAA73371.1; JOINED.
R EMBL; Y12868; CAA73371.1; JOINED.
R EMBL; Y12869; CAA73371.1; JOINED.
R EMBL; Y12869; CAA73371.1; JOINED.
R EMBL; Y12870; CAA73370.1; --
R EMBL; Y12870; CAA7370.1; --
R EMBL; Y12870; CAA7370.1; --
R EMBL; Y12870; CAA7370.1; --
R EMBL; Y12870; CAA7370; CAA7370.1; --
R EMBL; Y12870; CAA7370.
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Best Local Similarity
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                                                                                                                                   TISSUE-SALIVARY GLAND;
Case S.T., Cox C., Bell W.C., H
Submitted (APR-1996) to the EMB
EMBL; U54641; AAA99804.1; -.
InterPro; IPR000561; -.
InterPro; IPR000853; -.
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      PRINTS; P
PROSITE;
PROSITE;
SEQUENCE
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SP220.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Chironomus thummi thummi (Midge).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;

Chironomoidea; Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7155;
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PR00876; MTNEMATODE.
; PS00022; EGF_1; UNKNOWN_2.
; PS01186; EGF_2; UNKNOWN_1.
E 1704 AA; 185745 MW; 3A3F20247C8F1E28
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7 (TrEMBLrel.
0 (TrEMBLrel.
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Last sequence update)
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                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
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Pred. No. 9.6e-20;
7; Mismatches 49
                                                                                                                                                                                                                                                                             Hoffman
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                                                                                                                                                                                                                                                                           ProDom; PD001629; ; 1.
PROSITE; PS00249; PDGF_1; 1
PROSITE; PS50278; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
SEQUENCE 358 AA; 40908 M
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000072; -. Pfam; PF00341; PDGF; 1. ProDom: PDOO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-MAR-2001 (TrEMBLrel. 16,
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EMBL; X99572; CAA67892.1;
EMBL; D89628; BAA14002.1;
HSSP; P15692; 1VPP.
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family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97030254; PubMed=8876195; Ordandini M., Marconcini L., Ferruz "Identification of a c-fos-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Molecular cloning or
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DICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDEN
                                                                   RHPYSIIRRSIQTPEEDECPHSKKLCPIDMLWDNTKCKCVLQDETPL---
                                                                                                     RQVHSIIRRSLPA-TLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFH
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57; Conser
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., Shimane M., Hirata
g of a novel vascular
                                                                                                                                                                                   19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GROWTH
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                                                                                                                                                      Score 241.5; I
Pred. No. 2e-1:
23; Mismatches
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FACTOR D (C-FOS, INDUCED
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l; Mismatches
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Sciurognathi; Muridae;
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                                                                                                                                                                                   241.5; DB 11;
No. 2e-18;
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CASE S.T., COX C., Bell W.C., H.
Submitted (APR-1996) to the EMB
EMBL; U54640; AAA99803.1; -.
InterPro; IPR000561; -.
InterPro; IPR000853; -.
PRINTS; PR00876; MTNEMATODE.
PROSITE; PS00022; EGF_1; UNKNOW
SEQUENCE 1698 AA; 186164 MW;
                                                                                                                                           035251;
035251;
01-JAN-1998
01-JAN-1998
01-MAR-2001
                                                                                            01-JAN-1998 (Tremblrel. 05, 01-JAN-1998 (Tremblrel. 05, 01-MAR-2001 (Tremblrel. 16, VASCULAR ENDOTHELIAL GROWTH
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01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-OCT-2000 (TrEMBLrel. 15,
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Chironomoidea; Chironomidae; Chironominae; Chironomus.
                                                        VEGF-D
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63; Conserv
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A; 186164 MW; 82
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25.7%;
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                                                                                                  Last sequence up Last annotation FACTOR D.
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les 79;
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Best Local S
Matches 52
                                                  Matches
                                                               Query Match
Best Local
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Pfam; Pf00341; PDGF; 1.
ProDom; P0001629; -; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS00249; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
SEQUENCE 326 AA; 37112 MW;
                                                                                                            STRAIN=CECT 2413;

MEDLINE=9826335; PubMed=9600944;

Rey M., Ohno S.A., Pintor-Toro J.A., Jose A., Llobell A., Benitez T.;

"Unexpected homology between inducible cell wall protein QID74 of
filamentous fungi and BR3 salivary protein of the insect Chironomus.";

Proc. Natl. Acad. Sci. U.S.A. 95:8212-6216(1998).

EMBL; X95671; CAA64974.1;
InterPro; IPRO00561; -.

PROSITE; PS01186; EGF_2; 1.

SEQUENCE 704 AA; 77925 MW; 63414BDDEC365EBC CRC64;
                                                                                                                                                                                                                                                                                                                                         O74567 PRELIMINARY;
074567;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                        Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                   QID74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 42:483-488(1997).
EMBL; AF014827; AAB66557.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SPRAGUE DAWLEY:
MEDLINE-97349118; PubMed-9205122;
Yamada Y., Nezu J., Shimane M., Hirata
"Molecular cloning of a novel vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          NCBI_TaxID=5544
                                                                                                                                                                                                                                                                                                    Trichoderma harzianum
                                                                                                                                                                                                                                                                                                                               Q174 PROTEIN.
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HSSP; P15692; 1VPP
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              CPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHD-ICGPNKEL---DEETCQCV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHPYSIIRRSI--QIPEEDQCPHSKKLCPVDMLWDNTKCKCVLQD
CPSGYTWNGHQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDRCECVCKAPCPGDLIQHPENCSCFECKESLESCCQKHKMFHPDTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RQVHSIIRRSLPATLP----QCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDG
                                                   Similarity 58; Conserv
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52; Conser
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                                                                                                                                                                                                                                                                                        Ascomycota; mitosporic Ascomycota; Trichoderma.
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31.18;
                                                              14.1%; 22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
-VHDCGKDATWQYGNCVCNKKGEVYNPKDKTCSCPPGQY 127
                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation updat
                                              Score 217.5; DB 1
Pred. No. 7.3e-16;
9; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                               704
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endothelial
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                                                   103;
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                                             Archosauria; Aves Gallus.
NCBI_TaxID=9031;
[1]
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NON_TER
NON_TER
SEQUENCE
                                       Eukaryota; Metazoa;
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Submitted (OCT-1998) to the
EMBL; AF099135; AAG29747.1;
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9GLX1;
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae;
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                                                                                                                                                                                                              FHDICGPNKELDEETCQCVCRAGLRPASCGPH-KELDRNSCQCVCKNKLFPSQCGANREF 124
                                                                                                                                                                                                                                 RHPFSIIRRSI--QIPEEDRCSHSKKLCPVDMLWDSNKCKCVLQEE---
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122 AA;
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(TrEMBLrel. 16,
(TrEMBLrel. 16,
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                             Aves;
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13820 !
                              Neognathae;
                                       Chordata; Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                12.6%;
25.5%;
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01, Last sequence update)
16, Last annotation update)
                                                                                                                                                                                                                                                                                                                      MW.
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; actyla; Ruminantia; Pecora; Bovoidea;
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                              Galliformes;
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                            tebrata; Euteleostomi;
Phasianidae; Phasiani
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                              Phasianinae;
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Best Local S
Matches 61
                                                                                                                                                                                                                                                              Q9VB78;
01-MAY-2000
01-MAR-2001
01-MAR-2001
MEDLINE-20196006: PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
Evans C.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones F.S., Hoffman S., Cunningham B.A., Edelman G.M.;
"A detailed structural model of cytotactin: protein homologies,
alternative RNA splicing, and binding regions.";
Proc. Natl. Acad. Sci. U.S.A. 86:1905-1909(1989).
EMBL; J04519; AAA48745.1; -.
HSSP; P24821; 1TEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00008; EGF; 13.
pfam; PF00041; fn3; 11.
pfam; PF00147; fibrinogen_C; 1.
pROSITE: PS00022; EGF_1; UNKNOWN_14.
PROSITE: PS01186; EGF_2; 14.
SMART; SM00186; FBG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-like domain; Glycoprotein; Signal.
                                                                                                                       STRAIN-BERKELEY
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  CG6124 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                            419
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                                                                                                                                                                                                                                                                                                                                                                                                                      CTNRQKACEPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKCAC-----ECTES--PQKCLLKGKKFHHQTCSCY----
                                                                                                                                                                                                                                                                                                                                                                                            CINGQCVCDEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLCVCHEGFVGDDCSQKRCPKTCNNRGRCVDGR-CVCHEGYLGEDCGELRCPNDCHNRGR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVCDEGYTGEDCGELICPNDCFDRGRCINGTCFCEEGYTGEDCGELTCPNNCNGNGRCEN 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CVCKNKLFPSQCG----ANREFDENTC---QCVCKR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGYTGP--DCGEELCPHGCGIHGRCVGGRCVCHEGFTGEDCNEPLCPNNCHNRGRCVDNE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNC--SEPACPRNCL-NRGLCVRAKCICEEGFTGEDCSQARCPSDCNDQGKCVDGVCVCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQCQAANKTCPTNYMWNNHIC---RCLAQEDF-----MFSSDAGDDS--TDG----F 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HDICGPNKELDEETC------QCVCRAGLRPASCG----PHKELDRNSC---Q 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000561; -. IPR001777; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1810 AA;
                                                                                                                                                                                                                                                            (TrEMBLrel. 13, (TrEMBLrel. 16, (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199304 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                            Created)
Last sequence up
Last annotation
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                      800
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.4e-08;
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                                                                                                                                                                                                                                                            update)
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RA POSIER C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C., Ra, Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Ra Hostin D., Lei Y., Lei Y., Levitsky A.A., Li J., Li J., Liang Y., Lin X., Ra Liako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Mount S.M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Ra Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Ra Syler E., Spradling A.C., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Ra Syler E., Spradling A.C., Stapleton M., Strong R., Sun E., Ra Syler E., Spradling A.C., Stapleton M., Strong R., Sun E., Ra Syler E., Spradling A.C., Stapleton M., Strong R., Sun E., Ra Syler E., Spradling A.C., Stapleton M., Strong R., Sun E., Ra Syler E., Spradling A.C., Stapleton M., Strong R., Sun E., Ra Syler E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling S.M., Weinstock G.M., Weissenbach J., Ra Sheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Ra Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Ra Sheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Ra Sheng X.H., Zhong F.N., Zhong M., Venter J.C., RT "The genome sequence of Drosophila melanogaster."; Escience 287:2185-2195(2000).
    RESULT
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Best Local :
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                                                                                                                                                                                                               090994 PRELIMINARY; PRT; 090994; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence of the control of the control
NCBI_TaxID=9031;
                                                   Gallus
                                                                                              Archosauria;
                                                                                                                               Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P02876; 9WGA.
FlyBase; FBgn0039484; CG6124.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 CVAPNECSCNAGYTKLEGVCTPVCK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRCSPVCSGGCKNGFCVAPGKCSCDEGYIKGTGNSCKPICSKGCENGFCDAPEKCSCNDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T-CQCVCRAGLRPASC-GPHK-ELDR----NSCQCVCKNKL-----FPSQCGANRE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQKACEPGFSYSEEVCRCVPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- KGCENGFCDAPEKCSCNDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEMDGENRCSPVCSGGCKNGFCVAPGKCSCD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FD---ENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS01186; EGF_2; UNKNOWN_9.
800 AA; 87721 MW; A7CA1C171DA189C8 CRC64;
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                                                                                              Aves;
                                                                                         Neognathae;
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                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
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Pred. No. 5.7e-08;
                                                                                         Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 800;
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                                                                                         Phasianinae;
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Best Local
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                                                                                              Q90995;
Q90995;
Q1-NOV-1996 (TrEMBLrel. 01, C
Q1-NOV-1996 (TrEMBLrel. 16, L
Q1-MAR-2001 (TrEMBLrel. 16, L
200 KDA TENASCIN PRECURSOR.
                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
Archosauria; Aves; Neogn
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CHAIN
SEQUENCE
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Pfam; PF00041; fn3; 8.
Pfam; PF00147; fibrinogen_C;
Submitted (JUL-1989) to the EMBL/GenBank/DDBJ databases
                      SEQUENCE FROM N.A.
                                             NCBI_TaxID=9031;
                                                                                                                                                                 Q90995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00022; EGF_PROSITE; PS01186; EGF_SMART; SM00060; FN3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M23121; AAA49085.1; -. HSSP; P24821; 1TEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant tenascin fragments."; Cell 59:325-334(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001777; -.
InterPro; IPR002181; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90030407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                      14
                                                                                                                                                                                                                        CINGQCVCDEGF
                                                                                                                                                                                                                                                                                                                    CVCDEGYTGEDCGELICPNDCFDRGRCINGTCFCEEGYTGEDCGELTCPNNCNGNGRCEN 359
                                                                                                                                                                                                                                              CTNRQKACEPGF
                                                                                                                                                                                                                                                                                              GKCAC-----
                                                                                                                                                                                                                                                                                                                                           CVCKNKLFPSQCG----ANREFDENTC---QCVCKR-----TCPRNQPLN----P 145
                                                                                                                                                                                                                                                                       GLCVCHEGFVGDDCSQKRCPKDCNNRGHCVDGR-CVCHEGYLGEDCGELRCPNDCHNRGR
                                                                                                                                                                                                                                                                                                                                                                   EGYTGP -- DCGEELCPHGCGIHGRCVGGRCVCHEGFTGEDCNEPLCPNNCHNRGRCVDNE
                                                                                                                                                                                                                                                                                                                                                                                                                 PNC--SEPACPRNCL-NRGLCVRGKCICEEGFTGEDCSQAACPSDCNDQGKCVDGVCVCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1043
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                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                             ECTES - - POKCLLKGKKFHHQTCSCY - - - -
                                                                                                                                                                                                                          430
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1532
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                                                                    Chordata; Craniata; Vertebrata; Eutel
Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.2%;
24.2%;
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_2; 14.
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                                                                                                                                          Created)
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                                                                                                                 Last sequence update)
Last annotation updat
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POTENTIAL.
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Pred. No. 1e-07;
0; Mismatches 79;
                                                                                                                                                                PRT;
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                                                                             Euteleostomi
                                                                     Phasianinae;
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Best Local
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Pfam; PF000041; fn3; 10.
Pfam; PF000147; fibrinogen_C; 1
PROSITE; PS00022; EGF_1; UNKNC
PROSITE; PS01186; EGF_2; 14.
                                                                                                                          Q9VJU5 PRELIMINARY; PRT; 543 AA.
Q9VJU5;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2001 (TrEMBLrel. 16, Last annotation update)
BG:DSO0180.10 PROTEIN.
BG:DSO0180.10 OR CG8942.
MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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CHAIN
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SEQUENCE
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EGF-like
                                      STRAIN-BERKELEY
                                                                      Ephydroidea; Drosophilidae; NCBI_TaxID=7227;
                                                                                              Eukaryota; Metazoa; I Pterygota; Neoptera;
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                                                 SEQUENCE FROM N.A.
                                                                                                                     Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M23121; AAA49084.1; -. HSSP; P24821; 1TEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000561; -. InterPro; IPR001777; -. InterPro; IPR002181; -.
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                                                                                                                                                                                                                                                                                                           GLCVCHEGFVGDDCSQKRCPKDCNNRGHCVDGR-CVCHEGYLGEDCGELRCPNDCHNRGR 418
                                                                                                                                                                                                                                                                                                                                 GKCAC-----ECTES--PQKCLLKGKKFHHQTCSCY------
                                                                                                                                                                                                                                                                                                                                                         CVCDEGYTGEDCGELICPNDCFDRGRCINGTCFCEEGYTGEDCGELTCPNNCNGNGRCEN
                                                                                                                                                                                                                                                                                                                                                                                CVCKNKLEPSQCG----ANREFDENTC---QCVCKR------
                                                                                                                                                                                                                                                                                                                                                                                                      EGYTGP--DCGEELCPHGCGIHGRCVGGRCVCHEGFTGEDCNEPLCPNNCHNRGRCVDNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQCQAANKTCPTNYMWNNHIC---RCLAQEDF-----MFSSDAGDDS--TDG----F
                                                                                                                                                                                                                                                                                                                                                                                                                            HDICGPNKELDEETC-----QCVCRAGLRPASCG----PHKELDRNSC---Q 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00186; FBG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain; Glycoprotein;
                                                                                    melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Metazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;
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A; 188515
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Pred. No. 1.1e
20; Mismatches
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POTENTIAL.
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W; A6FB0CFD623CDE53
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.1e-07;
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R.F.,
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Cherriera S., Fleischmann W.,
RA Codson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Chodson K., J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Meinton D.R., Nelson K.A., Nixon K., Musphy L., Muzny D.M., Nelson D.L.,
RA Meinton D.R., Pacleb J.M.,
RA Meinton D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Sampson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y. Wassarman D.A., Weinstock G.M., Weinschach J.,
RA Yeng X.H., Zhong F.M., Zhong K.G., Wang S., Yao Q.A.,
RA Yeng X.H., Zhong F.M., Ra Weinstock G.M., Weinschach J.,
Ra Schen R., Schen R., Schen R., Schen R., Shu S.,
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Best Local
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PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF-like
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Pallin, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 287:2185-2195(2000).
EMBL; AE003642; AAF53364.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0028545;
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                                                196
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    203 WKRP 206
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                                                                                       CTESPQKCLLKGKKFHHQTCSCY-----RRPCTNR-QKACEPGFSYSEEVCRCVPSY
                                                                                                                                   CGQNSRCVRPGVCECENGYAGDDGGTNCRPVCS-TCPENGLCLSPGVCVCKPGYVMRNDL
                                                                                                                                                                               CGAN-REFDENTCQC----
                                                                                                                                                                                                                                                                  TDGFHDICGPNKELDEETCQCVCRAGLRPASCGP-----HKELDRNSCQCVCKNKLFPSQ 117
                                                                                                                                                                                                                                                                                                                                                       SLPATLPQCQA-----ANKTCPTNYMWNNHICR----CLAQEDFMFSSDAGD-----DS
                                              CQPHCEKCSDNAHCVAPNQCECFPGYESSGADKKCVPKCSKGCTNGFCFAPETCVCSIGY
                                                                                                                                                                                                                        ECGHHSFC----SEPGKCECEPGYEKVGNGTVFPDGYKNNSNGNCSPIC----
                                                                                                                                                                                                                                                                                                             SSPNTC-SCNAGYGGIDCHPVCPT-VCGKNEFCDRPGVCSCQNGYKRTSPSDNCLPVCEK 88
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57; Conserv
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543 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein.
A; 58562 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                   Score 145; DB 5;
Pred. No. 8.7e-08;
9; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F419FDAFC4AD0D2A CRC64;
                                                                                                                                                                            - VCKRTCPRN-QPLNPGKCACE - - -
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В

256 QMGP

259

Search completed: October 17, 2001, 14:50:53 Job time: 419 sec

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4.5 Compugen Ltd

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Result
No.
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                                                                                                                                                                                                                                                                              Score
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1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*
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13: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*
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/SIDSB/gcgdata/geneseq/yeneseqp/AA1985.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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ALIGNMENTS

RESULT AAW86225

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16-FEB-1999 (first entry)

AAW86225;

AAW86225 standard; protein;

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VEGF; VRP; vascular endothelial growth factor; VEGF-related protein; recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia; coronary; collateral vessel development; cell growth; migration; heart; lower limb ischaemia; stroke; peripheral vascular disease; intestine; wound healing; skin; vascular permeability.
New truncated vascular endothelial growth factor-related subunits - lack part of the N-terminal sequence, used to
                                        WPI; 1999-009426/01.
                                                                                                                                                  20-APR-1998;
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                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                          Human VEGF-C truncated fragment 4.
                                                                                            (COLL-) COLLATERAL THERAPEUTICS
                                                                                                                       25-APR-1997;
                                                                                                                       97US-0842984.
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                                                                                           25-APR-1997;
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                                          (COLL-) COLLATERAL THERAPEUTICS
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Pred. No. 2.2e-82;
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                                                                                                                                                  VEGF; VRP; vascular endothelial growth factor; VEGF-related protein; recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia; coronary; collateral vessel development; cell growth; migration; heart; lower limb ischaemia; stroke; peripheral vascular disease; intestine; wound healing; skin; vascular permeability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to truncated VRP (vascular endothelial growth factor (VEGF)-related protein) subunits that have at least one amino acid N-terminal to the first Cys of the core sequence deleted. Host cells transformed or transfected with expression vectors containing
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                                                                                                                                                                                                                                                                Human VEGF-C
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                                                                                    WO9849300-A2
                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                               16-FEB-1999 (first entry)
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100.0%; Pred. No. 2.2e-82;
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25-APR-1997;

97US-0842984.

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RESULT
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Best Local
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                                                             VEGF; VRP; vascular endothelial growth factor; VEGF-related protein; recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia; coronary; collateral vessel development; cell growth; migration; heart; lower limb ischaemia; stroke; peripheral vascular disease; intestine; wound healing; skin; vascular permeability.
                                Homo sapiens
                                                                                                                                                                     Human VEGF-C truncated fragment 1.
                                                                                                                                                                                                         16-FEB-1999
                                                                                                                                                                                                                                                                      AAW86222 standard; protein; 307 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                302 AA;
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                                                                                                                                                                                                       (first entry)
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Pred. No. 2.3
0; Mismatches
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hes 0;
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WO9849300-A2

Homo sapiens

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acids encoding the truncated VRP subunits are used to produce the truncated proteins recombinantly. The truncated VRP subunits, optionally expressed from gene therapy vectors, have in vivo and in vitro angiogenic activity and are used to stimulate angiogenesis, particularly coronary collateral vessel development in cases of cardiac ischaemia; to stimulate endothelial cell growth and migration in vitro; to treat heart disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic lower limb ischaemia; stroke and peripheral vascular disease); to promote healing of wounds (of skin or intestines), and to increase vascular permeability. Sequences AAW86222 to AAW86225 represent truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor (VEGF)-related protein) subunits that have at least one amin acid N-terminal to the first Cys of the core sequence deleted. Host cells transformed or transfected with expression vectors containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New truncated vascular endothelial growth factor-related protein subunits - lack part of the N-terminal sequence, used to stimulate angiogenesis, e.g. for treating heart disease and ischaemia
                               pharmaceutical
                                              Growth factor; human;
                                                                                                            14-JUL-1999
                                                                                                                                                                         AAY08284 standard; Protein; 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              permeability. Sequences fragments of VEGF-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-009426/01
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                                                                                                                                                                                                                                                        296 cvpsywkrpqms 307
                                                                                                                                                                                                                                                                                      181 CVPSYWKRPQMS 192
                                                                                                                                                                                                                                                                                                                       236
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                                                                                                                                                                                                                                                                                                                                                                                     176
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                                                                            growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 AA;
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                                                                            factor protein
                                                                                                          (first entry)
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                                              dimer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                            fragment VEGF-C
                                            cysteine knot; cellular inclusion body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1130; DB 20;
Pred. No. 2.3e-82;
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RESULT
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                                                                            VEGF; VRP; vascular endothelial growth factor; VEGF-related protein; recombinant; truncated; gene therapy; anglogenesis; cardiac ischaemia; coronary; collateral vessel development; cell growth; migration; heart; lower limb ischaemia; stroke; peripheral vascular disease; intestine; wound healing; skin; vascular permeability.
05-NOV-1998
                          WO9849300-A2
                                                    Homo sapiens
                                                                                                                                                              Human VEGF-C full length sequence
                                                                                                                                                                                          16-FEB-1999
                                                                                                                                                                                                                     AAW86237;
                                                                                                                                                                                                                                             AAW86237 standard; protein; 399 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein fragments used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preparing active growth factor dimers
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                                                                                                                                                                                                                                                                                                                                                                                                                           eetcqcvcraglrpascgphkeldrnscqcvcknklfpsqcganrefdentcqcvckrtc 246
                                                                                                                                                                                                                                                                                                                                                                                                                                       EETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 8; 14pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 AA;
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Pred. No. 2
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thes 0;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     optionally expressed from gene therapy vectors, have in vivo and in vitro angiogenic activity and are used to stimulate angiogenesis, particularly coronary collateral vessel development in cases of cardiac ischaemia; to stimulate endothelial cell growth and migration in vitro; to treat heart disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic lower limb ischaemia; stroke and peripheral vascular disease); to promote healing of wounds (of skin or intestines), and to increase vascular permeability. Sequences AAM86234 to AAW86239 represent full length VRP sequences from which the truncated fragments are created.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor (VEGF)-related protein) subunits that have at least one amino acid N-terminal to the first Cys of the core sequence deleted. Host cells transformed or transfected with expression vectors containing nucleic acids encoding the truncated VRP subunits are used to produce the truncated proteins recombinantly. The truncated VRP subunits,
                                                                                   Foetal liver kinase 1 binding protein; human; flk-1bp;
                                                                                                                                                            13-JAN-1998
                                                                                                                                                                                                                                   AAW17837 standard; Protein; 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                angiogenesis, e.g. for treating heart disease and ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New truncated vascular endothelial growth factor-related protein subunits - lack part of the N-terminal sequence, used to stimulate
                                                                     receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-009426/01.
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                                                                                                                                                                                                                                                                                                                       388 cvpsywkrpqms
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                                                healing;
                                                                                                                         foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine kinase; vasculogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1130; DB 20; ilarity 100.0%; Pred. No. 2.9e-82; Conservative 0; Mismatches 0;
                                                                                                                   liver kinase A binding protein
                                                                                                                                                          (first entry)
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                                                  tumour; therapy;
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                                                                                                                                                                                                                                                                                                                           399
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                                                  antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (vascular endothelial
                                                                     angiogenesis;
                                                                                                                       flk-1bp.
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Homo sapiens

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                                                                                                                                                                                                                                                                                                        This polypeptide comprises a human foetal liver kinase 1 binding protein (flk-lbp) (see AAW17837) that binds to the receptor tyrosine kinase flk-l expressed on vascular endothelial and other cells. The mature flk1-bp can be secreted from host cells transformed with an expression vector including an isolated flk-lbp cDNA clone (see AAT68811). Flk-lbp can be used to isolate cells to which it binds, for use in studying the roles of such cells and of flk-l in vasculogenesis and angiogenesis. Angiogenesis inhibition or increased vascularisation may be clinically desirable (e.g. to suppress solid tumour growth or in wound healing, respectively). The flk-lbp can be administered to treat conditions with defective or insufficient flk-l. Polypeptides may also act as carriers to deliver diagnostic/therapeutic agents to cells to which flk1-bp binds, to generate antibodies, and to identify flk-lbp antagonists of useful for treating flk-lbp mediated conditions.
                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 192; Conserv
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 30-32; 43pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding a human foetal liver kinase 1 binding protein to treat conditions with insufficient protein, deliver agents cells and identify antagonists to treat protein-mediated cond
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cvpsywkrpqms
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                            CVPSYWKRPQMS
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                                                                                                                                                                                                                                                                                      419 AA;
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21..35
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  419
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                            192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                               Score 1130; DB 18;
Pred. No. 3.1e-82;
                                                                                                                                                                                                                   Mismatches
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RESULT AAW00932

The polypeptide, or

active fragments,

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01-AUG-1995;
12-JAN-1996;
14-FEB-1996;
     This polypeptide comprises the pre-pro sequence of human VEGF-C, a novel ligand that binds specifically to human Flt4 receptor tyrosine kinase (VEGFR-3), stimulating phosphorylation of the receptor. Its sequence was deduced from a cDNA clone (AAT84276) obtd. from a PC-3 prostatic adenocarcinoma cell (ATCC CRL 1435)
                                                                                          Flt4 receptor tyrosine kinase ligand and related nucleic acid to modulate growth of endothelial cells and for diagnosis of endothelial cell diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vascular endothelial growth factor receptor-3; ligand;
angiogenesis; wound healing; lymph vessel; lymphangioma;
cancer; metastasis; therapy; diagnosis; antibody; inhibitor
                                                                                                                                     N-PSDB;
                                                                                                                                                                   Alitalo K,
                                                                                                                                                                                                                                                                 01-AUG-1996;
                                                                                                                                                                                        (UYHE-) UNIV HELSINKI LICENSING
                                                                                                                                                                                                                                                                                     13-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW00932 standard; Protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eptide
                                                                                                                                   1997-145688/13.
DB; AAT84276.
                                                                      7;
                                                                     Page 112-113; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor tyrosine kinase ligand VEGF-C.
                                                                                                                                                                   Joukov
                                                                                                                                                                                                          96US-0671573.
95US-0510133.
96US-0585895.
96US-0601132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor tyrosine kinase; VEGFR-3;
                                                                                                                                                                                                                                                                96WO-FI00427
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                                                                                                                                                                                                                                                                                                                                                                                                                         "preferred
retaining
                                                                                                                                                                                                                                                                                                                            "preferred
retaining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "preferred active fragment of VEGF-C, retaining Flt4 ligand activity (Clai
                                                                                                                                                                                                                                                                                                                                                                      "preferred
                                                                                                                                                                                                                                                                                                                                                                                                    "preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "preferred
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Flt4 li
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Flt4 lj
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F1t4 li
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                                                                                                                                                                                                                                                                                                                                                                                          active fragm
Flt4 ligand
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Flt4 ligand
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igand activity (Claim 11)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity (Claim 12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity (Claim 15)"
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RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed in transformed or transfected host cells for use in claimed methods for detecting endothelial cells (e.g. to image lymphatic vessels, endothelial venules, Fit4 receptor in histochemical tissue) and also to modulate the growth of mammalian endothelial cells (e.g. to accelerate angiogenesis and to promote endothelial function of lymphatic vessels). Inhibitors of VEGF-C, such as antibodies, can be used to control endothelial cell proliferation, e.g. lymphangioma or metastatic cancer. Mouse and quail VEGF-C sequences (see AAW00934-35) have also been
         Lee J,
                               (GETH ) GENENTECH
                                                      08-SEP-1995;
                                                                              30-AUG-1996;
                                                                                                     13-MAR-1997.
                                                                                                                             WO9709427-A1
                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                Protein
                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                            receptor protein tyrosine kinase; Flt4; signal transduction; wound healing; vulnerary; rheumatoid arthritis; Kaposi's sarcoma; therapy; diagnosis; angiogenesis; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                 Vascular endothelial growth factor-releated protein; VRP; VEGF;
                                                                                                                                                                                                                                                                                                                                        Human vascular endothelial growth factor-related protein VRP.
                                                                                                                                                                                                                                                                                                                                                                05-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                        AAW13833;
                                                                                                                                                                                                                                                                                                                                                                                                              AAW13833 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prnqplnpgkcacectespqkcllkgkkfhhqtcscyrrpctnrqkacepgfsyseevcr 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192;
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          Wood
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                                                        95US-0003491
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                                                                               96WO-US14075
                                                                                                                                                                                                                     Location/Qualifiers 1..20
                                                                                                                                                                                                /label= Sig_peptide 20..419
                                                                                                                                                              /note=
                                                                                                                                                                                    /label= Mat_protein
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                                                                                                                                                             "deduced residue
                                                                                                                                                  tyrosine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1130;
Pred. No. 3
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                                                                                                                                                             from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.1e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 18;
                                                                                                                                                             nucleotide sequence
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AAW75751
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A human vascular endothelial growth factor (VEGF)-related protein (VRP) (AAW1833) has been identified that binds to, and stimulates the phosphorylation of, the receptor tyrosine kinase Flt4. It is postulated to be a third member of the VEGF protein family. Its amino acid sequence was deduced from a cDNA clone (AAT59929) obtd. from a glioma G61 library. Recombinant VRF can be produced in transformed host cells and used: to promote growth of vascular and lymph endothelial cells; to stimulate phosphorylation of the tyrosine kinase domain of a Flt4 receptor; as a diagnostic; as an additive to cell cultures; to screen for (ant)agonists: and to raise monoclonal antibodies used to treat conditions associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with excessive neovascularisation or vascular permeability. may make it possible to avoid coronary by-pass surgery by stimulating growth of the collateral circulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein similar to treat e.g. wounds,
                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                           Flt4; vascular endothelial growth factor C; vascular endothelial cell; lymphatic endothelial cell; myelopoiesis; anglogeneses; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vascular endothelial growth factor C protein analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW75751 standard; Protein; 419
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                                                                                       WO9833917-A1
                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                lymphangiogenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                         Location/Qualifiers 156
                                                                                                                                                                           /note=
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                                                                                                                                                                           "Xaa
                                                                                                                                                can
                                                                                                                                                                                                                                                                                                                                                   ; myelopoiesis;
elephantiasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.
                                                                                                                                             can be anything be nothing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1130; DB 18;
Pred. No. 3.1e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                      angiogeneses; in:
Milroy's disease
                                                                                                                                                                           other than cysteine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·_
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06-AUG-1998

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                                                                                                                                           Flt4; vascular endothelial growth factor C; vascular endothelial cell; lymphatic endothelial cell; myelopoiesis; angiogeneses; inflammation; lymphangiogenesis; oedema; elephantiasis; Milroy's disease.
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                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                   Human vascular endothelial growth factor C protein.
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Pred. No. 3.1e-82;
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WO9833917-A1

recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia; coronary; collateral vessel development; cell growth; migration; heart; lower limb ischaemia; stroke; peripheral vascular disease; intestine; wound healing; skin; vascular permeability.

VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;

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RESULT 1
AAW86203
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Matches 192
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                             Human VEGC protein.
                                                                                          AAB10648
                                                                                                                         AAB10648 standard; Protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                            eetcqcvcraglrpascgphkeldrnscqcvcknklfpsqcganrefdentcqcvckrtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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stimulate
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Best Local Similarity
Matches 192; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel vascular endothelial growth factor-X (YEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vascularization including formation and proliferation of new blood vascularization in subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote the products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1998;
18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth; VEGC.
                                                                                                                                                                                                                                                                                                                                                                                                                              tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGC protein used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     skin graft growth, tissue repair, proliferation of new blood vessels,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 11; 127pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-442669/38
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                                                                      SLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELD 60
                                    CVPSYWKRPQMS 192
                                                                                                                                                                   EETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTC
                                                                                                                                                                                                                      {\tt slpatlpqcqaanktcptnymwnnhicrclaqedfmfssdagddstdgfhdicgpnkeld}
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cvpsywkrpqms
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99US-0124967.
99US-0164131.
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                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                 Score 1130; DB 21;
Pred. No. 3.1e-82;
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VEGF-X;

vascular endothelial growth factor; human; vulnerary; cytostatic;

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                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                           onset
                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                    altering the sequence receptor-3 -
                                                                                                                                                                                                                                                                                                                                                                                                                                             disorder,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, Flt4, fms-like tyrosine kinase 4; lymphoedema; vascular endothelial growth factor receptor 3; VEGFR-Milroy-Nonne syndrome; lymphoedema praecox; VEGF-C; vascular endothelial growth factor C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human VEGF-C
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                                                                                                                                         slpatlpqcqaanktcptnymwnnhicrclaqedfmfssdagddstdgfhdicgpnkeld 287
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cvpsywkrpqms
                                                                    PRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCR 180
                                                                                          eetcqcvcraglrpascgphkeldrnscqcvcknklfpsqcganrefdentcqcvckrtc
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)B; AAC62406.
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UNIV HELSINKI LICENSING
                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                  early onset lymphoedema and lymphoedema praecox, which is late
                                                                                                                                                                                                                                                                                                                                                                                                                                a human subject for increased risk of developing a lymphatic comprises assaying a nucleic acid to determine a mutation the sequence of a vascular endothelial growth factor
                                                                                                                                                                                                                                                    419
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                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              76pp; English.
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                      The patent discloses a method to treat neoplastic disease characterised by expression of fms-like tyrosine kinase 4 (F1t4) receptor (also referred as vascular endothelial growth factor receptor-3) VBGFR-3) in endothelial cells of blood vessels adjacent to malignant neoplasm. The method involves administering a compound that inhibits binding of a ligand to F1t4 thereby inhibiting F1t4 mediated proliferation of vascular endothelial cells. The compound is useful for treating neoplastic disease such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas,
                                                                                                                                                                                                                                                                                                                    Treating neoplastic diseases such as lymphoma, cand sarcomas, involves administering a compound binding of ligand proteins to fms-like tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis; neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma; sarcoma; malignancy; VEGF-C; vascular endothelial growth factor C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIND
                                                                                                                                                                                                                                                                     15-17; Page 140-142; 148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LUDWIG INST CANCER RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaipainen A,
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  Flt4 receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note- "Has a pattern of spaced cysteine residues reminiscent of a Balbiani ring 3 protein (BR3P) sequence; cleavage of signal peptide and the C-terminal peptide produces a partially processed form of VEGF-C of about 29 kD which has high affinity to Flt4 (VEGFR-3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at position 156 i
165 is essential
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/note= "cleavage of this peptide from partially processed
VEGF-C produces a fully processed mature form of VEGF-C
of 21-23 kD which has high affinity to VEGFR-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "important for VEGF-C activity"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-terminal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds and stimulates VEGF-C
156 is essential for VEC
ntial for VEGFR-2 and VEC
  tyrosine kinase binding
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and VEGFR-3
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Search completed: October 17, 2001, 14:46:01 Job time: 127 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for manufacturing medicament useful for diagnostic screening, imaging and treatment of malignancies characterised by Flt4-expressing blood cells. The Flt4 gene maps to chromosomal region 5q35 and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in their 3' sequences and are differentially expressed in HEL and DAMI cell lines. Flt4 belongs to a subfamily of class III receptor tyrosine kinases (RTKs). It is used as a target for tumour imaging and anti-tumour therapy. The present sequence is a human prepro-vascular endothelial growth factor C (VEGF-C), a specific example of Flt4 binding compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                           408 cvpsywkrpqms 419
                                                                                                             181 CVPSYWKRPQMS 192
                                                                                                                                                                                         121 PRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCR 180
                                                                                                                                                                                                                                         348 prnqplnpgkcacectespqkcllkgkkfhhqtcscyrrpctnrqkacepgfsyseevcr 407
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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1 SLPATLPQCQAANKTCPTNY.....SYSEEVCRCVPSYWKRPQMS
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US-08-99-042-105-4
US-08-99-042-105-18
US-09-042-105-18
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159 SLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELD 218

Qy 1 SLPATIPOCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDSTDGFHDICGPNKELD	Query Match 100.0%; Score 1130; DB 4; Length 350; Best Local Similarity 100.0%; Pred. No. 3e-95; Matches 192; Conservative 0; Mismatches 0; Indels 0; Ga	JENUTH: 350 amino acids TYPE: amino acids TYPE: amino acids TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 33: US-08-510-133A-33 ()	REFERENCE/DOCKET NUMBER: 38113/32863 ; REFERENCE/DOCKET NUMBER: 28113/32863 ; TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300 ; TELEPAX: 312/474-0448 ; INFORMATION FOR SEQ ID NO: 33: INFORMATION FOR SEQ ID NO: 33:	10,133A	STATE: Illinois COUNTRY: United States of America TIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPATION STATEM PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25	JOUKDAY, VIAGOMÍT TITLE OF INVENTION: Receptor Ligand NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago	ion US/08	28 130 11.5 1218 2 US-08-400-159-6 Sequence 6. 29 130 11.5 1218 3 US-08-611-729A-6 Sequence 6. 30 130 11.5 1218 4 US-08-82-046-2 Sequence 2. 31 130 11.5 2199 5 PCT-US95-11684-2 Sequence 2. 32 128 11.3 2703 1 US-08-820-170A-25 Sequence 2. 33 125.5 11.1 374 2 US-08-820-170A-25 Sequence 2. 34 125.5 11.1 374 3 US-09-055-699-25 Sequence 2. 35 125.5 11.1 374 4 PCT-US95-06385-25 Sequence 2. 36 125.5 11.1 374 5 PCT-US95-06385-25 Sequence 2. 37 125 11.1 2556 1 US-08-083-590A-20 Sequence 2. 38 125 11.1 2556 1 US-08-083-590A-20 Sequence 2. 39 124 11.0 314 2 US-08-60-309-19 Sequence 2. 40 124 11.0 314 2 US-08-60-309-19 Sequence 1. 41 123 10.9 2050 2 US-08-32-07-19 Sequence 1. 42 12 10.8 1193 3 US-08-611-729A-10 Sequence 1. 43 122 10.8 1193 3 US-08-611-729A-10 Sequence 1. 44 122 10.8 2556 1 US-08-882-046-6 Sequence 6.
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Best Local Similarity
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 35
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181
                                                                                          219 EETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTC 278
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
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100.0%; Pred. No. 3e
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South Wacker Drive
                                                                                                                                                                                                                  0; DB 4; Length 350;
3e-95;
hes 0; Indels 0
                                                                                                                                                                                                                    0;
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                                                                                     Query Match
Best Local Similarity
                                                                       Matches
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APPLICANT: Alitalo,
APPLICANT: Joukov,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F196/004
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION NUMBER: 08/601,132
APPLICATION NUMBER: 08/601,132
                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 14-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 12-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/5
FILING DATE: 01-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,011
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                                                                                                                                                                                                                                                                   TELEFAX: 25-3856
TYPE: ami
TOPOLOGY:
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STATE: Illinois
COUNTRY: United States of America
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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o. 6130071
                                                                                                                                                                                                      4: 419 amino acids amino acid
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Llarity 100.0%;
Conservative 0
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00 Sears Tower, 233
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                                                                     Score 1130; DB 4; Pred. No. 3.6e-95; Mismatches 0;
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-08-510-133A-35
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                                                                                                                                                                                                                                                                            Best Local Sin
Matches 192;
                                                                                                                                                                                                                                                                                                                    Query Match
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INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                       348
                                                                            121
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181 CVPSYWKRPQMS 192
                                                                                                                                                                                                                                                                                           Local Similarity
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REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFFICATION: «Unknown»
ATTORNEY/AGENT_INFORMATION:
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MEDIUM TYPE: Floppy disk
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Joukov, Vladomir
                                                                                                                                        EETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTC 120
                                                       PRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCR 180
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                                       PRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCR
                                                                                                                   EETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTC
                                                                                                                                                                                              SLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELD 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
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COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 419 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 312/474-0448
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Pred. No. 3.6e-95;
Nismatches 0;
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                                                                                                                                                                                                                                                                                                                                                       Matches 191;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202)371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/4
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 8-MAR-1994
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NUMBER OF SEQUENCES: 15
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TITLE OF INVENTION: VA
                                                                                                                                    121 PRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCR 180
                                                                                                                                                                                              219
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                                                                      181 CVPSYWKRPQMS 192
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                                                                                                                                                                                                                   61 EETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTC 120
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                                   CVPSYWQRPQMS 350
                                                                                                                 PRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCR
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GY: linear
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ROSEN, CRAIG A.
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                                                                                                                                                                                                                                                                                                                                                                       99.6%;
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Pred. No. 6.9e-95;
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Length 350; Indels

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-824-996-2
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen, Craig A.
APPLICANT: Cao, Liang
APPLICANT: Cao, Liang
TITLE OF INVENTION: Polynucelotides Encoding Vascular Endothelial Growth
TITLE OF INVENTION: Factor 2
FILE REFERENCE: PF112D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: 08/207,550
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER FILING DATE: 1994-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hu, Jing-Shan
                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                  PRIOR APPLICATION DATA:
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                                FILING DATE: H
                                                                                                                                                                                                                            CITY: WASHINGTON STATE: DC
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                                                                                                                                                                                                          COUNTRY:
                                                               APPLICATION NUMBER:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                  CAO, LIANG
                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                  HU, JING-SHAN
ROSEN, CRAIG !
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                                                  HEREWITH
                                                                                                                                                                                                                                                                                                                                                                    CRAIG A.
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99.5%;
                                                                                                                                                                                                                                                                                 KESSLER, GOLDSTEIN & FOX
US 08/207,550
                                                                   US/09/042,105
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Pred. No. 6.9e-95;
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RESULT 8
US-08-999-811-2
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Best Local Similarity
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                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIA REPLICATION DATA:
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED
                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                         COUNTRY: U
ZIP: 20005
                                                                                                                                                                                                         STREET: 1100 NEW CITY: WASHINGTON
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CLASSIFICATION:
                APPLICATION NUMBER: FILING DATE: HEREW
                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                             ADDRESSEE: STERNE, KESSLER, OSTREET: 1100 NEW YORK AVENUE
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                                                                    PatentIn Release #1.0, Version #1.30
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                HEREWITH
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                                                                                                                                                                                                                                                                                                   VASCULAR ENDOTHELIAL GROWTH FACTOR
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Pred. No. 6.9e-95;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:

06-JUN-1995

US 08/465,968

FILING DATE:

8-MAR-1994

US 08/207,550

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

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US-09-042-105-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09042105 Patent No. 6040157
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Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: | |
FILING DATE: 8-MAR-1:
CLASSIFICATION:
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STRRET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                         APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
NUMBER OF SEQUENCES: 35
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEPAY. '2020-201
                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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LENGTH: 419 amino acids
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ATTORNEY/AGENT INFORMATION:
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                                                                  APPLICATION NUMBER: FILING DATE: HEREW CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408 CVPSYWQRPQMS 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 CVPSYWKRPOMS 192
                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                     STATE:
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ROSEN, CRAIG A.
                  8-MAR-1994
                                                                                        HEREWITH
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99.5%;
                                    US 08/207,550
                                                                                                        US/09/042,105
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Patent No. 6040157
GENERAL INFORMATION:
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Best Local Similarity
Matches 191; Conserv
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                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HEREWITH
                 CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 CVPSYWKRPQMS 192
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APPLICATION NUMBER:
                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                            USA
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(777 TO NO: 2:
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99.5%;
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us 08/207,550
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 06-JU

06-JUN-1995

US 08/465,968

FILING DATE: 8
CLASSIFICATION:

8-MAR-1994

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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                       ADDARLA
STREET: 6 L.
CITY: ROSELAND
STATE: NEW JERSEY
STATE: USA
                            SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
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                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               APPLICANT:
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FILING DATE:
                                                                 OPERATING SYSTEM:
                                                                                    COMPUTER:
                                                                                                                                                                                                    ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTC 120
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                APPLICATION NUMBER: PCT/US96/09001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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99.5%;
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    Mismatches

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Pred. No. 8.2e-95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/465,
FILING DATE: 6 JUN 95
APPLICATION NUMBER: 08/207,
FILING DATE: 8 MAR 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
                                       CLASSIEICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/F196/00427
                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Too
STREET: 6300 Sears Tower,
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REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 57
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LENGTH: 419 AMINO ACIDS
                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                         STREET: 6300 (CITY: Chicago STATE: Illino:
                                APPLICATION NUMBER: PCT/1
FILING DATE: 01-AUG-1996
                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                      ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCR
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                                                                                                                                                                                                                                                    TRY: United States of America 60606-6402
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ower, 233 South Wacker Drive
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Pred. No. 8.2e-95;
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PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
APPLICATION NUMBER:

14-FEB-1996

08/601,132

APPLICATION NUMBER: 08/585,895

FILING DATE:

28-JUN-1996

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RESULT 13
US-08-795-430-13
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Best Local Similarity
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
TOPOLOGY: line
WOLECUTE
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                    APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular
TITLE OF INVENTION: Protein
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NAME: Gass, David A.
NAME: Gass, David A.
NAME: Gass, David A.
NAME: 38,153
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 CVPSYWKRPQMS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                           404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 PRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 312/474-0448
                                                                                       COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                            CITY: Chicago
                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/5: FILING DATE: 01-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                       CVPSYWKRPHLN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRNQPLNPGKCACECTENTQKCFLKGKKFHHQTCSCYRRPCANRLKHCDPGLSFSEEVCR 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDTCQCVCKGGLRPSSCGPHKELDRDSCQCVCKNKLFPNSCGANREFDENTCQCVCKRTC 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLPATLPQCQAANKTCPTNYVWNNYMCRCLAQQDFIFYSNVEDDSTNGFHDVCGPNKELD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162;
                                                                                                                           Illinois
                                                                                                                                                           E: Marshall, O'Toole, 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JAN-1996
                                                                                                                                                                                                                     Protein and Gene, Mutants Thereof, and Uses Thereof 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.3%; Score 998; DB 4; Length 415; 84.4%; Pred. No. 3.2e-83;
                                                                                                                                                                                                                                                       Vascular Endothelial Growth Factor C (VEGF-C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08/510,133
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                                                                                                                                                              Gerstein, Murray & Borun
South Wacker Drive
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                                                                                                                                                                                                             US-08-915-795-3
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                                                                                                                                                   Sequence 3, Application US/08915795 Patent No. 6235713 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.2%; Score 839; DB 4; Best Local Similarity 73.1%; Pred. No. 8.1e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
TOPOLOGY: line-
WOLECUTE
                                                                           APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Karl ALITALO
                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acid
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/5
FILING DATE: 01-AUG-1995
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                         TITLE OF INVENTION:
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APPLICATION NUMBER:
FILING DATE: 28-JUN-
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                                                                                                                                                                                                                                                                                                                                                                       346
                                                                                                                                                                                                                                                                                                                               180 RCVPSYWKRPQMS 192
                                                                                                                                                                                                                                                                                                                                                                                                        120 CPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                            286 DEETCQCVCKGGVRPISCGPHKELDRASCQCMCKNKLLPSSCGPNKEFDEEKCQCVCKKT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 SLPATQTQCHVANKTCPKNHVWNNQICRCLAQHDFGFSSHLGDSDTSEGFH-ICGPNKEL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 DEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-NOV-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/585,895 FILING DATE: 12-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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FILING DATE: 01-AUG-1996
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                                                                                                                                                                                                                                                                                         RCVRTSWKRPLMN 418
                                                                                                                                                                                                                                                                                                                                                                     CPKHHPLNPAKCICECTESPNKCFLKGKRFHHQTCSCYRPPCTVRTKRCDAGFLLAEEVC
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Evenson, McKeown, Edwards & Lenahan P.L.L.C.
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                                       GROWTH FACTOR: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 418;
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STREET: 1200 G St CITY: Washington

1200 G Street, NW, Suite 700

COUNTRY:

United States of America

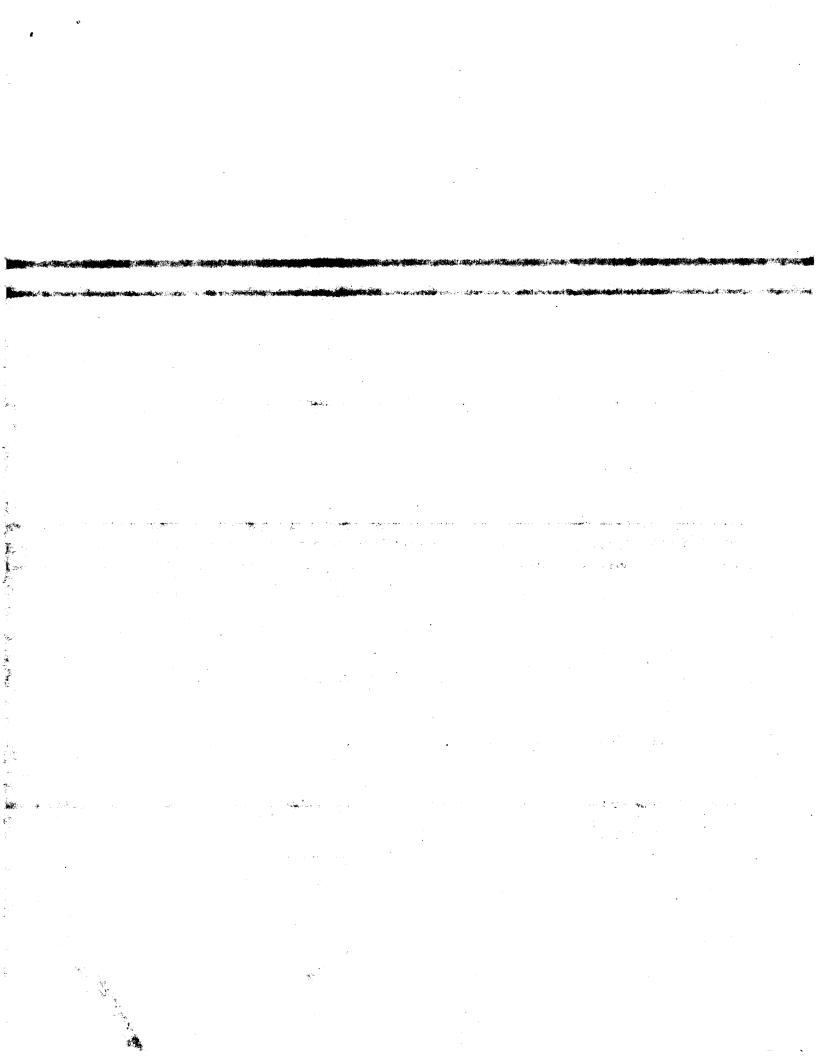
RY: U 20005

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US-08-915-795-5
; Sequence 5, Application US/08915795
. patent No. 6235713
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Best Local Similarity
Matches 51; Conserv
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                         APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                  APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 PGKCAC-ECTESPQKCLLKGKKFHHQTCSC-----YRRPCTNRQKACEPGFSYSEE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 -----PALCGPH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 RCSHSKKLCPIDMLWDSNKCKCVLQE-----ENPLAGTED----HSHLQE----- 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 PKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKE 312
                                                                                                                 STREET: 1200 G STREET: Washington
                                                              COUNTRY: UZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                         E: Evenson, McKeown, Edwards & Lenahan P.L.L.C. 1200 G Street, NW, Suite 700
                                                                                 United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 628-8844
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.7%; Score 234; DB 4; Length 325; 28.8%; Pred. No. 3.9e-14;
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; TISSUE TYPE: Human Lung
US-08-915-795-5
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: N/A
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
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SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 100
PELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
285 PKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKE 341
                                       128 PGKCAC-ECTESPQKCLLKGKKFHHQTCSC-----YRRPCTNRQKACEPGFSYSEE 177
                                                                                                                                                               214 RCSHSKKLCPIDMLWDSNKCKCVLQE-----ENPLAGTED----HSftLQE----- 254
                                                                                                                     68 CRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLN 127
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                                                                                                                                                                                                      8 QCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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n Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                 20.7%; Score 234; DB 4; Length 354; 28.8%; Pred. No. 4.3e-14;
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                                                                                                                                                                                                                                                  24; Mismatches
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Search completed: October 17, 2001, 14:47:10 Job time: 196 sec



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Result
No.
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Maximum DB seq
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Maximum Match 100%
Listing first 45 summaries
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A;Accession: G02659 A;Status: preliminary A;Status: preliminary A;Status: preliminary A;Accessione: GDS: Translated from GB/EMBL/DDBJ A;Accule type: mRNA A;Residues: 1-419 <mor> A;Cross-references: EMBL: U58111; NID: g1373426; PIDN: AAB02909.1; PID: g1373427 C;Genetics: A;Gene: GDB: VEGFC; VRP A;Cross-references: GDB: 3890883; OMIM: 601528 A;Cross-references: GDB: 3890883; OMIM: 601528 F;1-12/Domain: signal sequence #status predicted <stg> F;1-12/Domain: propeptide #status predicted <pro></pro></stg></mor>	A; Molecule type: protein A; Residues: 'X',104-120 <jou2> A; Residues: 'X',104-120 <jou2> R; Lee, J; Gray, A; Yuan, J; Luoh, S.M.; Avraham, H.; Wood, W.I. submitted to the EMBL Data Library, December 1995 A; Description: Vascular endothelial growth factor related protein (VRP): A ligand and A; Reference number: S69208 A; Accession: S69208 A; Molecule type: mRNA A; Residues: 1-419 <lee> A; Cross-references: EMBL:043142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989 R; Morris, J.C. submitted to the EMBL Data Library, May 1996 A; Reference number: H01557</lee></jou2></jou2>	RESULT 1 S69207 vascular endothelial growth factor C precursor - human N;Alternate names: FLT4 ligand DHM C:Species: Homo sapiens (man) C:Species: Homo sapiens (man) C:Species: Homo sapiens (man) C:Caccession: S69207; S61795; S71443; S69208; G02659 R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel EMBO J. 15, 1751, 1996 A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand A;Reference number: S69207; MUID:96203094 A;Reference number: S69207 A;Status: nucleic acid sequence not shown A;Molecula type: mRNA A;Residues: 1-419 <joud 15,="" 1995="" 1996="" 290-288,="" 70-419="" <joui="" a="" a.;="" a;accession:="" a;cross-references:="" a;molecula="" a;note:="" a;reference="" a;residues:="" a;scatus:="" a;title:="" acid="" chilov,="" compared="" conceptual="" d.;="" data="" december="" e.;="" embl="" embl:x94216;="" embo="" endothelial="" factor,="" fit4="" for="" from="" growth="" i.;="" is="" j.="" k.;="" kalpainen,="" kukk,="" lahtinen,="" library,="" ligand="" mrna="" muid:96178224="" nid:g1177488;="" not="" novel="" nucleic="" nucleotide="" number:="" of="" only="" pajusola,="" part="" pid:e221096;="" pid:g118="" pidn:caa63907.1;="" r;joukov,="" reference="" revision="" s61795="" s61795;="" s7195="" saksel="" sequence="" shown="" shown;="" submitted="" the="" this="" to="" translation="" type:="" v.;="" vascular="" vegf-c,="" was="" with=""> A;Accession: S71443 B;Accession: S71443 B;Accession: S71443 B;Accession: S71443</joud>	35 125.5 11.1 1111 2 73.07 inypoline Lical processor of the composition of the compositio

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C;Species: Chironomus tentans
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C;Superfamily: unassigned Balbiani ring
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A;Title: The balbiani ring 3 gene in Chironomus
A;Reference number: S08167; MUID:90172404
A;Accession: S08167
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R; Paulsson, G.;
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A; Residues: 1-1700 <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Best Local
 secretory
                                                                                       1429
                                                                                                                                                         1372
                                                                                                                                                                                                                                                                                                                                                                 1204
                                                                                                                                                                                                                         1312 KSWNDDSCSCQCKSKMPCGGCPPNQQWNEKDCECKCSATGNCPAGQTWNSQTCQCSCPAT 137:
                                                                                                                                                                                                                                                                                            1260 -----C-KTKWWNDEMCQCVCKPGCPEGGCKGVMKWNANTCSCECPADKAKPASCGDK 131
                                                                                                                                                                                           129
                                                                                                                       176 EEVC
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                                                                                       DATC 1432
                                                                                                                                                       GKCTGAQVWCSKACKCVCPAQKKCDSPKTWDENSCSCQCPKNMRPPTG---GCNAGRTWD 1428
                                                                                                                                                                                                                                                                                                                            TDGFHDICGPNKELDEETCQCVCRAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVPSYWKRPQMS 192
                                                                                                                                                                                        GKC------ACECTESPQKCLLKGKKFHHQTCSCY----RRPCTNRQKACEPGFSYS 175
                                                                                                                                                                                                                                                          KELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRT--CPRNQPLN------P 128
                                                                                                                                                                                                                                                                                                                                                              PTPAPTCSNNQKYSNVSCSCGCNPGKPKNGCPGNQIWCDNTCRCVCPKNMEKPADN---- 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCR 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTC
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                                                                                                                         179
 protein
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 midge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.1%;
25.4%;
(Chironomus
                                                                                                                                                                                                                                                                                                                                                                                                -----TCPTNYMWNNHICRCLAQEDFMFSSDAGDDS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 238; DB 2;
Pred. No. 4.3e-11;
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Pred. No. 2.7e-80;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins
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tentans) (fragment)
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                                                                                                                                                                                                                                                                                                                            -LRPASCGPH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                  82;
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C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A32230; B32230; A33379; B33379; C33379; S01292; A30903
R;Jones, F.S.; Hoffman, S.; Cunningham, B.A.; Edelman, G.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1905-1909, 1989
A;Title: A detailed structural model of cytotactin: protein homologies, alternative R A;Reference number: A32230; MUID:89184536
                                   A;Molecule type: mRNA
A;Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',45
A;Cross-references: GB:M23121; NID:g212746; PIDN:AAA49086.1; PID:g212749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Dignam, S.S.; Case, S.T. Gene 88, 133-140, 1990
A;Title: Balbiani ring 3 in A;Reference number: JQ0542;
A;Accession: JQ0542
                                                                                                                                                                                                       A;Cross-references: GB:J04519
R;Spring, J.; Beck, K.; Chiquet-Ehrismann, R.
Cell 59, 325-334, 1989
A;Title: Two contrary functions of tenascin: dissection of the active sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
                        A; Accession: B33379
                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                       A;Reference number: A33379; MUID:90030407
A;Accession: A33379
                                                                                                                                                                                                                                                                                                        A; Residues: 1-1044, 1318-1810 < JO2>
                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: B32230
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:J04519; NID:g211717; PIDN:AAA48745.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-1810 <JON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N; Alternate names: cytotactin; hexabrachion N; Contains: tenascin 190K; tenascin 200K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tenascin precursor - chicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB:M24160
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A; Residues: 1-160 <DIG>
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C;Accession: JQ0542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 GKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRC-VPSYWK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 NCGNKKFFDKPSCECKCKNN--PST--SPQVWDADDCECKCPKDKQKPQGGCDGGQKWND 101
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Pred. No. 2.3e-07;
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A;Residues: A;Accession:

A; Molecule type: mRNA

-204, 'G', 206-221, 'A', 223-380, 'D', 382-386, 'H', 388-444, 'HN', 44**7-**450, 'V', 45

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F;223-249/Domain: EGF homology <EGFI>
F;316-342/Domain: EGF homology <EGFI>
F;316-342/Domain: EGF homology <EGF>
F;592-673/Domain: fibronectin type III repeat homology <FN3B>
F;681-65/Domain: fibronectin type III repeat homology <FN3B>
F;773-857/Domain: fibronectin type III repeat homology <FN3D>
F;865-949/Domain: fibronectin type III repeat homology <FN3D>
F;957-1037/Domain: fibronectin type III repeat homology <FN3E>
F;1046-1128/Domain: fibronectin type III repeat homology <FN3E>
F;1137-1219/Domain: fibronectin type III repeat homology <FN3H>
F;1138-1399/Domain: fibronectin type III repeat homology <FN3H>
F;1318-1399/Domain: fibronectin type III repeat homology <FN3I>
F;1495-1575/Domain: fibronectin type III repeat homology <FN3I>
F;1495-1575/Domain: fibronectin type III repeat homology <FN3X>
F;1590-1798/Domain: fibronectin type III repeat homology <FN3X>
F;1590-1798/Domain: fibronectin type III repeat homology <FN3X>
F;1590-1798/Domain: fibronectin type III repeat homology <FN3X>
F;1734-1747/Domain: calcium binding #status predicted <CAB>
                                                                                  adhesive plaque protein Mgfp2 precursor - Mediterranean mussel C;Species: Mytilus galloprovincialis (Mediterranean mussel) C;Date: 27-Apr-1995 #sequence_revision 03-Oct-1995 #text_chang. C;Accession: A56175 R;Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, S. J. Biol. Chem. 270, 6698-6701, 1995
                                                                                                                                                                                                                                                                                       RESULT
A56175
J. Biol. Chem. 270, 6698-6701, 1995
A;Title: Mussel adhesive plaque protein gene
A;Reference number: A56175; MUID:95204464
A;Accession: A56175
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A; Residues: 27-181,'R',183-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447
A; Cross-references: EMBL:X08030
A; Cross-references: EMBL:X08030
A; Note: part of this sequence was confirmed by protein sequencing
A; Note: part of this sequence was confirmed by protein sequencing
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A; Accession: S01292
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EMBO J. 7, 2977-2982, 1988
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A; Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',452-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVCDEGYTGEDCGELICPNDCFDRGRCINGTCFCEEGYTGEDCGELTCPNNCNGNGRCEN 359
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                                                           of epidermal growth
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C;Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF hom C;Superfamily: EGF homology CEGX1>
                                                                                                                                                                                                                                                                                                                                                                                                   Exp. Cell Res. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed A;Reference number: A49175; MUID:93178563
A;Accession: A49175
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                                                                                                                                           F;560-591/Domain:
F;674-705/Domain:
                                                                                                                                                                                   F;482-513/Domain:
                                                                                                                                                                                                                                                                                A; Experimental source: embryo
A; Note: sequence extracted from NCBI backbone (NCBIP:126158)
                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1203 <LAR>
A;Cross-references: EMBL:X68279; NID:g287989; PIDN:CAA48340.1; PID:g287990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lardelli, M.;
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C;Accession: A49175; PH1570; S32113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Mus musculus (house mouse)
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Best Local S
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                    Query Match
Best Local
    Matches
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nes 67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVSKPCKNRGKCIWNGKAYRCKCAYGYGGRHCTKKSYKKNPCASRPCKNRGKCTDKGNGY
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    l Similarity
62; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   names: Notch
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es: Notch homolog
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                                                                                                 EGF homology <EGF1>
EGF homology <EGF>
EGF homology <EGX2>
EGF homology <EGF3>
EGF homology <EGF3>
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    Conservative
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                    12.3%;
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  Score 139.5; DB 2;
Pred. No. 0.0013;
6; Mismatches 68;
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    Indels 115;
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                                     Length 1203;
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16 CPTNYMWNNHICRCL----

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STDG-FHDIC----

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A;Molecule type: mRNA
A;Residues: 1-1746 < NIS>
A;Residues: 1-1746 < NIS>
A;Cross-references: EMBL:X61599; NID:g2124; PIDN:CAA43796.1; PID:g2125
A;Cross-references: EMBL:X61599; NID:g2124; PIDN:CAA43796.1; PID:g2125
C;Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type
C;Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracell
E;1-22/Domain: signal sequence #status predicted <NAT>
F;346-372/Domain: signal sequence #status predicted <NAT>
F;346-372/Domain: EGF homology <EGFP>
F;377-403/Domain: fibronectin type III repeat homology <FN3D>
F;622-703/Domain: fibronectin type III repeat homology <FN3D>
F;892-93/Domain: fibronectin type III repeat homology <FN3D>
F;984-1064/Domain: fibronectin type III repeat homology <FN3E>
F;1164-1246/Domain: fibronectin type III repeat homology <FN3E>
F;1164-1246/Domain: fibronectin type III repeat homology <FN3SP>
F;1343-1423/Domain: fibronectin type III repeat homology <FN3SP>
F;1341-1511/Domain: fibronectin type III repeat homology <FN3SP>
F;1341-1511/Domain: fibronectin type III repeat homology <FN3SP>
F;1431-1511/Domain: 
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R;Nishi, T.; Weinstein, J.; Gillespie, W.M.; Paulson, J.
Eur. J. Biochem. 202, 643-648, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: contactin; hexabrachion
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete primary structure of porcine tenascin. Detection A;Reference number: S19694; MUID:92104189
A;Accession: S19694
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                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                          12 ANKTCPTNYMWNNHIC --- RCLAQEDFMFSSDAGDDSTDG -- FHDICGPNKELDEETCQC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92
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                                                                                     EGQCVCDEGFAGADCSERRCP-SDCHNRGRCLDGRCECDDG--
                                                                                                                                           --QCVC-----
                                                                                                                                                                                                 VCDEGFTGEDCGELICPKDCFDRGRCINGTCYCDEGFEGEDCG
                                                                                                                                                                                                                                                 VCRAGLRPASCG----PHKELDRNSC---QCVCKNKLFPSQCGANREFDENTC-----
                                                                                                                                                                                                                                                                                                       SRETCPVPCSEEHGRCVDGRCVCQEGF----AGEDCNEPLCLHNCHGRGRCVENE---C
                               RRP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDGRCIDLVNGYQCNCQPGTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDTNPLNGQYICTCPQGYKGADCTEDVDECAMANSNPCEHAGKCVNTDGAFHCECLKGYA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SPQKCLLKGKKFHHQTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \tt NGQCVDKVNRFQCLCPPGFTGPVCQ-IDIDDCSSTPCLNGAKCIDHPNGYECQCATGFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPRCEMDINECHSDPCQNDATCLDKIGGFTCLCMPGFK----GVHCELEVNECQSNPCVN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPNKELD----EETCQ-----
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                                                                                                                                        -KRTCPRNQPLNPGKC---ACECTESPQKCLLKGKKFHHQTCSCY 157
                                                                                                                                                                                                                                                                                                                                                                                                                12.3%; Score 139.5; DB 26.2%; Pred. No. 0.0017; Live 17; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                     -FEGEDCGEL
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                                                                                                                                                                                                                                                                                                                                                                                                                63;
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                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell-fate determining gene Notch2 protein - G;Species: Rattus norvegicus (Norway rat) C;Date: 21-Jan-1994 #sequence_revision 18-No C;Accession: A49128 R;Weinmaster, G.; Roberts, V.J.; Lemke, G. Development 116, 931-941, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Notch2: a second mammalian Notch A;Reference number: A49128; MUID:93202015 A;Accession: A49128
                         F;1909-1941/Domain:
F;1943-1975/Domain:
                                                                               F;1191-1222/Domain:
F;1876-1908/Domain:
                                                                                                      F;1129-1060/Domain: EGF homology <EGF>
F;1067-1099/Domain: EGF homology <EGX3>
F;1153-1184/Domain: EGF homology <EGF3>
F;1153-1222/Domain: EGF homology <EGX4>
                                                                                                                                                                                                                                                                        C;Superfamily: unassigned ankyrin repeat F;264-295/Domain: EGF homology <EGX1>
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                                                                                                                                                                                                                        F;877-908/Domain:
                                                                                                                                                                                                                                                 F;799-830/Domain:
                                                                                                                                                                                                                                                                                                                                 A; Note: sequence extracted from NCBI backbone (NCBIP:127811)
                                                                                                                                                                                                                                                                                                                                                        A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-2471 <W
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; not
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A; Introns: 19/3; 61/3;
629/3; 1721/3; 1767/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U41624; PIDN:AAA83316.1; CESP:F46C8.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-2195 <
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A;Description: The sequence of C. elegans cosmid |
A;Reference number: Z21497
A;Accession: T34264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Wilcox,
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #t
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1736 NCVQHVVPDMGNCQRQCGNNQVCIQDQCQCRNGYYAQTE 1774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 VCRAGL--RPASCGPHKELDRNSCQCV-----CKNKLFPSQCGANREFDENTCQC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --VCKRTC--PRNQPLNP-----GKCACECTES----POKCLLK-GKKFHHQTCSCYRR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CQAANKTCPTNYMWNNHICRCLAQEDFMFS--SDAGDDSTDGFHDICGPNKELDEETCQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -CRPGYYQQPGSC-----LQDRCNCIQEVESDSCLNR----QCGMNQVCIQDQCQCRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCPGGCSGHGRCVNGQCVCDEG
                                                                                                                                                                                                                                                                                                                                                                                       1-2471 <WEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                     EGF homology <EGX2>
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                                                ankyrin repeat homology ankyrin repeat homology
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                                                                                                                                                                                                                                              homology <EGX1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80/1; 159/1; 182/1; 208/2; 246/1; 308/1; 367/1; 1811/1; 1874/1; 1920/1; 2011/2; 2068/3; 2117/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 139.5; DB Pred. No. 0.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB/EMBL/DDB
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                                                                                                                                                                                                                                                                                                  proteins; ankyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                         <AN2>
<AN4>
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                                                                                  <AN1>
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2161/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: sequence extracted from NCBI backbone (NCBIN:64543, NCBIP:64547)
C;Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type
C;Keywords: extracellular matrix; glycoprotein; tandem repeat
F;287-313/Domain: EGF homology <EGF>
F;346-427/Domain: fibronectin type III repeat homology <FN1>
F;435-517/Domain: fibronectin type III repeat homology <FN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Onda, H.; Poulin, M.L.; Tassava, R.A.; Chiu, I.M.
Dev. Biol. 148, 219-232, 1991
A;Title: Characterization of a newt tenascin cDNA and localization of tenascin mRNA dur.
A;Reference number: A43902; MUID:92038434
A;Accession: A43902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tenascin - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Feb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-647 < OND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: A43902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M76615
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
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                                                                            201 RGRCVNGQCVCDEGF 215
                                                                                                                                                           152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           565 TLCDENIDNCDPDPC-----HHGQCQDGIDSYTCICNPGYMGAICSDQIDECYSSPCL 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        506 NGQCVDKVNRFQCLCPPGFTGPVCQ-IDIDDCSSTPCLNGAKCIDHPNGYECQCATGFTG 564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                  ---CTNRQKACEPGF 172
                                                                                                                                                         GFMGEDCADLRCP-NDCNNRGRCVNGQCVCDEG--
                                                                                                                                                                                                                                      TGEDCGELTCPNNCNNRGRCVNGLCVCDDGFQGDDCSELRCPNDCNDRGRCVNGKCVCKE 151
                                                                                                                                                                                                                                                                         RPASCG----PHKELDRNSC---QCVCKNKLFPSQCG----ANREFDENTC---QCVCKR 118
                                                                                                                                                                                                                                                                                                                   CPNNC---NNRGRCVEDECVCDEGFTGDDCSE---LIC-PNDCFDRGRCINGVCFCDEGF
                                                                                                                                                                                                                                                                                                                                                        CPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC---QCVCRAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SPQKCLLKGKKFHHQTC----
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                                                                                                                                                                                            -----TCPRNQPLNPGKCA---CECTESPQKCLLKGKKFHHQTCSCYRRP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-----RQKACEPGFS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---CKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKC-----ACECTE---- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPRCEMDINECHSDPCQNDATCLDKIGGFTCLCMPGFK----GVHCELEVNECQSNPCVN 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
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                                                                                                                                                                                                                                                                                                                                                                                                                    12.2%; Score 138; DB 2; 28.2%; Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Mismatches
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Pred. No. 0.0022;
6; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----CVCRAGLRPASCGPHKELDRNSCQ---CV- 91
                                                                                                                                                         -- FMGEDCSDLRCPGDCNN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 647
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                                                                                                                                                                                                                                                                                                                                                                                                 56;
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                                                                                         F; 222-254/Domain:
                                                                                                                  F;184-215/Domain:
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C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol C;Keywords: transmembrane protein F;146-177/Domain: EGF homology <EGX1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Xenopus laevis (African clawed frog)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1
C;Accession: A35844
                                                                                  F;757-788/Domain:
                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-2524 <COF>
                                                                                                                                                                                                                                                                                                           A; Status: preliminary; nucleic acid sequence not shown; not compared with
                                                                                                                                                                                                                                                                                                                                   Science 249, 1438-1441, 1990
A;Title: Xotch, the Xenopus homolog of Drosophila notch
A;Reference number: A35844; MUID:90385285
A;Accession: A35844
                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Coffman, C.; Harris, W.; Kintner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Notch protein - African clawed frog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1915-1947/Domain: ankyrin repeat homology F;1948-1980/Domain: ankyrin repeat homology
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A;Residues: 1-2437 <BIE>
A;Cross-references: EMBL:X69088; NID:g433866; PIDN:CAA48831.1; PID:g433867
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; F;755-786/Domain: EGF homology <EGF1>
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A; Accession: S42612
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Mech. Dev. 43, 87-100,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: S42612
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;1924-1956/Domain: ankyrin
;1957-1989/Domain: ankyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 57; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          655 DKINGYECVCEPGYSGSMCNINIDDCALNPCHNGGTCIDGVNSFTCLCPDGFRDATCLSQ 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 DSTDGFHDICGP-----NKELDE-----ETC-----QCVCRAGLRPASC-GP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVCK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCKNGGVCRESEDFQSFSCNCPAGWQGQTCEVDINECVRNPCTN-GGVCENLRGGFQ---
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                                                                            EGF homology <EGX1>
EGF homology <EGF1>
EGF homology <EGF2>
EGF homology <EGX2>
EGF homology <EGX2>
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                                                     EGF homology <EGX3>
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  repeat homology repeat homology
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C;Superfamily: unassigned EGF-related p:
C;Keywords: tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tenascin-like protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jan-2000
C;Accession: A61625; S28463
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                                                                                                                                                                                                                                                                                                                           F;1-62/Domain: signal sequence #status predicted F;63-782/Product: tenascin-like protein #status | F;497-524/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-782 < BAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Ten(a), a Drosophila gene related A;Reference number: A61625; MUID:93264270 A;Accession: A61625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Baumgartner, S.; Chiquet-Ehrismann, Mech. Dev. 40, 165-176, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: ten-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references; EMBL:X68794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status:
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Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
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 CYR----RPCTNRQKACEPGFS-----YSEEVCRCVPSY
                                   HWTGPDCSQAVCSLDCGRNGVCESGKCRCNSGWTGNLCDQLPCDSRCSEHG-QCKNGTCV
                                                                                                      GTCVAGQCYCKAGWQGEDCG---TIDQQVYQCL--
                                                                                                                                      ETC---QCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKR 118
                                                                                                                                                                        VPNCSSHGRCIEGECHCERGWKGPYC-------DQHDCLDPLCS-----GH
                                                                                                                                                                                                          LPQCQAANK----TCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGINTETCQCPPGF 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --YSEEVCRCVPSY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----PGYTGRNCEMDIDDCQ-----PNPCHNGGSCSDGINMFFCNCPAG-----FRG 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGPNKELDE-ETCQCVCRAGLRPASCGPHKELDRNSC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKFHHQTCSCYRRPCTNRQK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GRCKESEDFETFSCECPPGWQGQTC----EIDMNECVNRPCRNGATCQNTNGSYKCNCK 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKCEEDINECASNPCKNGANCTDCVNSYTCTCQPGFSGIHCESNTPDCTESSCFNGGTCI 999
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55; Conserv
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                                                                                                                                                                                                                                             Conservative
                                                                     TCPRNQPLNPGKCACE-----CTESP--QKCLLKGKKFHHQTCS 155
                                                                                                                                                                                                                                         12.0%; Score 136; DB 2; I 23.4%; Pred. No. 0.0018; tive 19; Mismatches 75;
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Pred. No. 0.0031;
""" atches 77;
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C; Species: Mus musculus (house mouse)
C; Date: 23-Feb-1996 #sequence_revision 23-Feb-1
C; Accession: A57278
R; Zhang, H.; Hu, W.; Ramirez, F.
J. Cell Biol. 129, 1165-1176, 1995
J. Title: Developmental expression of fibrillin
A; Heference number: A57278; MUID: 95263670
A; Accession: A57278
                                                                                                                                                                                                                                                                                                    A;Title: An amplifiable DNA region from the Mycoplasma A;Reference number: Z18888; MUID:95014025 A;Accession: T18355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
T18355
                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-1187 <
                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mycoplasma hyorhinis
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
C;Accession: T18355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:L39790; NID:g762830; PIDN:AAA74908.1; C;Superfamily: unassigned EGF-related proteins; EGF homology F;1239-1274/Domain: EGF homology <EGF1> F;2488-2523/Domain: EGF homology <EGFP>
                                                                                                                                                                           A; Genetic code:
                                                                                                                                                                                                                   A; Cross-references: EMBL:Ll1447; NID:g150156;
                                                                                                                                                                                                                                                                                A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                   R;Deng, G.; McIntosh, M.A.
J. Bacteriol. 176, 5929-5937, 1994
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A; Residues: 1-2907 <ZHA>
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Matches 60
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                                                               Local Similarity nes 47; Conserv
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                      26 ICRCLAQEDFMFSSDAG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPLNPGKC---ACECTESPQKCLL-KGKKFHHQTCSCYR-RPCTNRQKACEPGFSYSE-- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDECSQSPKPC--NFICKNTKGSYQCSCPRGYVLQEDGKTCKDLDECQTKQHNCQFLCVN 2542
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ycoplasma hyorhinis
                                                                 Conservative
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    Mycoplasma hyorhinis

                                                                                   12.0%;
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                                                                 17;
                                                                                   Score 135.5; DB Pred. No. 0.0027;
                                                                                                                                                                                                                                                                                    from GB/EMBL/DDBJ
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                      -DDSTDGFH----
                                                                 Mismatches
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                                                                                                                                                                                                                   PID:g664956;
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                    -DICGPNKELDEETCOC-
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                                                                 Indels
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	Search completed: October 17, 2001, 14:48:40 Job time: 286 sec	
	Db 430 CSEEHCECV 438	
	Qy 174 YSEEVCRCV 182	
429	CTEEHCECTESTCGCENEPCECEEEACD	
173	QY 119 TCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFS 173	
393		
118	;	
354	Db 295 ICKNLEHSEILYRLKNGQVVNLLETELETEELHYADSPVQEGKEPCGCSLKETEESCDCE 354	

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Result
No.
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/

Wood C.R.; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL

SEQUENCE FROM N.A.

Fitz L., Morris J.C., Towler P.S., Long A.J., Greco R.,

Fitz L., Morris J.C., Towler P.S., Long A.J., Greco R.,

Burgess P., Glannotti J., Ciarletta A., Hennessey D., Kovacic

Fitzgerald M., Scaltreto H., Weich N., Neben S., Finnerty H.,

Fitzgerald M., Scaltreto H., Weich N., Neben S., Finnerty H.,

Fitzgerald C. R., Wang J., Nickbarg E., Gassaway R., Turner K.,

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MEDLINE=96203094; PubMed=8612600; JOUKOV V., PajusOla K., Kalpainen Saksela O., Kalkkinen N., Alitalo EMBO J. 15:1751-1751(1996).

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OF 103-120. A., Chilov D., K., wth factor, VEGF -2) receptor tyr	a; Craniata; Vertebrata; s; Catarrhini; Hominidae;	P49/6/; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-2000 (Rel. 40, Last annotation update) VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR VASCULAR ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND) (FLT4-	PRT; 419 AA.	ALIGNMENTS	BAR1_CHIPA FBP1_STRPU	LRP1_HUMAN	TGFB_HUMAN	NTC4_MOUSE	LML2_CAEEL	NTC1_RAT	ITB3 MOUSE
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STRAIN=BALB/C;
MEDLINE=97164697; PubMed=9012504;
Kukk E., Lymboussaki A., Taira S., Kaipain
Joukov V., Alitalo K.;
"VEGF-C receptor binding and pattern of ex
suggests a role in Lymphatic vascular deve
Development 122:3829-3837(1996).
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(POTENTIAL).
                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                   Murinae;
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BAR3_CHITE
ID BAR3_CI
AC Q03376
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Best Local S
Matches 162
BAR3_CHITE
Q03376;
Q1-OCT-1993
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EMBL; U58112; I
HSSP; P15692; 1
                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  REPEAT
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97388482; PubMed=9247316;
Fitz L.J., Morris J.C., Towler P., Long A., Bur
Wang J., Gassaway R., Nickbarg E., Kovacic S.,
Giannotti J., Finnerty H., Zollner R., Beier D.
Turner K.J., Wood C.R.;
"Characterization of murine Flt4 ligand/VEGF-C.
Oncogene 15:613-618(1997).
                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                         PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0438; GECYSKNOT.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000072; -.
InterPro; IPR002400; -.
Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:109124; Vegfc.
                                                                                 404
                                                                                                       181
                                                                                                                             344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HOMODIMER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL GROWTH
                                                                                              CVPSYWKRPQMS
                                                                                                                                           PRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCR
                                                                                 CVPSYWKRPHLN
                                                                                                                                                                                       EETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTC
                                                                                                                                                                                                                         SLPATLPQCQAANKTCPTNYVWNNYMCRCLAQQDFIFYSNVEDDSTNGFHDVCGPNKELD
                                                                                                                                                                                                                                    SLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELD
                                                                                                                               PRNQPLNPGKCACECTENTQKCFLKGKKFHHQTCSCYRRPCANRLKHCDPGLSFSEEVCR
                                                                                                                                                                             EDTCQCVCKGGLRPSSCGPHKELDRDSCQCVCKNKLFPNSCGANREFDENTCQCVCKRTC
                                                                                                                                                                                                                                                                        162;
                                                                                                                                                                                                                                                                                    Similarity
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271
271
295
295
319
343
171
201
236
415 F
                                                                                                                                                                                                                                                                        Conservative
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AAB46707.1; -.
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                                                                                                                                                                                                                                                                                                                                 ΑĄ,
                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                         factor; Glycoprotein; Signal; Repeat.

POTENTIAL.

98 POTENTIAL.

415 VASCULAR ENDOTHELIAL GROWTH FACTOR

361 4 X 24 AA TANDEM REPEATS.
                                                                                 415
                                                                                                         192
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415
361
294
318
342
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1771
201
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TO THE PDGF/VEGF FAMILY OF GROWTH
                                                                                                                                                                                                                                                                                                                                 W.
                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                               4 (PARTIAL).

N-LINKED (GLCNAC. . .) (
D9D3DD3CECC659D6 CRC64
                                                                                                                                                                                                                                                                      Score 998; DE
Pred. No. 1.6e
L8; Mismatches
                         1700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g A., Burgess P., (acic S., Ciarletta
Beier D.R., Leak I
                        ₽
                                                                                                                                                                                                                                                                                   DB 1;
.6e-76;
                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
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(Rel.

27, Created)

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RESULT 4
TENA_CHICK
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SIGNAL
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
TENA_CHICK
                                                                       1429
                                                                                                                              1372
                                                                                                                                                                                                                                              1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paulsson G., Lendahl U., Galli J., Ericsson C., Wieslander L.;
"The Balbiani ring 3 gene in Chironomus tentans has a diverged repetitive structure split by many introns.";
J. Mol. Biol. 21:331-349(1990).
-!- FUNCTION: USED BY THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR STRUCTION: USED BY THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR STRUCTURE, THE LARVAL TUBE. BALBIANI RING PROTEIN 3 COULD PLAY ROLE AS A TRANSPORT PROTEIN THAT BINDS TO OTHER PROTEINS INTRACELLULARLY AND IN THE GLAND LUMEN IN ORDER TO PREVENT THES CHEMOTITED BY CONSTRUCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P18055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Salivary gland;
MEDLINE-90172404; Pubm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BALBIANI RING
                                                                                                  176
                                                                                                                                                          129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: HAS 82 APPROXIMATE REPEATS OF CYS-X-CYS-X-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: SECRETED. TISSUE SPECIFICITY: SALIVARY GLAND.
                                                                       DATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                x52263; CAA36506.1;
S08167; S08167
                                                                                                EEVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboratic sen the Swiss Institute of Bioinformatics and the EMBL outstation guropean Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no war
                                                                                                                           GKCTGAQVWCSKACKCVCPAQKKCDSPKTWDENSCSCQCPKNMRPPTG---GCNAGRTWD 1428
                                                                                                                                                                                                                                                                         TDGFHDICGPNKELDEETCQCVCRAG--
                                                                                                                                                         GKC-----
                                                                                                                                                                                     KSWNDDSCSCQCKSKMPCGGCPPNQQWNEKDCECKCSATGNCPAGQTWNSQTCQCSCPAT
                                                                                                                                                                                                                KELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRT--CPRNQPLN-----P 128
                                                                                                                                                                                                                                                                                                                                PATLPQCQAANK------TCPTNYMWNNHICRCLAQEDFMFSSDAGDDS 45
                                                                                                                                                                                                                                                                                                    PTPAPTCSNNQKYSNVSCSCGCNPGKPKNGCPGNQIWCDNTCRCVCPKNMEKPADN----
                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR00876; MINEMATODE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                       1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000853;
                                                                                                                                                                                                                                                                                                                                                                                                                                  1700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel.
                                                                                                                                                                                                                                            -C-KTKWWNDEMCQCVCKPGCPEGGCKGVMKWNANTCSCECPADKAKPASCGDK 131:
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chironomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                       ACECTESPOKCLLKGKKFHHQTCSCY----RRPCTNRQKACEPGFSYS 175
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30,
                                                                                                                                                                                                                                                                                                                                                                                                                                              1700
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25.4%;
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Last annotation update)
3 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                            26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  MW.
                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
BALBIANI RING PROTEIN
MW; 34202B28521B0815 (
                                                                                                                                                                                                                                                                                                                                                                          Score 238;
Pred. No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chironominae;
PRT;
1808 AA
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                                                                                                                                                                                                                                                                                                                                                                                       1.
                                                                                                                                                                                                                                                                                                                                                            74;
                                                                                                                                                                                                                                                                                                                                                                                      Length 1700;
                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
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L outstation -
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в33379; С33379;

A33379;

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MATKIA MILLOW, MATKIA MILLOW, MATKIA MILLOW, MATKIA MILLOW, MATKIA METAZOA; Chordata; Craniata; Vertebrata; Eutel Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae;
                                                  PIR;
                                                                                                     EMBL;
                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P10039; P13132; O73584; O73585;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
TEMASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN)
(GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR
MATRIX ANTICEN) (GP 150-225).
                                                                                                                                                                                                                                                                                modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth factor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 27-722 TISSUE=Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by recombinant tenascin Cell 59:325-334(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spring J., Beck K., Chiquet-Ehrismann R.; "Two contrary functions of tenascin: dissection of the active sites by recombinant tenascin fragments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fibrinogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A cDNA clone for cytotactin contains sequences similar to growth factor-like repeats and segments of fibronectin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Edelman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88176910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 464-1018 AND 1412-1661 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBO J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chiquet-Ehrismann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pearson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.

ALTERNATIVE PRODUCTS: 3 ISOFORMS; 230 KDA (SHOWN HERE), 200 K

AND 190 KDA; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ARE

PRODUCED IN A TISSUE-AND TIME-SPECIFIC MANNER DURING DEVELOPM

INDUCTION: BY TGF-BETA.

SIMILARITY: CONTAINS 13.5 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 13 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: CONTAINS 11 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: CONTAINS 13 FOMAIN RELATED TO THE C-TERMINAL PART

THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF EPITHELIAL TUMORS.
SUBUNIT: HEXAMERIC. A HOMOTRIMER MAY BE FORMED IN THE TRIPLE
COILED-COIL REGION AND MAY BE STABILIZED BY DISULFIDE RINGS &
BOTH ENDS. TWO OF SUCH HALF-HEXABRACHIONS MAY BE DISULFIDE LI
WITHIN THE CENTRAL GLOBULE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. Natl. Acad. Sci. U.S.A. 85:2186-2190(1988).
FUNCTION: SAM (SUBSTRATE-ADHESION MOLECULE) THAT APPEARS INHIBIT CELL MIGRATION. MAY PLAY A ROLE IN SUPPORTING THE
                                                                                                1; M23121; AAA49086.1;

2; X08031; CAB40811.1;

3; X08030; CAA30824.1;

3; J03641; AAA48748.1;

3; M20816; AAA48749.1;
                                                  A30903;
A31930;
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A31930.
A33379.
B33379.
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                                                                                A30903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=2478295;
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                                                                                                ALT_TERM.
ALT_SEQ.
ALT_SEQ.
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                                                                                                                                                                                                                                                                                                          Usage
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                                                                                                                                                                                                                                                                                                                                        its content
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Interpro; | IPRO00561; | Interpro; | IPRO01777; | Interpro; | IPRO01777; | Interpro; | IPRO01777; | Interpro; | IPRO01777; | IPRO0186; | EGF; | 13. | IPRO0186; | EGF | 1; | 14. | IPROSITE; | PSO0104; | fibrinogen_C; | 1. | IPFam; | PF000041; | fibrinogen_C; | 1. | IPFam; | IPFam; | PF000041; | fibrinogen_C; | 1. | IPFam; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR;
HSSP;
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  TENASCIN.

COLLED COIL (POTENTIAL).

EGG-LIKE 1 (INCOMPLETE).

EGF-LIKE 2.

EGF-LIKE 3.

EGF-LIKE 4.

EGF-LIKE 5.

EGF-LIKE 5.

EGF-LIKE 10.

EGF-LIKE 11.

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                                                           RESULT 5

FP2_MYTGA STANDARD;

ID FP2_MYTGA STANDARD;

AC Q25464;

AC Q35464;

DT 30-MAY-2000 (Rel. 39, Cro
DT 30-MAY-2000 (Rel. 40, Las
DE ADHESIVE PLAQUE MATRIX PI
DE (MGFP-2).
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Best Local S
Matches 61
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CARBOHYD
Mytilus galloprovincialis
Eukaryota; Metazoa; Mollus
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61; Conserv
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                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                ECTES - - PQKCLLKGKKFHHQTCSCY - -
                                                                          39, Created)
39, Last sequence update)
40, Last annotation update)
4TRIX PROTEIN 2 PRECURSOR (FOOT
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24.2%;
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    (Mediterranean
sca; Bivalvia; I
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N-LINKED (GLCNAC..
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N-LINKED (GLCNAC.

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                                                                                                                                                                                        PRT;
    Pteriomorphia;
                         mussel).
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.3e-05;
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Length 1808;

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160 359 128 299 89 241 49 CRC64;

PROTEIN

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(MGFP2)

Mytiloida;

ISOFORM).

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(POTENTIAL)

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PARTE TERRETOR OF COCCOCC COCCOCC ARE FERRETER TO THE PROPERT OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Mussel adhesive plaque protein gene is a novel member of epider growth factor-like gene family.";

J. Biol. Chem. 270:6698-6701(1995).

-i. FUNCTION: PROVIDES ADHESIVENESS TO THE MUSSEL'S FOOT. MUSSEL PRODUCE ONE OF THE STRONGEST WATER INSOLUBLE GLUE. THE MUSSEL ADHESIVE IS A BUNDLE OF THREADS, CALLED A BYSSUS, FORMED BY FIBROUS COLLAGENOUS CORE COATED WITH ADHESIVE PROTEINS.

-i. SUBCELLULAR LOCATION: SECRETED.
-i. SUBCELLULAR LOCATION: SECRETED.
-i. TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.
-i. PEVELOPMENTAL STAGE: EXPRESSION STARTS AT THE PEDIVELIGER, F FORMATION, STAGE.
   CARBONYD
DISULFID
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the Euro
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DOMAIN
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NCBI_TaxID=29158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a comment the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIHYDROXYPHENYLALANINE).
SIMILARITY: CONTAINS 11 EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00022; EGF_1;
PS01186; EGF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00010;
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   BAA07852.1; -.
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   Y., Miki D.,
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EGF-LIKE 1.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 9.
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EGF-LIKE 11.
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DOPA.
N-LINKED
Y SIMILARITY.
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gene is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal; Hydroxylation
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RESULT 6

WWF_CANFA. STANDARD; PRT; 2813 AA.

ID VWF_CANFA. STANDARD; PRT; 2813 AA.

AC Q28295; Q28311; Q9TSI4;
DT Q1-NOV-1997 (Rel. 35, Created)
DT Q1-CT-2000 (Rel. 40, Last sequence update)
DT Q1-OCT-2000 (Rel. 40, Last annotation update)
UNN WILLEBRAND FACTOR PRECURSOR (VWF).
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                                                                                Johnson G. Submitted
SEQUENCE FROM N.A. Venta P.J., Li J., "Complete sequence
                                      SEQUENCE FROM N.A.
Montgomery R.R., Fahs
Submitted (AUG-1996) t
                                                                                                   SEQUENCE FROM N.A.
Stoy S.J., Shibuya H.,
                                                                                                                                                                 Canis
                                                                                                                                 NCBI_TaxID=9615
                                                                                                                                             Mammalia; Eutheria; Carnivora;
                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                            F8VWF OR VWF.
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                                                                                                                                                                                                                                                                                                              SEEVCRCVPSY 185
                                                                                                                                                                                                                                                                                                                                  VVSKPCKNRGKCIWNGKAYRCKCAYGYGGRHCTKKSYKKNPCASRPCKNRGKCTDKGNGY
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                                                                                                                                                                                                                                                                                                                                                                                              CQCV-----CK---RTCPRNQPLNPGKC-----ACECT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GPHKELDR-----NSCQCVCKNKLFPSQCGAN------REFDENT----
                                                                                                                                                    familiaris (Dog)
mora: Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                           -VCKCARGY 455
                                                                                           'n
                                                                                (AUG-1996)
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                                       Montgomery M.W.;
he EMBL/GenBank/DDBJ
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                                                                                EMBL/GenBank/DDBJ
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         Brewer G.J.,
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er G.J., Schall W.D.; canine von Willebrand
                                        databases
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RA Mancuso D.J., Christopherson P.A., Kroner P.A., Montgomery R.R.;

RA "The canine von Willebrand factor gene: sequence and expression of refer a region encoding the glycoprotein ID/IX binding domain.";

RL Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.

C : PARTICIPARES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF VASCULAR INJURY (BY SIMILARITY).

C : SUBUNIT: MULTIMERIC (BY SIMILARITY).

C : TISSUE SPECIFICITY: BLOOD.

C : PTM: ALL CYSTEIME RESIDUES ARE INVOLVED IN INTRACHAIN OR INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).

C : SIMILARITY: CONTAINS 3 VWFA DOMAINS.

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C : SIMILARITY: CONTAINS 3 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK SIMILARITY: SOME, TO SILKWORM HEMOCYTIN.
  Plasma;
SIGNAL
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CHAIN
DOMAIN
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Pfam; PF00107; Cys.knot; 1.
Pfam; PF01826; TIL; 4.
Pfam; PF001826; VWA; 3.
Pfam; PF00092; VWA; 3.
Pfam; PF00093; VWG; 3.
Pfam; PF00094; VWG; 4.
PRINTS; PR00453; VWFADDMAIN.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01208; VWFA; 3.
PROSITE; PS01208; VWFA; 3.
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Submitted (OCT-1998) to the pure 'A
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InterPro; IPR001007; -.
InterPro; IPR001846; -.
InterPro; IPR002035; -.
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; L16903; AAA30903.1; -.
; AF099154; AAD04919.1; -.
; U66246; AAB93766.1; -.
; P04275; LATZ.
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Pred. No. 0.0002;
""" matches 56;
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"Isolation and characterization of a 230 kba
specifically expressed in fetal brains: its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C) (P230).
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                   astrocytes."
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                                                                                                                                                                                                                                                                                              outgrowth from rat cerebral cortex neurons
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TISSUE=Submaxillary gland;
MEDLINE=92104189; PubMed=1722152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2432
                                                                                                                                                                                                                                                                                                                                      MEDLINE=98158323; PubMed=9498558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
Mammalia;
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                                                                                                                                                                                                                                                                          Biochem. 122:1146-1152(1997).
                                           WITHIN THE CENTRAL GLOBULE.

SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.

ALTERNATIVE PRODUCTS: 3 ISOFORMS; MAJOR, MINOR-1 AND MINOR-2

ALTERNATIVE PRODUCTS: 3 ISOFORMS; MAJOR, MINOR-1 AND MINOR-2

(SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ARE

PRODUCED IN A TISSUE-AND TIME-SPECIFIC MANNER DURING DEVELOPMENT.

TISSUE SPECIFICITY: SUBMAXILLARY GLANDS AND BRAIN.

DEVELOPMENTAL STAGE: PREDOMINANTLY EXPRESSED IN THE EMBRYONIC AND

EARLY POSTNATAL STAGES. LITTLE OR NO DETECTION IN ADULT BRAIN.

SIMILARITY: CONTAINS 15 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 11 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 FIBRINOGEN-LIKE DOMAIN.
                                                                                                                                                                                                                                OF EPITHEI FUNCTION:
                                                                                                                                                                           IN GROWTH CONE GUIDANCE. INVOLVED IN NEURITE OUTGROWTH FROM CORTICAL NEURONS GROWN ON THE MONOLARYER OF ASTROCYTES.
SUBUNIT: HESTAMERIC. A HOMOTRIMER MAY BE FORMED IN THE TRIPLE COILED-COIL REGION AND MAY BE STABILIZED BY DISULFIDE RINGS AT BOTH ENDS. TWO OF SUCH HALF-HEXABRACHIONS MAY BE DISULFIDE LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scrofa
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                                                                                                                                                                                                                                                    FUNCTION: SAM (SUBSTRATE-ADHESION MOLECULE) INHIBIT CELL MIGRATION. MAY PLAY A ROLE IN
          SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation suropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHRGTIYPVGQFWEEACDVCTCTDLEDSVMGLRVAQCSQKPCEDN----CLSGFTYVLHEG
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                                                                                                                                                                                                                                          EPITHELIAL TUMORS
                                                                                                                                                                                                                                                                                                                                                                               Biochem.
                                                                                                                                                                                                                                                                                                                                                                              e primary structure of porcine tenascin:
transcript in adult submaxillary glands
Biochem. 202:643-648(1991).
                                                                                                                                                                                                                                                                                                                                                          OF 813-825; 887-917; 998-1011; 1597-1608
                                                                                                                                                                                                                                                                                                                                                                                                   Weinstein J., Gillespie W.M., primary structure of porcine 1
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Eutheria;
                                                                                                                                                                                                                                                                                                                                                 brain;
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                                                                                                                                                                                                                                 PLAYS A ROLE DURING
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Cetartiodactyla; Suina;
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PS01186;
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IPR002181;
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Eukaryota; Metazoa; Chordata; Craniata
Actinopterygii; Neopterygii; Teleostei
Cypriniformes; Cyprinidae; Rasborinae;
                                                                                                                                        01-NOV-1995
15-JUL-1998
              MEDLINE=94128602; PubMed=8297791;
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                                                         NCBI_TaxID=7955;
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Pred. No. 0.00
L7; Mismatches
                                                                             ) (Zebra danio).
; Craniata; Vertebrata; I
Teleostei; Euteleostei;
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   InterPro; IPRO00152; -.
InterPro; IPRO00561; -.
InterPro; IPRO00800; -.
InterPro; IPRO01336; -.
InterPro; IPRO01438; -.
InterPro; IPRO01438; -.
InterPro; IPRO01438; -.
InterPro; IPRO01810; -.
Pfam; PF00008; EGF; 36.
Pfam; PF000023; ank; 6.
Pfam; PF000023; ank; 6.
Pfam; PF00006; notch; 3.
Pfam; PF00006; EGFTGF.
PRINTS; PR00010; EGFTGF.
PRINTS; PR00010; EGFTGF.
PROSITE; PS50088; ANK_REPEAT; 4.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS00010; ASX_HYDROXYL; 23.
PROSITE; PS00010; ASX_HYDROXYL; 23.
PROSITE; PS001187; EGF_2; 28.
PROSITE; PS01187; EGF_2; 28.
PROSITE; PS01187; EGF_CA; 22.
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HSSP; P00740; 1IXA.
ZFIN; ZDB-GENE-990415-173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A zebrafish homologue of the Drosophila neurogenic gene Notch its pattern of transcription during early embryogenesis."; Mech. Dev. 43:87-100(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMERTION: IMPLICATED IN CELL FATE SPECIFICATIONS DURING EMERGY DEVELOPMENT. MAY BE INVOLVED IN THE FORMATION OF THE NEURAL PLATE, NOTOCHORD AND BRAIN VESICLES.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

DEVELOPMENTAL STAGE: EXPRESSED IN ALL CELLS IN PREGASTRULATION STAGES. DURING GASTRULATION IS DIFFERENTIALLY EXPRESSED,

ACCUMULATING PREDOMINANTLY IN THE PRECHORDAL MESODERM AND NOTOCHORD. AT THE END OF GASTRULATION, EXPRESSED ALONG THE ANYELOPING ASIA INCLUDING THE DEVELOPING HERAL PLATE ANYERIOR POSTERIOR AXIS INCLUDING THE DEVELOPING HERAL PLATE AND DIFFERENTIATING MESODERM. ALSO PRESENT IN THE DEVELOPING AND DIFFERENTIATING MESODERM.
                                                                                                                                                                                                                                                                                                                                                                                                 AND DIFFERENTIATING MESODERM. ALSO PRESEN ERAIN AND HEAD RECTONS. SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE FAIMLARITY: CONTAINS 36 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS. SIMILARITY: CONTAINS 6 ANK REPEATS.
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MEDLING=90385285; PubMed=2402639;

Coffman C., Harris W., Kintner C.;

"Notch, the Xenopus homolog of Drosophila notch.";

Science 249:1438-1441(1990).

[2]

REVISIONS TO 1759-1782.

Kintner C.;

Submitted (JUN-1996) to the EMBL/GenBank/DDBJ datal
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN EARLY EMBRYOS.
SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.
SIMILARITY: CONTAINS 36 EGF-LIKE DOWAINS.
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 6 ANK REPEATS.
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TE; PS0008; ANK. REPEAT; 4.
TE; PS50297; ANK. REP. REGION; 1.
TE; PS00010; ASX_HYDROXYL; 23.
TE; PS00002; EGF_1; 34.
TE; PS01187; EGF_CA; 21.
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21.7%;
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Pred. No. 0.00
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InterPro; IPRO00561; -.
InterPro; IPR00082; -.
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InterPro; IPR001438; -.
InterPro; IPR001438; -.
InterPro; IPR001881; -.
InterPro; IPR002212; -.
Pfam; PF00008; EGF; 46.
Pfam; PF00008; EGF; 46.
Pfam; PF000010; EGFBLOOD.
PROSITE; PS001010; ASX, HYDROXYL; 43. -.
PROSITE; PS01186; EGF 2; 36.
PROSITE; PS01187; EGF CA; 43.
EXTTROCELULAR matrix; Calcium-binding; Gl
 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Fibrillin genes map to regions of conserved mouse/human syn mouse chromosomes 2 and 18.";

Genomics 18:667-672(1993).

-I- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICR THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.

-I- SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIU EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE OF 210-317 FROM N.A.
MEDLINE-94140368; PubMed-8307578;
** Pereira L., Zhang H., Sang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE STANDARD; PRT; 2907 AA. 061555; 063957; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) FIBRILLIN 2 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L39790; AAA74908.1; -. EMBL; S69359; AAC60685.1; -. MGD; MGI:95490; Fbn2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang H., Hu W., Ramirez F.;
"Developmental expression of fibrillin of extracellular microfibrils.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
MCBI_TaxID=10090;
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                                                          ASCGPHKELDRN-SCQCVCKNKLFPSQCGA---
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01-JUN-1994
01-FEB-1996
01-NOV-1997
FIBRILLIN 2
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Putham E.A., Zhang H., Ramirez F., Milewicz D.M.;
"Fibrillin-2 (FBN2) mutations result in the Marfan-like disorder,
congenital contractural arachnodactyly.";
Nat. Genet. 11:456-458(1995).
-i- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
THAT BINDS CALCIUM. FIBRILLIN-2-CONTAINING MICROFIBRILS REGULATE
THE EARLY PROCESS OF ELASTIC FIBRE ASSEMBLY CONGENITAL CONTRACTURAL
-i- DISEASE: DEFECTS IN FBN2 ARE THE CAUSE OF CONGENITAL CONTRACTURAL
-i- DISEASE: DEFECTS IN FBN2 ARE THE CAUSE OF CONGENITAL CONTRACTURAL
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2653
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Zhang H., Apfelroth S.D., Hu W.,
Bonadio J., Mechan R.P., Ramirez
"Structure and expression of fibr
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P; P35555; 1EMO.; 121050; -.
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SIMILARITY: CONTAINS 43 CALCIUM-BINDING EGF-LIKE DOMAINS.
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x62009; -; NOT_ANNO
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Biochem. Biophys. Res. Commun. 194:1019-1024(1993).

Biochem. Biophys. Res. Commun. 194:1019-1024(1993).

FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEOSTASIS, IT PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING MONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE VASCULAR INJURY (BY SIMILARITY).

-I- SUBUNIT: MULTIMERIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lavergne J.M., Plao Y.C., Ferreira V., Kerull
Bahnak B.R., Meyer D.;
"Primary structure of the factor VIII binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VI-UCT-ZUUU (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
VON WILLEBRAND FACTOR PRECURSOR (VWF) (FRAGMENT):
F8VWF OR VWF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2716
                                                                                                                                     HSSP;
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                                                          InterPro;
                                                                                                                                                     EMBL;
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Mammalia; Eutheria;
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                                                                       InterPro;
                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                   PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR INVERCHAIN DISULETDE BONDS (BY SIMILARITY).
SIMILARITY: CONTAINS 3 WEFC DOMAINS.
SIMILARITY: CONTAINS A C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
SIMILARITY: SOME, TO SILKWORM HEMOCYTIN.
                                                                       L; AF052036; AAC06229.1; -.
L; S64541; AAB27829.2; -.
P; P04275; IATZ.
arPro; IPR000359; -.
arPro; IPR001806; -.
arPro; IPR001846; -.
arPro; IPR002035; -.
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         PF00007; Cys_knot;
PF00092; vwa; 3.
PF00093; vwc; 3.
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PubMed=8352759;
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the EMBL/GenBank/DDBJ databases.
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PR00365; PR00453;

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; PS01208; VWFC; 3.
; PS01185; CTCK_1; 1.
; PS01225; CTCK_2; 1.
; PS01225; CTCK_2; 1.
coagulation; Platelet; Glycoprotein; Extracellular matrix; Endothelial cell; Repeat; Cell adhesion.
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PS01208;
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GELCNAC
.) (POTENTIAL).
) (POTENTIAL).
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Query Match Best Local Similarity

11 25

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Score Pred.

134.5; DB 1; No. 0.00056;

Length

2482;

IPR000152;

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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence updated)
01-OCT-2000 (Rel. 40, Last annotation updated)
CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR
                                   EMBL; X93328;
EMBL; U66888;
HSSP; P07204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _MOUSE
                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                    MEDLINE-97312684; PubMed-9169125;
Lin H.H., Stubbs L.J., Mucenski M.L.;
"Identification and characterization of a seven
receptor using differential display.";
Genomics 41:301-308(1997).
                                                                                         use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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          GCRDb; GCR_1309; MGD; MGI:106912;
                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning of F4/80, a murine macrophage-restricted surface glycoprotein with homology to the G-protein-linked transmembrane 7 hormone receptor family.";
J. Biol. Chem. 271:486-489(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BALB/C; TISSUE=Peritoneal cavity; MEDLINE=96132946; PubMed=8550607; McKnight A.J., Macfarlane A.J., Dri P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BALB/C; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Elemopean Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PRO
TISSUE SPECIFICITY: IN MACROPHAGES; BUT ASS
ARE LOCALIZED WITHIN T-CELL AREAS OF LYMPH
LOW LEVEL OF EXPRESSION ON BLOOD MONOCYTES.
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SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS
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                                                                                                                                                                                                                                                                                                        FUNCTION: PROBABLY INVOLVED IN CELL ADHESION WITHIN
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InterPro; IPR000561; -.
InterPro; IPR000832; -.
InterPro; IPR0001740; -.
InterPro; IPR001881; -.
Pfam; PF00002; 7tm 2; 1.
Pfam; PF00008; EGF; 7.
Pfam; PF01825; GPS; 1.
PRINTS; PR01128; EMR1HORMONER.
PROSITE; PF001650; G_PROTEIN_RECEP_F2_2; 1.
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Matches 65
                                                                                                                                         MEDLINE=95155442; PubMed=7531707; Gherzi R., Carnemolla B., Siri A., Ponassi M., Balza E., Zardi L., "Human tenascin gene. Structure of the 5'-region, identification, characterization of the transcription regulatory sequences."; D. Biol. Chem. 270:3429-3434(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                         TENA_HUMAN STANDARD; PRT; 2201 AA.

P24821; Q15567; Q14583;

01-MAR-1992 (Rel. 21, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

01-OCT-2000 (Rel. 40, Last annotation update)

TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN)

(GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR
MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C).
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606;
                                                                                                                                                                                                                                             "Human tenascin: primary structure, pre-mRNA splicing localization of the epitopes recognized by two monocle antibodies.";
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE TISSUE=Fetal brain, and Melanoma; MEDLINE=91187670; PubMed=1707164;
                                                                                                                                                                                                                                                                                                                                                                                                      Homo
SEQUENCE FROM N.A.
MEDLINE=92052108; PubMed=1719530;
                                                              multidomain
                                                                            Nies D.E., Her
"The complete
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                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=95155442;
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ath T.J., Kim J.H., (
NA sequence of human
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Interpro; IPRO00561; -...

Interpro; IPRO00777; -...

Interpro; IPRO01777; -...

Interpro; IPRO0177; -...

Pfam; PF00008; EGF; 14.

DR Pfam; PF000147; fibrinogen_C; 1.

Pfam; PF00041; fibrinogen_C; 1.

Pfam; PF00041; fin3; 15.

DR PROSITE; PS00022; EGF_1; "

PROSITE; PS01186; EGF Glycoprotein; Ce"

Extracellul="Signature" of the property of the pro
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"An alternatively spliced region of the human hexabrachion repeat of potential N-glycosylation sites.";
Proc. Natl. Acad. Sci. U.S.A. 86:1588-1592(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Glioblastoma;
MEDLINE=89160821; Pul
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OF EPITHELIAL TUMORS.

ISUBUNIT: HEXAMERIC. A HOMOTRIMER MAY BE FORMED IN THE COLLED-COIL REGION AND MAY BE STABILLIZED BY DISULFIL BOTH ENDS. TWO OF SUCH HALF-HEXABRACHIONS MAY BE DISULFIL BOTH ENDS. TWO OF SUCH HALF-HEXABRACHIONS MAY BE DISUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.

ALTERNATIVE PRODUCTS: FOUR VARIANTS ARE PRODUCED FROGENE IN A TISSUE- AND TIME-SPECIFIC MANNER DURING DEIL INDUCTION: BY TOF-BETA.

SIMILARITY: CONTAINS 15 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 FIBRINOGEN-LIKE DOMAIN.
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email to license@isb-sib.ch).
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RA Oliva A.A. Jr., Chan S.J., Steiner D.F.;
RT "Evolution of the prohormone convertases: identification of a monologue of pc6 in the protochordate amphioxus.";
RI BIOCHIM. BLOPHYS. ACTA 1477:338-348 (2000).
CC -!- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPROTEASE ACTIVITY CONTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE CONTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE COFTLEAVAGE ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR PROPECTEINS BY CLEAVAGE OF ARG-YAA-YAA-ARG-[-ZAA BONDS, WHERE XAA CA. SUBCELLULAR LOCATION: ISOFORM A AND ISOFORM C ARE SECRETED.
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EMBL; AF184617; AAF26302.1;
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the European Bioliformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
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                                              CEAGCPPGQFLHHGDCDSCHRECKTCDGP---
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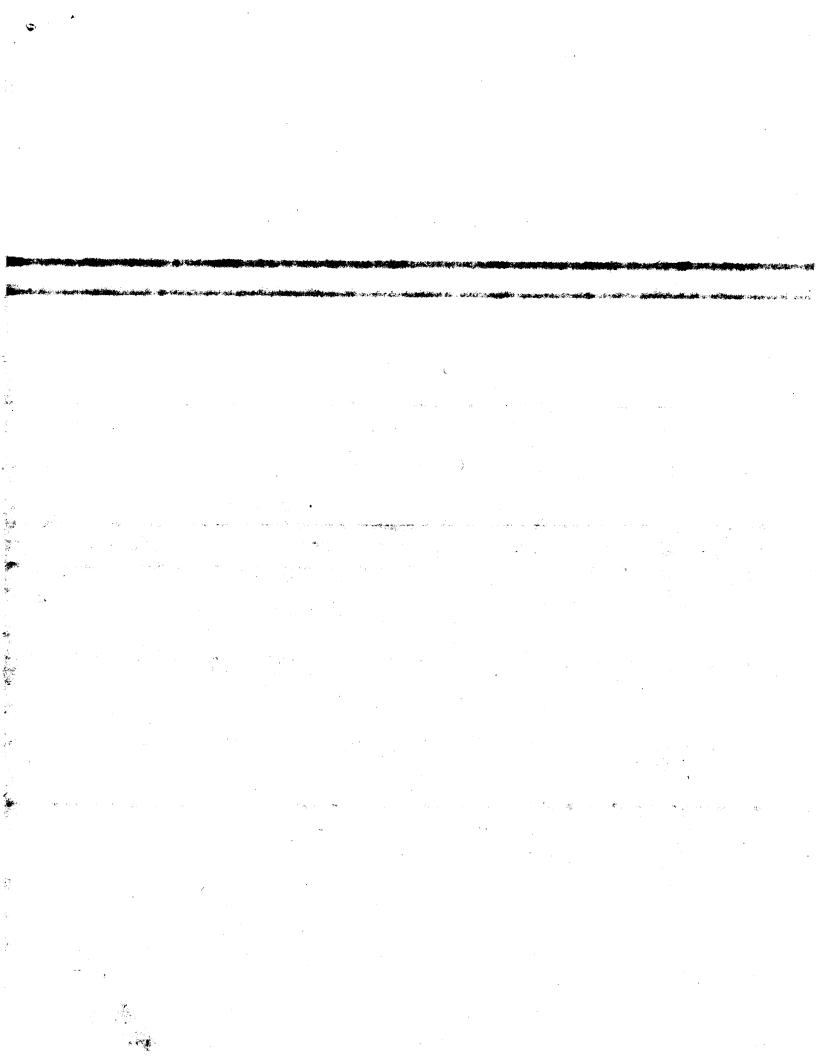
SUBTILASE_SER; 1.

protease; Glycoprotein; Zymogen; Signal;

protease; Glycoprotein; Zymogen; Signal;

protease; Glycoprotein; Zymogen; Signal;
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CLEAVAGE (AUTO-) [BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Pred. No. 0.00
P); Mismatches
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MISSING (IN ISOFORM C).
CHPTCKECSDEYDDTCTACNDGFLLTDASSCEAGCPPGQFL
HHGDCDSCHRECKTC -> IARCVDRXDRXWCDLVLRFNFC
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                                                                                            -EC - - SDEYDDTCTACNDGFLLTDASS
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Search completed: October 17, 2001, 14:51:45 Job time: 471 sec



GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                           sp_unclassified:*
sp_vertebrate:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_mammal:*
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                                                                                                                                                                                                                                                                                                                                                                                                                             sp_plant:*
                                                                                                                                                                                                                                                            Length DB
                                                                              126
1704
1698
354
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p97946 mus musculu
035251 rattus norv
074567 trichoderma
090824 gallus gall
090878 drosophila
090994 gallus gall
090995 gallus gall
090995 gallus gall
090996 gallus gall
090916 drosophila
090916 drosophila
090868 drosophila
041701 homo sapien
044447 hemicentrot
006008 mus musculu
                                                                                                                                                                057352 coturnix co
037757 rattus norv
094446 chironomus
094438 chironomus
094438 chironomus
043915 homo sapien
                                                                                                                                                                                                                                   Q9xs50 bos taurus
                                                                                                                                                                                                                                                           Description
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
133	134	134	134	134	134	134	134.5	135	135	135.5	135.5	135.5	135.5	136	136	136	136.5	138	138	138.5	139.5	139.5	139.5	139.5	139.5
11.8	11.9	11.9	11.9	11.9	11.9	11.9	11.9	11.9	11.9	12.0	12.0	12.0	12.0	12.0	12.0	12.0	12.1	12.2	12.2	12.3	12.3	12.3	12.3	12.3	12.3
2019	2906	2352	1664	1219	1218	642	999	1587	778	4114	4006	1511	1187	2653	777	777	122	701	648	765	2475	2471	2471	2471	2470
11	11	υ	Ç,	11	11	13	4	4	13	11	11	ហ	2	თ	σı	UI	6	u	G	G	G	11	4	4	11
Q64706	Q9WUH9	061240	Q9TVQ2	Q63722	Q9QXXO	P79941	Q9NQ36	000508	Q9IBG4	054796	035452	Q9VB21	Q49549	Q25253	Q9VYP1	Q24550	Q9GLX1	Q9VJU4	Q9NKD7	Q9NL50	Q9GP97	Q9QW30	Q9H240	Q04721	035516
Q64706 mus musculu	Q9wuh9 rattus norv	061240 halocynthia	Q9tvq2 caenorhabdi	Q63722 rattus norv		P79941 xenopus lae	homo	000508 homo sapien	Q9ibg4 xenopus lae	054796 mus musculu	O35452 mus musculu	Q9vb21 drosophila	Q49549 mycoplasma	Q25253 lucilia cup		Q24550 drosophila		Q9vju4 drosophila	Q9nkd7 drosophila	Q9n150 sarcophaga	Q9gp97 caenorhabdi	Q9qw30 rattus	Q9h240 homo sapien	Q04721 homo sapien	035516 mus musculu

ALIGNMENTS

	61 EETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLEPSQCGANREEDENTCQCVCKRTC 120	Qy	
		Db '	
	1 SLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELD 60	Qy	
_	Query Match 87.7%; Score 991; DB 6; Length 420; Best Local Similarity 84.4%; Pred. No. 5.8e-99; Matches 162; Conservative 14; Mismatches 16; Indels 0; Gaps	X B O	
	SHAGHACH 440 MG, 10001 MM, JOHNSHIITIGICHEAD CUCCHI	Ç	
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	1 20	ΕT	
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	PROSITE; PS50278; PDGF_2; 1.	DR	
	PROSITE; PS00249; PDGF_1; 1.	DR	
	Pfam; PF00341; PDGF; 1.	DR	
	InterPro; IPR000072;	DR	
		DR	
	EMBL; AB004275; BAA77687.1;	DR	
	Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.	RL	
		RT	
	Liu X., Yonekura H., Yamagishi S., Yamamoto Y., Yamamoto H.;	RA	
	TISSUE=HEART;	RC	
	SEQUENCE FROM N.A.	RР	
		RZ Z	
	NCBI_TaxID=9913;	Q:	
	Bovinae; Bos.	റ്റ	
	Eutheria; Cetartiodactyla; Ruminantia; Pec	8	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	8	
		20	
	DOTHELIAL GROWTH	DE	
	(TrEMBLrel, 16, Last	Ŋ	
	(TrEMBLrel. 12,	ŢΩ	
	01-NOV-1999 (TremBLrel. 12, Created)	DT	
		AC	
	O9XS50 PRELIMINARY; PRT; 420 AA.	ij	
	O9XS50	O9X	
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В

289

EETCQCVCKGGLQASSCGPHKELDRDSCQCVCKNKLFPSSCGANREFDENTCQCICKKTC

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Best Local
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                               Signal
                                                                                                                                                                                                                                                                                                                                                         ProDom; PD001629; -; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000072; -.
InterPro; IPR002400; -.
Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Development 125:743-752(1998).
EMBL; Y15837; CAA75799.1; -.
HSSP; P15692; IVPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eichmann A., Corbel C., Jaffredo T., Breant Alitalo K., Le Douarin N.M.;
"Avian VEGF-C: cloning, embryonic expression of the differentiation of VEGFR2-expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=98167900; PubMed=9435294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  057352;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursors.
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                                                                                                                                                             DEETCQCYCRAGLRPASCGPHKELDRNSCQCYCKNKLFPSQCGANREFDENTCQCYCKRT 119
                                                                                                                                                                                                             SLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD-DSTDGFHDICGPNKEL 59
                                                                                                 CPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVC 179
                                                   RCVRTSWKRPLMN
                                                                                                                                                DEETCQCVCKGGVRPISCGPHKELDRASCQCMCKNKLLPSSCGPNKEFDEEKCQCVCKKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRNQPLNPGKCACECTENPQKCFLKGKKFQHQTCSCYRRPCTNRVKHCEQGLSFSEEVCR
                                                                        RCVPSYWKRPQMS 192
                                                                                                                                                                                               SLPATQTQCHVANKTCPKNHVWNNQICRCLAQHDFGFSSHLGDSDTSEGFH-ICGPNKEL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCR 180
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111
418 AA;
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73.1%;
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Last annotation update)
FACTOR C PRECURSOR.
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Pred. No. 1.4e
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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VASCULAR ENDOTHELIAL GROWTH

; 099BFCC79151BF2B CRC64;
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L.4e-82;
les 33;
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                                                                                                                                                                                                                                                                      Length 418;
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Best Local s
Matches 56
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Best Local S
Matches 41
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Q94446;
01-FEB-1997 (TIEMBLICEL 0
01-FEB-1997 (TIEMBLICEL 0
01-CCT-2000 (TIEMBLICEL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; S
                                                                         1210
                                                                                                                                                                                                                                                                                                                                                                           TISSUE-SALIVARY GLAND;
Case S.T., Cox C., Bell W.C., Hoffman R.T., Ma
Submitted (APR-1996) to the EMBL/GenBank/DDBJ
EMBL; U54641; AAA99804.1; -.
InterPro; IPR000561; -.
InterPro; IPR000853; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chironomus thummi thummi (Midge).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;

Chironomoidea; Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mandriota S.J., Pepper M.S. Submitted (JUN-1997) to the EMBL; AF010302; AAB63248.1; HSSP; P15692; 2VPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        035757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                   PRINTS; PR00876; MTNEMATODE

PROSITE; PS00122; EGF_1; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

SEQUENCE 1704 AA; 185745 MW; 3A3F20247C8F1E28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000072; -. Pfam; PF00341; PDGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VASCULAR ENDOTHELIAL GROWTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 KDA SILK PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                        TDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVC-KNKLFPSQCGAN 104
                                                                    PTPAPTCSASQKYSNVTCSCGCNPGMPAKGCPGNQVWCENSCQCVCPKNMEKPADN----
                                                                                                                     PATLPQCQAAN ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 22.7%;
l Similarity 74.5%;
41; Conservative
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                                                                                                                                                                   Similarity
56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS50278; PDGF_2; 1.
M00141; PDGF; 1.
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126 AA;
                                                                                                                                                                   Conservative
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13977
                                                                                                                                                                                         21.7%;
27.6%;
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15,
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                                                                                                                                                                 Score 245.5; DB 5;
Pred. No. 3.8e-18;
L; Mismatches 75;
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Pred. No. 2.4e-20;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hoffman R.T., Martin J., Hamilton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8F365AFBC4E037B0 CRC64;
                                                                                                                  KTCPTNYMWNNHICRCLAQEDFMFSSDAGDDS
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                                                                                                                                                                   Indels
                                                                                                                                                                                                             Length 1704;
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RESULT
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AC Q95

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Best Local Similarity
Matches 63; Conser
                           043915 PRELIMINARY;
043915;
01-JUN-1998 (TrEMBLrel. 0
01-JUN-1998 (TrEMBLrel. 0
01-MAR-2001 (TrEMBLrel. 1
GROWTH FACTOR FIGF.
FIGF OR VEGF-D.
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TISSUE-SALIVARY GLAND;
TISSUE-ST., Cox C., Bell W.C., Hoffman R.T., Martin J., Hamilton Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U54640; AAA99803.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chironomus pallidivittatus (Midge).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;

Chironomoidea; Chironomidae; Chironominae; Chironomus.
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01-FEB-1997 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTKCSDKQKFIESKCECGCDTQTQCKNGFRWSNLECGCLCDEKKCQGKQVFDKNTCQCKC
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Last annotation updat
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Pred. No. 4.5e-17;
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Best Local
        P97946 PRELIMINARY;
P97946;
01-MAY-1997 (TrEMBLrel. 03, C
01-MAY-1997 (TrEMBLrel. 03, I
01-MAR-2001 (TrEMBLrel. 16, I
VASCULAR ENDOTHELIAL GROWTH F
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EMBL; Y12865; CAA73371.1; JOINED.
EMBL; Y12866; CAA73371.1; JOINED.
EMBL; Y12867; CAA73371.1; JOINED.
EMBL; Y12869; CAA73371.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                 ProDom: PD001629; -; 1.

PROSITE; PS00249; PDGF_1; 1

PROSITE; PS50278; PDGF_2; 1.

SMART; SM00141; PDGF; 1.

SEQUENCE 354 AA; 40444 M
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EMBL; Y12864; CAA73371.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acnen M.G., Jeltsch M., Kukk E., Alitalo K., Stacker S.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97349118; PubMed=9205122;
Yamada Y., Nezu J., Shimane M., Hirata
"Molecular cloning of a novel vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98140120; pubMed=9479493;
Rocchigiani M., Lestingi M., Luddi A., Orlandini Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
"Human FIGF: cloning, gene structure, and mapping between the PIGA and the GRPR genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                               Local Similarity
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OR FIGE
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29; -; 1.
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                                                                                                                                                                                                                                                                                                                                                                   40444 MW;
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                                                                                                                                                                                                                                                                                                             20.7%;
                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                               Score 234; DB
Pred. No. 1.7e
24; Mismatches
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FACTOR D (C-FOS INDUCED
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            FACTOR).
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Best Local (
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                                                                                                                                                                                       O35251 PRELIMINARY; PRT; 326 AA.
035251;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR D.
                                                  STRAIN-SPRAGUE DAWLEY;
MEDLINE-97349118; PubMed-9205122;
Yamada Y., Nezu J., Shimane M., H
              Genomics 42:483-488(1997)
                                                                                                                     Rattus norvegicus (Rat),
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 42:483-488(1997).
EMBL; X99572; CAA67892.1;
EMBL; D89628; BAA14002.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ordandini M., Marconcini L., Ferruzzi R., Oliviero S.; "Identification of a c-fos-induced gene that is related platelet-derived growth factor/vascular endothelial grow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                           VEGF-D.";
                                     Yamada Y., Nezu J., Shimane M., Hirata Modecular cloning of a novel vascular
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97349118; PubMed=9205122;
Yamada Y., Nezu J., Shimane M., Hirata
"Molecular cloning of a novel vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 93:11675-11675(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97030254; PubMed=8876195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P15692;
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                                                                                                                                                                                                                                                                                                                                    290
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                                                                                                                                                                                                                                                                                                                                                PGKCAC-ECTESPQKCLLKGKKFHHQTCSC-----YRRPCTNRQKACEPGFSYSEE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:108037;
                                                                                                                                                                                                                                                                                                                                    PENCSCFECKESLESCCQKHKIFHPDTCSCEDRCPFHTRTCASRKPACGKHWRFPKE
                                                                                                                                                                                                                                                                                                                                                                                                                  CRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                              ECPHSKKLCPIDMLWDNTKCKCVLQDETPL--------
AF014827; AAB66557.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                         -EPTLCGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40908 MW;
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28.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 225;
Pred. No. 1.
                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6636B17FBF07037C CRC64;
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.6e-16;
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Matches 58
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Best Local S
Matches 44
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Pfam; per00341; pDGF; 1.
ProDom; pD001629; -; 1.
PROSITE; pS00249; pDGF_1; 1.
PROSITE; pS50278; pDGF_2; 1.
SMART; SM00141; pDGF; 1.
SEQUENCE 326 AA; 37112 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               074567
074567;
01-NOV-1998
01-NOV-1998
01-MAY-2000
                                                                                                                                                                                                                                                                           MEDLINE=98263335; PubMed=9600944;
Rey M., Ohno S.A., Pintor-Toro J.A., Jose A., Llobell A., Benitez T.;
"Unexpected homology between inducible cell wall protein QID74 of
filamentous fungi and BR3 salivary protein of the insect Chironomus.";
Proc. Natl. Acad. Sci. U.S.A. 95:6212-6216(1998).
EMBL; X95671; CAA64974.1; -.
InterPro; IPR000561; -.
PROSITE; PS01186; EGF_2; 1.
SEQUENCE 704 AA; 77925 MW; 63414BDDEC365EBC CRC64;
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InterPro; IPR000072;
Pfam; PF00341; PDGF;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-CECT 2413;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi;
NCBI_TaxID=5544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trichoderma harzianum.
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243
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                                                                                                                                                                                      16 CPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHD-ICGPNKEL----DEETCQCV---- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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GKEAHFDYNQKKCVCKNNGEVYNSAKKTCSCPDGQYWNGKQCVCPYGQVFNGKQCVPDCG
                                                                                                       WNGKNCQ-----VDCGKDASYDYKQKKCVCKKHGEIYNSNSKTCSCPPGQVWNGYACVVD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCV 67
                                                   CGKEAHFDNKQKKCVCNNYGEIYNSGSKTCACPGGQYFNGKKCVCPYGKVWNGKQCVEDC
                                                                            CGANREFDENTCQCVCKR----
                                                                                                                                CPSGYTWNGHQC------VHDCGKDATWQYGNCVCNKKGEVYNPKDKTCSCPPGQY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PENCSCFECKESLESCCQKHKMFHPDTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGKCAC-ECTESPQKCLLKGKKFHHQTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QCPHSKKLCPVDMLWDNTKCKCVLQD-----
                       ------SPQKCLLK--GKKFH--HQTCSC-----YRRPCTNRQ----KACEPG--
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ascomycota; mitosporic
                                                                                                                                                                                                                            15.2%;
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29.7%;
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Pred. No. 9.6e
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                              Score 171.5; DB 3; Pred. No. 1.7e-10; 6; Mismatches 67;
                                                                            ----TCPRNQPLNPGKCAC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1261AFA373596C00 CRC64;
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InterPro; IPR001777; -.
InterPro; IPR0012181; -.
Pfam; PF00008; ECF; 13.
Pfam; PF00041; fn3; 11.
Pfam; PF00041; fibrinogen_C; 1
 Q9VB78
Q9VB78;
01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00022; EGF_1; UNKNOWN_14.
PROSITE; PS01186; EGF_2; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad.
EMBL; J04519; AAA-
HSSP; P24821; ITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones F.S., Hoffman S., Cunningham B.A., Edelman G.M.; "A detailed structural model of cytotactin: protein ho alternative RNA splicing, and binding regions."; Proc. Natl. Acad. Sci. U.S.A. 86:1905-1909(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=89184536; PubMed=2467292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
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                                                                                               419
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                                                                                               CINGQCVCDEGF
                                                                                                                      CTNRQKACEPGF
                                                                                                                                            GLCVCHEGFVGDDCSQKRCPKTCNNRGRCVDGR-CVCHEGYLGEDCGELRCPNDCHNRGR 418
                                                                                                                                                                                         CVCDEGYTGEDCGELICPNDCFDRGRCINGTCFCEEGYTGEDCGELTCPNNCNGNGRCEN 359
                                                                                                                                                                     GKCAC
                                                                                                                                                                                                                CVCKNKLFPSQCG----ANREFDENTC---QCVCKR-----
                                                                                                                                                                                                                                        EGYTGP--DCGEELCPHGCGIHGRCVGGRCVCHEGFTGEDCNEPLCPNNCHNRGRCVDNE
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                                                                                                                                                                                                                                                                                                                                     61;
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1 33 POTENTIA
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 (TrEMBLrel. 13, (TrEMBLrel. 16,
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                                     PRELIMINARY;
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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24
                                                                                                                                                                                                                                                                                                                                                                                              199304 MW;
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01, Last sequence update)
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                               Score 151; DB : Pred. No. 6e-08
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Kodira C.D., Krafft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Supskin M.P., Smith T.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter E., Wang A.H., Wang Y.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong G.D., Rabinia melanogaster.";
REMBL, AEO03759, AAF56664.2; -.
                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               George R.A., Lewis S.E., Richards S., Asnburuer m., neuverson, Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basun A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basun A., Baxendale J., Bayraktaroglu L., Beasley E.M., Barden B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muso Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Last annotation update) CG6124 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0039484; CG6124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG6124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132;
395
                                           107
                                                                                    335
                                                                                                                                                                            285
                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro;
                                                                                                                                63
                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                     9
                                                                                  NRCSPVCSGGCKNGFCVAPGKCSCDEGYIKGTGNSCKPICSKGCENGFCDAPEKCSCNDG 394
YEMDGENRCSPVCSGGCKNGFCVAPGKCSCD-----
                                      FD---ENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN 163
                                                                                                                                                                       CVAPNECSCNAGYTKLEGVCTPVCK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE003759;
P02876; 9W
                                                                                                                           T-CQCVCRAGLRPASC-GPHK-ELDR-----NSCQCVCKNKL----
                                                                                                                                                                                                                CQAANK-TCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGF-----HDICGPNKELDEE
                                                                                                                                                                                                                                                              50;
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                              PS01186;
                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000561;
                                                                                                                                                                                                                                                                                                                                                                          800 AA;
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Celniker S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9WGA
                                                                                                                                                                                                                                                                                                                                                                        EGF_2; UNKNOWN_9.
; 87721 MW; A7CA1C171DA189C8 CRC64;
                                                                                                                                                                                                                                                                                13.1%;
                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holt R.A.,
                                                                                                                                                                                                                                                       Pred. No. 6.36
3; Mismatches
                                                                                                                                                                                                                                                                                                   Score 148;
                                                                                                                                                                         -----DGCVNGFCASPEKCSCNDGYEMDSE
                                                                                                                                                                                                                                                     ,; DB 5;
6.3e-08;
79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evans C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachycera; Muscomorpha;
-EGYSKETGNSCKPICS-
                                                                                                                                                                                                                                                                                                     Length 800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gocayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ayne J.
Galle
                                                                                                                           -FPSQCGANRE
                                                                                                                                                                                                                                                              50;
                                                                                                                                                                                                                                                            Gaps
                                                                                                                              106
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P Q

164

RQKACEPGFSYSEEVCRCVPSY

-- KGCENGFCDAPEKCSCNDGY

461

185

442

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Best Local Similarity 24.2
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01186; EGF_SMART; SM00060; FN3; 1
EGF-like domain; Glyco
                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00008; EGF; 13.
Pfam; PF00041; fn3; 8.
Pfam; PF00147; fibrinogen_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spring J., Beck K.F., Chiquet-Ehrismann R.; "Two contrary functions of tenascin: dissection recombinant tenascin fragments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spring J.; Submitted (JUL-1989) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2001 (TrEMBLrel. 16, 190 KDA TENASCIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      090994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q90994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M23121; AAA49085.1; -. HSSP; P24821; ITEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell 59:325-334(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=90030407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00022; EGF_1; UNKI
PROSITE; PS01186; EGF_2; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000561; -.
InterPro; IPR001777; -.
InterPro; IPR002181; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
419
                     161 CTNRQKACEPGF
                                             360
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CINGQCVCDEGF
                                                                    GKCAC ---
                                                                                          CVCDEGYTGEDCGELICPNDCFDRGRCINGTCFCEEGYTGEDCGELTCPNNCNGNGRCEN
                                                                                                                 CVCKNKLFPSQCG----ANREFDENTC---QCVCKR-----
                                            GLCVCHEGFYGDDCSQKRCPKDCNNRGHCVDGR-CVCHEGYLGEDCGELRCPNDCHNRGR 418
                                                                                                                                       EGYTGP--DCGEELCPHGCGIHGRCVGGRCVCHEGFTGEDCNEPLCPNNCHNRGRCVDNE
                                                                                                                                                               HDICGPNKELDEETC----
                                                                                                                                                                                     PNC--SEPACPRNCL-NRGLCVRGKCICEEGFTGEDCSQAACPSDCNDQGKCVDGVCVCF 241
                                                                                                                                                                                                          PQCQAANKTCPTNYMWNNHIC---RCLAQEDF-----MFSSDAGDDS--TDG----F 49
                                                                                                                                                                                                                                                                                                                                                   domain; Glycoprotein; Signal.

1 33 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                  ---ECTES--POKCLLKGKKFHHOTCSCY--
                                                                                                                                                                                                                                                                                          ΑĄ;
                      172
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1224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
                                                                                                                                                                                                                                           13.1%;
24.2%;
                                                                                                                                                                                                                                                                                          168632 MW; 1E62E9ED8AFC3ACB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01,
                                                                                                                                                                                                                                                                                                                                                                                              UNKNOWN_14
                                                                                                                                                                                                                                 20;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                Score 148; DB 13;
Pred. No. 1.1e-07;
0; Mismatches 79
                                                                                                                                                                                                                                                                                                                POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                            -QCVCRAGLRPASCG----PHKELDRNSC---Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1532
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                                                                                                                                                                                                                                                      Length 1532;
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                                                                                                                 -TCPRNQPLN----P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            active
                                                                                                                                                                                                                                 92;
                                                                   RRP 160
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                                                                                          359
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Best Local
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InterPro; IPR00177; -.
InterPro; IPR002181; -.
InterPro; IPR002181; -.
InterPro; IPR00208; EGF; 13.
Pfam; PF00008; EGF; 13.
Pfam; PF000147; fibrinogen_C; 1.
Pfam; PF00147; fibrinogen_C; 1.
PROSITE; PS00022; EGF_1; UNKNOWN_14.
PROSITE; PS01186; EGF_2; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
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SEQUENCE
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Q90995;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M23121; AAA49084.1; -. HSSP; P24821; ITEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2001 (TrEMBLrel. 16, 200 KDA TENASCIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00186; FBG; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recombinant tenascin
Cell 59:325-334(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spring J., Beck K.F., Chiquet-Ehrismann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=90030407; PubMed=2478295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-like domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
419
                                            161 CTNRQKACEPGF 172
                                                                                          360
                                                                                                                                         129
                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                     242
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CINGQCVCDEGF 430
                                                                                                                                       GKCAC-----ECTES--PQKCLLKGKKFHHQTCSCY----
                                                                                                                                                                                        CVCDEGYTGEDCGELICPNDCFDRGRCINGTCFCEEGYTGEDCGELTCPNNCNGNGRCEN 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contrary functions of tenascin:
                                                                                          GLCVCHEGFVGDDCSQKRCPKDCNNRGHCVDGR-CVCHEGYLGEDCGELRCPNDCHNRGR 418
                                                                                                                                                                                                                                       CVCKNKLFPSQCG---
                                                                                                                                                                                                                                                                                     EGYTGP--DCGEELCPHGCGIHGRCVGGRCVCHEGFTGEDCNEPLCPNNCHNRGRCVDNE 299
                                                                                                                                                                                                                                                                                                                                  HDICGPNKELDEETC-----QCVCRAGLRPASCG----PHKELDRNSC---Q 89
                                                                                                                                                                                                                                                                                                                                                                                PNC--SEPACPRNCL-NRGLCVRGKCICEEGFTGEDCSQAACPSDCNDQGKCVDGVCVCF
                                                                                                                                                                                                                                                                                                                                                                                                                             PQCQAANKTCPTNYMWNNHTC----RCLAQEDF-----MFSSDAGDDS--TDG----F 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1225 17
1714 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.A.
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1224
1714
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1714
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24.2%;
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                                                                                                                                                                                                                                       -ANREFDENTC - - - QCVCKR - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the EMBL/GenBank/DDBJ
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Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 148;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n; Signal. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A6FB0CFD623CDE53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dissection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                       -TCPRNQPLN----P 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the active sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
                                                                                                                                         -RRP
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                                                                                                                                                                                                                                                                                                                                                                              241
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Q9VJU5; Q9VJU5; 01-MAY-2000

PRELIMINARY;

PRT;

543 AA

VI MAY - 2000 (TIEMBLIEL 13, 01-MAY - 2000 (TIEMBLIEL 13, 01-MAR - 2001 (TIEMBLIEL 16, BG; DSQ00180 10 FORMETTE

Last sequence update)
Last annotation update)

BG:DS00180.10 PROTEIN. BG:DS00180.10 OR CG8942.

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Qγ
                                                                                                                                                                                                                                                                                                                                                     RA Ballew R.M., Basu A., Barendale J., Andrews FrankNoch C., Beatsley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boalshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Lord S., Dough L.E., Correll J.H., Gu Z., Gubart W.M., Glasser K.,

RA Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPerson D.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPerson D.L.,

RA Meison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Meison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Meison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Siden-Kiamos I., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Wang A.H., Wang X.,

RA Kimsh S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

"The genome sequence of Drosophila melanogaster.";

The Matter S., Shankov S., Shankov
                                         Matches
                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                              EMBL; AE003642; AAF53364.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M.D., Celn:
Amanatides P.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0028545; BG:DS00180.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7227;
                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                             InterPro; IPR000561; -
InterPro; IPR001304; -
                                                                                                                                                                                                                                                                                                                       HSSP; P35555; 1EMN.
SLPATLPQCQA-----ANKTCPTNYMWNNHICR----CLAQEDFMFSSDAGD-----DS 45
                                                                                                                                                                               SM00181; EGF;
                                         Similarity
57; Conser
                                                                                                                                                                                                  PS00615; C_TYPE_
PS00022; EGF_1;
PS01186; EGF_2;
                                                                                                                                                               domain;
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Celniker S
                                                                                                                                            ĀΑ;
                                                                                                                                        Glycoprotein.
A; 58562 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iker S.E., Holt R.A., Ev
Scherer S.E., Li P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=10731132;
                                                                                                                                                                                                                                          TYPE_LECTIN_1; UNKNOWN_1
                                                            12.8%;
23.4%;
                                                                                                                                                                                                                       UNKNOWN_1.
                                         19;
                                     Score 145; DE
Pred. No. 9.6e
19; Mismatches
                                                                                                                                          F419FDAFC4AD0D2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hoskins
                                                          DB 5;
.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s C.A., octor
                                         98;
                                                                             Length 543;
                                       Indels
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Galle R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chandra I.,
                                                                                                                                                                                                                                                                                                                                                                                                                          Zheng L.,
Smith H.O.,
                                       70;
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ξ
                                       15;
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Query Match Best Local S Matches 57

Similarity 57; Conser

Conservative

19;

12.8%;

Score Pred.

core 145; DB 5; red. No. 1.1e-07; Mismatches 98

98;

70;

Gaps

15;

Length 620; Indels

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Qy
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01-OCT-2000 (TrEMBLrel. 15, I

01-OCT-2000 (TrEMBLrel. 15, I

01-MAR-2001 (TrEMBLrel. 16, I

BG:DS00180.10 PROTEIN.

BG:DS00180.10 OR CG8942.
                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Y, CN BW SF;

STRAIN=Y, CN BW SF;

Celniker S.E., Agbayani A., Arcaina T.T., Baarca.

Celniker S.E., Agbayani A., Arcaina T.T., Baarca.

Celniker S.E., Gabayani A., Arcaina T.T., Baarca.

Chew M., Ciesiolka L., Dotte Butchhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Dotte Butchhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Le Farfan D.E., Galle R., George R.A., Harris N.L., Kim E., Le Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Le Houston K.A., Hummasti S.R., Mazda P., Moshrefi A.R., Mosh
EGF-like SEQUENCE
                                                                      InterPro; IPR000561; ...
InterPro; IPR001304; ...
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS00022; EGF_1; UNKNOWN_1
PROSITE; PS01186; EGF_2; 7.
                                                                                                                                                                                                                                                                                                                                        Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Mos
Nixon K., Pacleb J.M., Park S., Péiffer B., Poon L., Seque
Sethi H., Snir E., Svirskag R P. War v. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K., Celniker S., Rubin G.M.;

"An exploration of the sequence of a 2.9-Mb region of the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Etarygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                              Zieran L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9NKD8
                                                                                                                                                                                                                      FlyBase; FBgn0028545; BG:DS00180.10
                                                                                                                                                                                                                                                      EMBL; AE003408; AAF44843.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99403001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGAN-REFDENTCQC-----------VCKRTCPRN-QPLNPGKCACE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSPNTC-SCNAGYGGIDCHPVCPT-VCGKNEFCDRPGVCSCQNGYKRTSPSDNCLPVCEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CQPHCEKCSDNAHCVAPNQCECFPGYESSGADKKCVPKCSKGCTNGFCFAPETCVCSIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGQNSRCVRPGVCECENGYAGDDGGTNCRPVCS-TCPENGLCLSPGVCVCKPGYVMRNDL
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                                                       SM00181; EGF;
domain; G: 620 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153:179-219(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         melanogaster:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                              ir E., Svirskas R.R.,
Rubin G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.A
Glycoprotein.
A; 67953 MW;
                                                                                                                                         C_TYPE_LECTIN_1; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10471707;
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Last sequence update)
Last annotation updat
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  29959AC3C8A51D43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  620
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                                                                                                                                                                                                                                                                                                                                                                        Sequeira
                                                                                                                                                                                                                                                                                                                                                                                                Moshrefi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doyle C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                В.,
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	333 Qmue 330	5
	333 ONC	3
	186 WKRP 189	Qy
332	273 CQPHCEKCSDNAHCVAPNQCECFPGYESSGADKKCVPKCSKGCTNGFCFAPETCVCSIGY 332	Db
185	135 CTESPQKCLLKGKKFHHQTCSCYRRPCTNR-QKACEPGFSYSEEVCRCVPSY 185	Qy
272	VRPGVCECENGYAGDDGGTNCRF	DЪ
134	101 CGAN-REFDENTCQC	Qy
213	GYEKVGNGTVFPDGYKNNSNGNCSPICPKD	В
100	46 TDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQ 100	Qy
165	108 SSPNTC-SCNAGYGGIDCHPVCPT-VCGKNEFCDRPGVCSCQNGYKRTSPSDNCLPVCEK 165	В
45	1 SLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDEMFSSDAGDDS 45	Qy

Search completed: October 17, 2001, 14:50:54 Job time: $420 \ \text{sec}$

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Result
No.
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Maximum |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on:
      110
110
110
                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of score greater than or equal and is derived by analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB seq length: 0
DB seq length: 2000000000
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    100
100
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11:
12:
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16:
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20:
21:
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| SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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Copyright (c) 1993 - 2000 Compugen
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							<pre>smooth muscle cell; chemotactic effect; psoriasis; arthritis;</pre>							: 1001	VEGF-2 prot	ted human V	cated	Fit4 r	lar end	vascul	e FIt4 r	VEGF-C	Human VEGF-B prote	pr	Human vEGr-C prote Vascular endotheli	Human VEGC protein	va	Vascular endotheli	Human F1t4 recepto Human vascular end	foetal	۲ ج ۱	growth	ascular	an growth	Mouse vascular end Murine c-Fos induc	musculus vasc	Homo sapiens vascu Human VEGF-D prote	

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                 AAW53241 standard;
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n in a dimeric form acts as a mitogen for fibroblasts or
cells. zvegf2 is claimed to be useful for stimulating the
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                                                            in the lung and/or gaseous exchange between the lungs and the blood stream or to improve blood circulation to the heart and 02 gas permeability in cases of cardiac insufficiency, to improve blood flow and gaseous exchange in chronic obstructive airway disease, or to treat malabsorptive syndromes in the intestinal tract. Quantitation of VEGF-D in cancer biopsy specimens may be useful as an indicator of future metastatic risk Antagonists can be used for treating e.g. conditions such as congestive heart failure, involving accumulations of fluid in the lung resulting from
                                                                                                                                                                                                                                                                                                                                                                                    products
heart or
                                                                                                                                                                                                              The sequence is that of human lung vascular endothelial growth factor D (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis in wound healing, tissue or organ transplantation, or to establish collateral circulation in tissue infarction or arterial stenosis, such as coronary artery disease, and inhibition of angiogenesis in the treatment of cancer or of diabetic retinopathy. It can also be used in the treatment of lung disorders to improve blood circulation and the treatment of lung disorders to improve the second circulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transplants; collateral circulation; infarction; arterial stenosis; coronary artery disease; inhibition; cancer; treatment; diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive airway disease; intestinal malabsorptive syndrome; blopsy; metastatic risk;
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Sequence
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10-FEB-1997;
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                                                                       The present sequence represents human vascular endothelial growth fa (VEGF-D). The VEGF-D protein, compounds and antibodies, which can the protein, may be useful in, e.g. gene therapy and in treatment of inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGDNA sequences may be used for screening for the compounds which bind
                                                                                                                                Claim 1;
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18-MAR-1999;
08-NOV-1999;
This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynuclectide (IIa) which has vulnerary, cytostatic, antirhematic, antirathritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularistoriatic; regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth; VEGD.
                                                                                                                  New vascular endothelial growth factor protein, useful for treating preventing diseases associated with inappropriate angiogenesis activ such as cancer, rheumatoid arthritis, psoriasis and wounds -
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                                                                                                                                                                                                  vascular endothelial growth factor receptor 3; VEGF Milroy-Nonne syndrome; lymphoedema praecox; VEGF-D; vascular endothelial growth factor D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VECD protein used to illustrate the method of the invention.
                                                                                                                                                      WO200058511-A1
                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                            Human; Flt4; fms-like tyrosine kinase 4; lymphoedema;
                                                                            26-MAR-1999;
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                                                                          Human; receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4 VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q3 cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis; neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melano sarcoma; malignancy; VEGF-D; vascular endothelial growth factor D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the protein sequence of the human vascular endothalial growth factor D (VEGF-D). It was used to demonstrate the methods of the invention, which involve the screening of individuals to determine which vascular endothalial growth factor receptor 3 (VEGFR-3, also known as Fl14 or fms-like tyrosine kinase 4) alleles they possess and thus their likelihood of developing hereditary lymphoedema. Conditions associated with lymphoedema include Milroy-Nonne syndrome, which is early onset lymphoedema and lymphoedema praecox, which is late
                                                                                                                                                                             Human prepro-vascular endothelial growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patent discloses a method to treat neoplastic disease characterised
expression of fms-like tyrosine kinase 4 (Flt4) receptor (also
                                                                                                                                                                                                                                                                                                                                                                                   MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
VKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEE 240
                                                                                                                                                                                                                                     ASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSVPELVP 180
                                                                                                                                                                                                                                                                                        myrewvvvnvfmmlyvqlvqgssnehgpvkrssqstlerseqqiraassleellrithse 60
                                       CQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354
                                                                                                             NPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETC
                                                                                                                                               vkvanhtgckclptaprhpysiirrsiqipeedrcshskklcpidmlwdsnkckcvlqee
                                                                                                                                                                                                                      aselgkstntffkppcvnvfrcggccneeslicmntstsyiskqlfeisvpltsvpelvp
                                                                         nplagtedhshlqepalcgphmmfdedrcecvcktpcpkdliqhpkncscfeckesletc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaipainen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HELSINKI LICENSING LTD OY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 142-143; 148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INST CANCER RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1963; DB 21;
Pred. No. 3.5e-149;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jussila
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RESULT
AAY70983
   PAR A 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vascular endothelial growth factor-D; VEGF; human; re-endothelialisation vascular endothelial growth factor receptor; VEGFR; vascular trauma; blood vessel; cardiovascular surgery; anti-restenosis agent; prevention;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Preventing stenosis and restenosis in mammals using vascular endothelial growth factor proteins or the nucleic acids encoding them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yla-herttuala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
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                                                            percutaneous
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UNIV HELSINKI LICENSING LTD
YLA-HERTTUALA S.
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                                                                                                                                                                                                                                                                                                                                                                            Page 53-55; 61pp; English.
                                                            transluminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Cleavage results in VEGF-D protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Carboxy_terminal_peptide
/note= "Cleavage results in partially-processed VEGF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Recombinantly_matured_VEGF_D_protein
/note= "Processed vascular epithelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1..21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Amino_terminal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 354
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                                                         coronary angioplasty.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        results in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     partially-processed VEGF-D
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Query Match
Best Local Sim
Matches 354;

Similarity

100.0%;

Score 1963; DB 21; Pred. No. 3.5e-149;

Conservative

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amellorate disease and to detect diseases, or susceptibility, by detecting mutations or the presence or amount of angiogenic protei expression. Particularly they are used to stimulate wound healing growth of damaged bone and tissue, and for repair of vascular tiss
                                                                                                                                                                                                                                                                  New nucleic acid encoding angiogenic proteins, useful e.g. for promoting healing of wounds and treating peripheral arterial disease critical limb ischaemia or coronary disease -
                                                                                                                                                                                                                           Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rheumatoid arthritis; autoimmune disease; alle infectious disease; neurodegeneration; vascular endothelial growth factor-D1; VEGF-D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; angiogenic protein; wound healing; vascular tissue repair; peripheral arterial disease; critical limb ischaemia; coronary disease; angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human VEGF-D1 protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                   quence is vascular endothelial growth factor-D1 (VEGF-D1), s an angiogenic protein of the invention. The angiogenic proteins DNA sequences encoding them, are used to prevent, treat or
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                                                                                                                                                     Human; gene therapy; lymphatic disorder; hereditary lymphedoema; Flt4; vascular endothelial growth factor receptor-3; VEGFR-3; VEGF-C; VEGF-D; fms-like tyrosine kinase 4.
26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.1%;
98.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1926; DB 22; Pred. No. 3.2e-146;
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is His"
                                                                    "residue 497
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stop codon
"residue 553
                       "residue 541 corresponds
                                      "residue 518 stop codon :
                                                                                                                                                                                                                                                                                                                                                              "residue 26
stop codon
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stop codon i
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in reading frame
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frame 2 of HF175"
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1 MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60

Query Match
Best Local Similarity
Matches 347; Conserv

97.7%; nilarity 98.0%; Conservative

Score 1917; DB 18; pred. No. 3.2e-145; 1; Mismatches 6;

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DRX PXX PR
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Examination of the 3 polypeptides indicates that reading frame 2 can be region free of nonsense codons. FIGF is a c.fos-cdependent autocrine growth factor able to induce cell division cc entry and, when over-expressed, a transformed phenotype in cliptoblasts. It could be implicated in tumours and development. CC Recombinant FIGF can be produced in transformed host (e.g. CHO) cc cells. It can be used to identify its receptors and in an assay cf or the identification of agonists and antagonists. Antibodies craised against FIGF can be used to block the function of the can be used to block the function of the can be used to block the function of the can be used to block the function of the can be used to block the function of the can be used to block the function of the can be used to block the function of the can be used to block the function of the can be used to block the function of the can be used to block the function of the control of the can be used to block the function of the control of the contr
                                                                                                                                                                                                                                                                                                                                                         Claim 3; Fig 2; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide molecule encoding c-Fos induced growth factor protein useful in therapy, in manufacture of compositions for treatment developmental disorders and in generation of transgenic animal
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Sequence
                                       research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT62961.
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29-SEP-1995;
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stop codon :
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stop codon i
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                                                         11-NOV-1996;
14-NOV-1996;
05-FEB-1997;
10-FEB-1997;
19-JUN-1997;
                                                                                                                                                                                                                                                                                                                        vascular endothelial growth factor; VEGF-D; angiogenesis; modification; acceleration; wound healing; tissue; organ; transplants; collateral circulation; infarction; arterial stenosis; coronary artery disease; inhibition; cancer; treatment; diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive airway disease; intestinal malabsorptive syndrome; biopsy; metastatic risk;
                            (LUDW-)
         Achen
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23-AUG-1996;
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                            LUDWIG INST CO
         Alitalo
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                                                        96AU-0003554.
96US-0031097.
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97US-0038814.
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                                      CANCER RES
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                            LICENSING LTD
         Stacker SA,
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Best Local
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                                                             Human VEGF-D
                                                                                           05-APR-2001
                                                                                                                                                       AAY97572 standard; Protein;
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in wound healing,
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ilarity 100.0%;
Conservative (
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Pred. No. 1.6e-136;
0; Mismatches 0;
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Human; angiogenic protein; wound healing; vascular tissue repair; peripheral arterial disease; critical limb ischaemia; coronary disea angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis;

disease;

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CC which is an anglogenic protein of the invention. The angiogenic proteins cand the DNA sequences encoding them, are used to prevent, treat or cameliorate disease and to detect diseases, or susceptibility, by content of detecting mutations or the presence or amount of angiogenic protein content of particularly they are used to stimulate wound healing, consisted the format of damaged bone and tissue, and for repair of vascular tissue, consequences are used to stimulate wound healing, consequences in tumours and to treat inflammation (where associated with increased vascular permeability), diabetic retinopathy, rheumatoid contracts of proteins are also used to identify specific contents of proteins are also used to identify specific contents and targeting of proteins are also used to identify specific contemplated in and targeting of proteins for in vivo or in vitro diagnosis (including imaging) or for therapy (including when linked to e.g. a label corrections); and for immunotyping of cells, e.g. for detecting minimal residual disease or haematopoietic progenitor/stem cells. It is also contemplated that the sequences might be useful for treating a very wide residual diseases (viral, bacterial, fungal or parasitic); cancer; concertion of the normal seater of contemplated that the sequences might be useful for treating a very wide resource of the content of the normal seater.
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infectious disease; neurodegeneration;
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                                           EEDRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCE
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                           such as coronary artery disease, and inhibition of angiogenesis in the treatment of cancer or of diabetic retinopathy. It can also be used in the treatment of lung disorders to improve blood circulation in the lung and/or gaseous exchange between the lungs and the blood stream or to improve blood circulation to the heart and O2 gas permeability in cases of cardiac insufficiency, to improve blood circulation to the heart and O2 gas permeability in cases of cardiac insufficiency, to improve blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transplants; collateral circulation; infarction; arterial stenosis; coronary artery disease; inhibition; cancer; treatment; diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive airway disease; intestinal malabsorptive syndrome; biopsy; metastatic risk; detection; diagnosis; congestive heart failure.
                                                                                                                                                           The sequence is that of mouse lung vascular endothelial growth factor D1 (VEGF-D1). VEGF-D1 can be used for e.g. acceleration of angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997;
23-AUG-1996;
                  flow and gaseous exchange in chronic obstructive airway disease
                                                                                                                              collateral circulation in tissue infarction or arterial stenosis,
                                                                                                                                           D1 (VEGF-D1). VEGF-D1 can be used for e.g. acceleration of angiogen in wound healing, tissue or organ transplantation, or to establish
                                                                                                                                                                                                                                      New isolated vascular endothelial growth factor-D - used products for use in e.g. modifying angiogenesis or treatiheart or intestinal disorders
                                                                                                                                                                                                                                                                                                        N-PSDB; AAV20808
                                                                                                                                                                                                                                                                                                                      WPI; 1998-179057/16.
                                                                                                                                                                                                                                                                                                                                                      Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                   (LUDW-)
                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9807832-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vascular endothelial growth factor; VEGF-D; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus vascular endothelial growth factor D1 (VEGF-D1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW53242 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAKHCRFPKEKRAAQGPHSRKNP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eedrcshskklcpidmlwdsnkckcvlqeenplagtedhshlqepalcgphmmfdedrce
   treat malabsorptive
                                                                                                                                                                                                                                                                                                                                                                                   LUDWIG INST CANCER RES. UNIV HELSINKI LICENSING
                                                                                                                                                                                                          Pages 63-64;
                                                                                                                                                                                                                                                                                                                                                      Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acceleration; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                 97AU-0004954.
97US-0038814.
97AU-0007435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0023751.
96AU-0003554.
96US-0031097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0051426
96AU-0001825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                     LICENSING LTD
                                                                                                                                                                                                          101pp; English.
                                                                                                                                                                                                                                                                                                                                                      Stacker SA,
syndromes in the
                                                                                                                                                                                                                                                                                                                                                      Wilks AF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue; organ
   intestinal tract
                                                                                                                                                                                                                                                        or treating
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Best Local
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Example 7; Page 32-35;
                                           VEGF-D protein encoded treating oedema
                                                                                                                     WPI; 1998-110591/10
N-PSDB; AAV15177.
                                                                                                                                                                                              Hirata Y,
                                                                                                                                                                                                                                                                                                                                                                                           22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9802543-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; vascular endothelial growth factor D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse vascular endothelial growth factor D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW44295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW44295 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                           15-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation;
                                                                                                                                                                                                                                          (CHUG-) CHUGAI RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKC 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mygewgmgnilmmfhvylvqgfrsehgpvkdfsferssrsmlerseqqiraassleellq 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                            Nezu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 AA;
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                                                                                                                                                                                                                                                                                          96JP-0185216.
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52pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1675; DB 19;
Pred. No. 3.7e-126;
20; Mismatches 32;
                                                                       useful
                                                                       for,
                                                                    e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGF-D; gene therapy;
                                                                    gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 358;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents mouse vascular endothelial growth factor D (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind the protein, may be useful in, e.g. gene therapy and in treatment of inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGF-D DNA sequences may be used for screening for the compounds which bind to the VEGF-D protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MYREWVVVVVEMMLYYQLVQGSSNEHGPVK-----RSSQSTLERSEQQIRAASSLEELLR
                                                                                                                                                          slesccqkhkifhpdtcscedrcpfhtrtcasrkpacgkhwrfpketr-aqglysqenp
                                      SLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354
                                                                                                                                                                                                                                                                                                                PELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRE 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tovevaselgkttntffkppcvnvfrcggconeegvmcmntstsyiskqlfeisvpltsv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.3%;
83.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1675; DB 19; Pred. No. 3.7e-126;
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Search completed: Job time: 128 sec October 17, 2001, 14:46:02

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using .sw model
     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/
2: /cgn2_6/ptodata/2/
3: /cgn2_6/ptodata/2/
4: /cgn2_6/ptodata/2/
5: /cgn2_6/ptodata/2/
6: /cgn2_6/ptodata/2/
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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US-08-795-430-8
US-08-795-430-11
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US-08-510-133A-3
US-08-510-133A-3
US-08-510-133A-3
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                       PCT-US96-09001-10
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Compugen Ltd.
                                                                                    Patent No. Patent No.
                                                                                Sequence 4, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 33, Appl
Sequence 33, Appl
Sequence 31, 4596
Patent No. 5219739
                                         Sequence 2, A
Sequence 2, A
Sequence 2, A
Sequence 56,
                                Patent No
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Sequence
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35, Appl
2, Appli
11, Appl
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Query Match
Best Local Similarity
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ALIGNMENTS

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HYPOTHETICAL: NO ORIGINAL SOURCE: TISSUE TYPE: HUS-08-915-795-5
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                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPh D.
REGISTRATION UMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Appli
Patent No. 623571
                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                TYPE: and the single STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein NO
                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: GROWTH FACTOR NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MARC G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: KARÍ ALITALO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C. STREET: 1200 G Street, NW, Suite 700 CITY: Washington
                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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                                                                                                                                                     354 amino acids
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                    Human Lung
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Score 1963; DB 4; Pred. No. 7.9e-172;

Length 354

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; HYPOTHETICAL: N
; ORIGINAL SOURCE:
; TISSUE TYPE:
US-08-915-795-3
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                                                                                                                                               TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
                                            TOPOLOGY: linear
MOLECULE TYPE: pro
MOLECULE TYPE: NO
                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acid
TYPE: amino acid
                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: GROWTH FACTOR NUMBER OF SEQUENCES: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Wa
STATE: L
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
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                                                                                                                                                                                TELEFAX:
                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C. STREET: 1200 G Street, NW, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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NO. 6235713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRETCVEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 354
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                                                                                                                    325 amino acids
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                                                                                                                                                                                 (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                         United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andrew F. WILKS
Steven A. STACKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                         linear
               Human Breast
                                                           protein
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Best Local Similarity
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                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
                                            SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acid
                                                                                                                             TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: GROWTH FACTOR NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 LICMNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIP 210
          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UI
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1200 G STREET: Washington
TOPOLOGY:
                                                                                                TELEX:
                                                                                                            TELEFAX:
                                                                                                                           TELEPHONE:
                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 RSSQSTLERSEQQIRAASSLEELLRITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEDRCSHSKKLCPIDMLWDSNKCKCYLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCE 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAKHCRFPKEKRAAQGPHSRKNP 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATFYDIETLKVIDEEWORTOCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEES 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSSQSTLERSEQQIRAASSLEELLRITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                N/A
                                                                                                                                                                                                                                                                                                                                                                                                               DC
                                         358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                            1200 G Street, NW, Suite
                                                                                                            (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kari ALITALO
                                                                                                                                                                                                                                                                                                                                                                                               United States of America
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linear
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Pred. No. 2.4e-157;
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1

; ORIGINAL SOURCE: ; TISSUE TYPE: US-08-915-795-8

Mouse

Lung

Query Match Best Local :

Score 1675; DB 4; Pred. No. 1.7e-145;

Length 358;

2;

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TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENCTH: 321 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08915795 Patent No. 6235713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Marc G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 628-8800
                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
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                                                                                                                                                                                                               CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56
                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                              United States of America
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Steven A. STACKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marc G. ACHEN
                                                                                                                                                                                                                                                                                                                                         Floppy disk
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                                                                                                                                                      26, 269
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                                                                                                                                       1064/42983
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US-08-999-811-2
; Sequence 2, Application US/08999811
; Patent No. 5932540
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Best Local Similarity
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                                                                                                                                                                                                                                                                             ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein ORIGINAL SOURCE: TISSUE TYPE: Mouse L
                         APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
BEGISTER MATTON NUMBER. 26,251
                                                                                              APPLICATION NUMBER:
FILING DATE: 8-MAR-1
PRIOR APPLICATION DATA:
                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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 REFERENCE/DOCKET NUMBER:
               REGISTRATION NUMBER:
                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                               CITY: WASHINGTON
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                                                                                                                 8-MAR-1994
                                                                                                                                                                                                                                                                                 Floppy disk
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86.5%;
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             36,351
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1488.1000004
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Pred. No. 1.4e-13
                                                                                                                                                                                                                                  Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09042105 Patent No. 6040157
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
NUMBER OF SEQUENCES: 35
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 8-MAR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 Q----CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC
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                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                    CLASSIFICATION:
                                                                                                            CLASSIFICATION:
                                                                                                                             FILING DATE:
                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLP
                                                                                                                                                                                                                                                                              20005
                                                                                                                                                                                                                                                                                                                                 WASHINGTON
                                                                                                                                                                                                                                                                                                                DC
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                                                                                                                                                                                                                                                                                               USA
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(202)371-2540
TD NO: 2:
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                                                     8-MAR-1994
                                                                                                                             HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.9%; Score 704.5; DB 2 38.9%; Pred. No. 1.1e-56;
 US 08/465,968
                                                                                                                                              US/09/042,105
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RESULT 7
US-09-042-105-18
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                                                                                                                                                                                                                                              ; Patent No. 6040157
; GENERAL INFORMATION:
; APPLICANT: HU, JINV
; APPLICANT: ROSEN, (
APPLICANT: CAO, LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEPAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/09042105 Patent No. 6040157
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ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,61
              COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSE: STERRE, KESSLER, (
STREET: 1100 NEW YORK AVENUE
                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175
                                                                                                                                                                                                                                                                                                                                                                                                                       352 PLNPGKCAC-ECTESPQKCLLKGKKFHHQTCSC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 IQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKE 341
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                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 114
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 SOFTWARE:
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PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                CRAIG A.
                                                                                                                                                                                                                                 VASCULAR ENDOTHELIAL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.9%; Score 704.5; 38.9%; Pred. No. 1.1
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                                                                                                                                                                            GOLDSTEIN &
Version
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: CLASSIFICATION: APPLICATION NUMBER:

US 08/207,550

CURRENT APPLICATION DATA:

HEREWITH

US/09/042,105

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US-08-795-430-8
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                                                                                                          Sequence 8, Application US/08795430 Patent No. 6130071
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Best Local Similarity
                                                                                          GENERAL INFORMATION:
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         APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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APPLICATION NUMBER:
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CLASSIFICATION:
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38.9%;
             Vascular Endothelial Growth Factor C (VEGF-C) Protein and Gene, Mutants Thereof, and Uses 1
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61; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 704.5; DB 3; Pred. No. 1.1e-56;
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                           Uses Thereof
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Best Local Similarity 38.9
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/5
FILING DATE: 12-JAN-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 28-JUN-
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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292 QCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQ 351
                                                                                                                                                                                   155 NTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIP 210
                                                                                                                                                                                                                       115 NTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCM 174
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FILING DATE: 01-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                         Q---CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC
                                                                                                           EEDRCSHSKKLCPIDMLWDSNKCKCVLQE----ENPLAGTED----HSHLQE---
                                                                                                                                                                                                                                         DIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICM 154
                                    -----PALCGPH-----
                                                                                                                                                NTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLP
                                                                                                                                                                                                                                                                                               EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 114
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                                  -----MMFDEDRCECVCKTPCPKDL 281
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US-08-510-133A-35
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 35:.
SEQUENCE CHARACTERISTICS:
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                                                                            235 Q----CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC
                                                                                                                    211 EEDRCSHSKKLCPIDMLWDSNKCKCVLQE----ENPLAGTED----HSHLQE---
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292 QCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQ
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REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/32863
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,133A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
CORRESPONDENCE Marshall, O'Toole, Gerstein, Murray & Borun
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Receptor Ligand NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Alitalo, Kari
Joukov, Vladomir
                                                                                                                                                                                  NTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIP 210
                                                                                                                                                                                                                                                               DIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICM 154
                                         -----PALCGPH-----
                                                                                                                                                           NTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLP
                                                                                                                                                                                                                                                                                                                                                            EQQIRAASSLEELLRITHSEDWKLWRCRLRL-----KSFTSMDSRSASHRSTRFAATFY 94
                                                                                                                                                                                                                                                                                                                       EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 114
                                                                                                                                                                                                                                                                                                                                                                                                        140;
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TELEFAX: 312/474-0448
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Illinois COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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1.1e-56;
                                   -----MMFDEDRCECVCKTPCPKDL 281
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GENERAL INFORMATION:
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APPLICATION NUMBER: 08/465
FILING DATE: 6 JUN 95
APPLICATION NUMBER: 08/207
APPLICATION NUMBER: 08/207
FILING DATE: 8 MAR 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
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STREET: ROSELAND
CITY: ROSELAND
CTATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: LI MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HU, ET AL.
TITLE OF INVENTION: Human Vascular EndothelialGrowth Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                  255
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                                                                                         211 EEDRCSHSKKLCPIDMLWDSNKCKCVLQE-----ENPLAGTED----HSHLQE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PS/2
OPERATING SYSTEM: |
SOFTWARE: WORD PER
                                                                                                                                                                                                                                                                                                               41 EQQIRAASSLEELLRITHSEDWKLWRCRLRL-----KSFTSMDSRSASHRSTRFAATFY 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS
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REFERENCE/DOCKET NUMBER: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME:
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                                                                                                                                            NTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIP 210
                                                                                                                                                                                                                        DIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICM 154
                                                                                                                                                                                                     NTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQCM 174
                                                                                                                                                                                                                                                                           EEQLRSVSSVDELMTVKYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAAAHY 114
                                                     Q----CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETC
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                  -PALCGPH-
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                 --MMFDEDRCECVCKTPCPKDL
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IQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKE 341

QCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQ 351

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                                 Matches
                                                Query Match
Best Local Similarity
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Patent No.
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                                                                                                                                                                                                           NFORMATION FOR SEQ ID NO:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acid
                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/34
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
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                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
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                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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GPVKRSSQSTLERSEQQIRAASSLEELLRITHSEDWKLWRCRLRLKSFTSMDSRSASHRS 86
                                  140;
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5. 6130071
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                                  Conservative
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Protein and Gene, Mutants Thereof, and Uses Thereof
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Patent No. 6130071
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                             FILING DATE: 01-AUG-PRIOR APPLICATION DATA: APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PCT/F196/00427
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                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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FILING DATE: 12-JAN-1996
                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
                                                                                                                                                                                 APPLICATION NUMBER:
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INFORMATION:
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                               08/340,011
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                                                                                                                                                                                                                                                                                                                                                                                   Version #1
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08999811
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Best Local Similarity 38.9%;
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REGISTRATION NUMBER: 2896
REFERENCE/DOCKET NUMBER: 2896
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
               PRIOR APPLICATION DATA:
                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 NPAKCIC-ECTESPNKCFLKGKRFHHQTCSCYRPPCTVRTKRCDAGFLLAEEVCR 406
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                                                                                                                                                                                                       COUNTRY: US
ZIP: 20005
                                                                                                                                                                                                                                                          STREET: 1100 NEW CITY: WASHINGTON
APPLICATION NUMBER:
                                   CLASSIFICATION:
                                                        FILING DATE:
                                                                                                                                                                                                                                               STATE:
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ROSEN, CRAIG A.
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                                                                      US/08/999,811
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               SEQ ID NO 2
LENGTH: 350
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08824996B Patent No. 5935820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 33.9%;
Best Local Similarity 38.3%;
Matches 133; Conservative 5
                                                                                             CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: 08/207,550
EARLIER FILING DATE: 1994-03-08
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                        APPLICANT: Cao, Liang
TITLE OF INVENTION: Polynucelotides Encoding Vascular Endothelial Growth
TITLE OF INVENTION: Factor 2
FILE REFERENCE: PF112D1
                                                                                                                                                                                                                                                                                    APPLICANT: Hu, Jing-Shan APPLICANT: Rosen, Craig A.
                                                                                SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202)371-254
ORGANISM: Homo
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEPHAX: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
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LENGTH: 350 amino acid
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Pred. No. 3.9e-53;
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RESULT 15
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: US
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, C
STREET: 1100 NEW YORK AVENUE
                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                            APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997 CLASSIFICATION:
                                                                                                                                                                                                                             APPLICATION NUMBER: US FILING DATE: 8-MAR-1994 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 20005
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                                                                                                                                                                                                                                                                                                            FILING DATE:
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ROSEN, CRAIG A.
CAO, LIANG
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                                                                                                                                                                                                                                                             us 08/207,550
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Pred. No. 3.9e-53;
5; Mismatches 87
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US-09-042-105-4
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Best Local Similarity 38.3
Matches 133; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                259
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                          LRITHSEDWKLWRCRLRL------KSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQ 107
                                                                                                                                                  TNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLRPASC
                                                                                                                                                                                                                                                                  ISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIPEEDRCSHSKKLCP 223
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ESPQKCLLKGKKFHHQTCSC----YRRPCTNRQKACEPGFSYSEE
                                    ESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKE 341
                                                                          GPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKCAC-ECT
                                                                                                                GPH-----
                                                                                                                                                                                                                              ITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQ----CQAANKTCP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.9%; Score 664.5; DB 3; 38.3%; Pred. No. 3.9e-53; Live 56; Mismatches 87;
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                                                                                                              -MMFDEDRCECVCKTPCPKDLIQHPKNCSCFECK 294
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Search completed: October 17, 2001, 14:47:11 Job time: 197 sec

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Title:
Perfect score:
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No.
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 2000000000
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111	111	111	111.5	111.5	112	112.5	113	113	114.5	114.5	115.5	116	118	119.5	120
5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.8	5.8	5.8	5.8	5.9	5.9	6.0	6.1	6.1
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tenascin-C - human	PDGF-related trans	platelet-derived g	hypothetical prote	polyferredoxin 4x2	laminin alpha 5 ch	hypothetical prote	integrin beta chai	platelet-derived g	zonadhesin - mouse	SIL protein - huma	notch4 - mouse	serine proteinase	hypothetical prote	hypothetical prote	platelet-derived g

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4552 residues	ALIGNMENTS	
osen parameters: 219241	7707778 1	
% summaries	SS9207 SS9207 vascular endothelial growth factor C precursor - human N;Alternate names: FLT4 ligand DHM C.Species: Homo sapiens (man) C.Species: 1996 #sequence_revision 01-Nov-1996 #te C;Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #te C;Accession: S69207; S61795; S71443; S69208; G02659 R.Joukov, V.; Palusola, K.; Kaipainen, A.; Chilov, D.;	- human 1996 #text_change 08-Oct-1999 02659 lov, D.: Lahtinen, I.: Kukk, E.: Saksel
····.	othe	ial growth factor, VEGF-C, is a ligand
esults predicted by chance to have a to the score of the result being printed, of the total score distribution.		PIDN:CAA63907.1; PID:e221096; PID:g118 to the EMBL Data Library, December 1995
SUMMARIES	R; Note: this is a revision to the sequence from reference. R; Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D EMBO J. 15, 290-298, 1996	From reference S61795 Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel
Description Description	A; Title: A novel vascular endothelial growth factor, A; Reference number: S61795; MUID: 96178224	VEGF-C, is a ligand for the Flt4
\$40080 vascular endotheli vascular endotheli vascular endotheli vascular endotheli	quence not shown; not	compared with conceptual translation
vascular vascular	A;Residues: 70-419 <joui> A;Note: this sequence has been revised in reference S69207</joui>	369207
	rary, December 1995	
16K vascular endocher	number: S69208	retated protein (vkr): A tigand and
41236 placental growth f	A; ACCESSION: S09208 A; Molecule type: mRNA	
piacentai growth vascular endothel	A;Residues: I-419 <lee> A;Cross-references: EMBL;U43142: NID;q1150988: PIDN;</lee>	PIDN:AAA85214.1; PID:q1150989
	Library May 1996	
	H01557	
FMSGB platelet-derived g	A:Status: preliminary: translated from GB/EMRI/DDRI	
FHUG1 platelet-derived g	A;Cross-references: EMBL:U58111; NID:g1373426; PIDN:	PIDN:AAB02909.1; PID:q1373427
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F;103-419/Product:

vascular endothelial growth

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#status experimental <MAT>

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A; Molecule type:
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R; Tischer, E.; N
J. Biol. Chem.
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C; Species: H
C; Date: 28-A
C; Accession:
R; Houck, K.A
A;Residues: 1-141,227-232 <TI3>
A;Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:MR;Keck, P.J.; Hauser, S.D.; Krivi, G.; Sanzo, K.; Warren,
                                                                         A;Cross-references: GB:M63971; GB:M63972;
A;Accession: B40454
A;Molecule type: DNA
A;Residues: 1-140,'N',183-232'<TI2>
A;Cross-references: GB:M63971; GB:M63972;
A;Accession: C40454
                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-140,'N',183-232 <HOU2> A;Accession: B41551 A;Status: nucleic acid sequence not shown A;Status: nucleic acid sequence not shown
                                                       A; Accession: C40454
A; Molecule type: DNA
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A; Accession: A41551
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Accession: A41551; C41551; B41551; A40454; B40454; C40454; A40079; A40080;
Houck, K.A.; Ferrara, N.; Winer, J.; Cachianes, G.; Li, B.; Leung, D.W.
ol. Endocrinol. 5, 1806-1814, 1991
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                                                                                                                                                                                                                                                                                  Mitchell, R.; Hartman, T.; 266, 11947-11954, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----PALCGPH----
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GB:M63974; GB:M
rren, T.; Feder,
                                                                                              GB:M63974;
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Connolly,
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GB:M63978
Connolly, D.
                                                                                            GB:M63977;
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                                                                                                                                                                                                                                                                                                   J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references:
A;Map position: 6p2
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 27-36;43-49, 'R';72-76,'Q'
C; Comment: The most common of several
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Molecule type: mRNA
A;Residues: 1-140, 'N. 183-232 <WEI>
A;Cross-references: EMBL:X62568; NID:g37658;
A;Experimental source: AIDS-Kaposi's sarcoma
A;Accession: JQ1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: AIDS-Kaposi's sarcoma R;Connolly, D.T.; Olander, J.V.; Heuvelman, J. Biol. Chem. 264, 20017-20024, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Weindel, K.; Marme, D.; Weich, H.A.
Biochem. Biophys. Res. Commun. 183, 1167-1
A; Title: AIDS-associated Kaposi's sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: VEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: A34492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Human vascular permeability factor. Isolation A; Reference number: A34492; MUID:90062112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-140,'N',227-232 <WE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: JQ1463; MUID:92231879
A; Accession: JQ1463
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A; Residues: 1-140,'N',183-232 <LEU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A40080; A; Accession: A40080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Vascular endothelial growth factor A; Reference number: A40080; MUID: 90069608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Leung, D.W.; Cachianes, G.; Kuang, Science 246, 1306-1309, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
A; Residues: 1-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 246, 1309-1312, 1989
A; Title: Vascular permeability factor, an
A; Reference number: A40079; MUID: 90069609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:M32977; NID:g181970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: not compared with conceptual translation
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Best Local
  185
                                           259
                                                                                         135
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                                                                                                                                                                                                                                                                                                               97
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                                         GPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE
                                                                                                                                DRCSHSKKLCPIDMLWDSNK---
                                                                                                                                                                                                                       STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
                                                                                                                                                                                                                                                                                                               ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT
                                                                                       DRARQEKKSVRGKGKGQKRKRKKSRYKSWSVYVGARCCLMPWS
                                                                                                                                                                            EESNITMQIMRIK-----PHQGQHIGEMSFLQHNKCECR------PKK 134
                                                                                                                                                                                                                                                                   EVVKFMD-VYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT
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                                                                                                                                                                                                                                                                                                                                                                               Similarity
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-CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD
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(uang, W.J.; (
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                                                                                                                                                                                                                                                                                                                                                    Score 200.5; DB 2;
Pred. No. 6.5e-08;
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Goeddel, D.V.;
                                                                                                                                -CKCVLQEENPLAGTEDHSHLQEPALC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN: AAA35789.1;
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cell
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rrara, N.
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                                                                                     -LPGPHPC
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Biochim. Biophys. Acta 1260, 235-238, 1995
A;Title: Nucleotide sequence and expression of the A;Reference number: $52130; MUID:95143284
A;Status: prelimina-
                                                                                                                                                                                         vascular endothelial growth factor - pig
c;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
C;Accession: S52130
R;Sharma, H.S.; Tang, Z.H.; Gho, B.C.G.; Verdouw, P.D.
                                                                                                                                                                                                                                                                                                                    RESULT
S52130
     A; Molecule type: mRNA
A; Residues: 1-190 <SHA>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 27-31 <FER>
C;Keywords: alternative splicing; glycoprotein
C;Keywords: alternative splicing; glycoprotein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-190/Product: vascular endothelial growth factor #status predicted
F;100/Binding site: carbohydrate (Asn) (covalent) #status predicted
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B40080
B40080
vascular endothelial growth factor precursor (version 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Ferrara, N.; Henzel, W.J.
Biochem. Biophys. Res. Commun. 161,
A; Title: Pituitary follicular cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 27-190 <TIS>
A; Cross-references: GB: M31836; NID: g163808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A33787; MUID:90121225 A; Accession: B33787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M32976; NID:g163006; PIDN:AAA30502.1; PID:g163007 R;Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J. Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Vascular endothelial growth factor A;Reference number: A40080; MUID:90069608
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C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Nov-1999
C:Accession: B40080; B33787; A33255
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A; Residues: 1-190 <LEU>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                              -CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSKKLCPIDMLWDSNKCKC-----VLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCEC 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEFNITMQIMRIK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVVKFMD-VYORSFCRPIETLVDIFQEYPDEIEFIFKPSCVPLMRCGGCCNDESLECVPT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
GB:X81380; NID:g587559; PIDN:CAA57143.1; PID:g587560
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                                                                                                                     e and expression of the porcine MUID:95143284
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A; Access.v.....A; Access.v....A; Access.v...A; Access.v...A; Access.v...A; Molecule type: mRNA A; Rolecule type: mRNA A; Residues: 1-116, 'ER',119-190 <CLA>A; Residues: 1-116, 'ER',119-190 <CLA>A; Ross-references: GB:M95200; NID:9202350; PIDN:AAA40547.1; A; Cross-references: GB:M95200; NID:9202350; NID
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A; Residues: 27-38 <ROS>
C; Keywords: alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Claffey, K.P.; Wilkison, W.O.; Spiegelman, J. Biol. Chem. 267, 16317-16322, 1992
A;Title: Vascular endothelial growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision
C;Accession: B44881; A43351; A61029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Conditioned medium from mouse sarcoma A;Reference number: A61029; MUID:91197543
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A;Accession: A43351
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A; Residues: 1-190 <BRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: B44881
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Development 114, 521-532, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Expression of vascular endothelial
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                                                                                                                                                                                                                                  114 RETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213
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                                                                                                                 SVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKC 233
KCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKD---
                                                          S-QHIGEMSFLQHSRCECR-
                                                                                                                                                                        IETLVDIFQEYPDEIEYIFKPSCVPLMRCAGCCNDEALECVPTSESNITMQIMRIK.PHQ 112
                                                                                                                                                                                                                                                                                            WVHWTLALLLYLHHAKWSQAAPTTEGEQKSH----
                                                                                                                                                                                                                                                                                                                                                   WKLWRCRLRL-----KSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVVKFMD-VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 198;
Pred. No. 8.
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Pred. No. 8.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 190
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-LIQHPKNCS 289
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NCBIP: 110675)
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                                                                                                                                                                                                                                                                                                                                                                                                              98;
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A; Residues: 27-33 <CLA>
R; Sugihara, T.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.
Biochim. Biophys. Acta 1224, 365-370, 1994
A; Title: Enhanced expression of multiple forms of VEGF
A; Reference number: S52136; MUID:95101726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:S38100; NID:g249860; PIDN:AAB22254.1; PID:g249861
A;Note: sequence extracted from NCBI backbone (NCBIN:107624, NCBI::107625)
R;Clauss, M.; Gerlach, M.; Gerlach, H.; Brett, J.; Wang, F.; Familletti, P.C.; Pan, Y.C.
J. Exp. Med. 172, 1535-1545, 1990
A;Title: Vascular permeability factor: a tumor-derived polypeptide that induces endothel A;Reference number: A60932; MUID:91079755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A44881; C44881; A60932; S52136
R;Breier, G.; Albrecht, U.; Sterrer, S.; Risau,
Development 114, 521-532, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C;Accession: A44881; C44881; A60932; S52136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-140, 209-214 <BR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: sequence extracted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N; Contains: vascular endothelial growth factor-2; vascular permeability factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A44881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                 290
                                                                                  150
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                                                                                                                                                                                                                                            174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 CFECKESLETCCQKHKLFHPDTCSCE
                                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 WKLWRCRLRL-----KSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      7
CFECKESLETCCQKHKLFHPDTCSCE
                                                                                                                                                                                                                                                                                                                         RETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLT 173
                                                                                  QKRKRKKSRFKSWSVH - -
                                                                                                                                 KCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKD----LIQHPKNCS 289
                                                                                                                                                                                        S-QHIGEMSFLQHSRCECR
                                                                                                                                                                                                                                       SVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKC 233
                                                                                                                                                                                                                                                                                           IETLVDIFQEYPDEIEYIFKPSCVPLMRCAGCCNDEALECVPTSESNITMQIMRIK-PHQ 112
                                                                                                                                                                                                                                                                                                                                                                                                    WVHWTLALLLYLHHAKWSQAAPTTEGEQKSH------EVIKFMD-VYQRSYCRP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 198; Ub ...
Pred. No. 9.3e-08;
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                                                                               -CE-----PCSERRKHLFVQDPQTCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is associated with spontaneous
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C;Species: Chironomus tentans
C;Sate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C;Accession: S08167
R;Paulsson, G;; Lendahl, U; Galli, J; Ericsson, C; Wieslander, L.
J. Mol. Biol. 211, 331-349, 1990
A;Title: The balbiani ring 3 gene in Chironomus tentans has a diverged repel A;Reference number: S08167; MUID:90172404
A;Accession: S08167
A;Accession: S08167
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                                                                                        В
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A;Residues: 1-1700 <PAU>
A;Cross-references: GB:X52263; NID:g7057; PIDN:CAA36506.1;
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C; Superfamily: una
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A;Title: Amino acid and CDNA sequences of a vascular endothelial cell mitogen that A;Reference number: A35987; MUID:90207249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Balbiani ring 3 protein - midge (Chironomus tentans) C;Species: Chironomus tentans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-190 <CON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glioma-derived vascular endothelial cell growth factor - C:Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                      A;Gene: BR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M32167; NID:g204287; PIDN:AAA41211.1; PID:g204288
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Best Local Similarity
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Best Local (
                                                                                      1073 TKCSDKQKFIESKCECGCETQT----QCKDGFRWSNLECGCLCDDKK--CP------GK 1119
                                          164 QLFEISVPLTSVPELVPVKVANH-----TGCKCLPTAPRHPYSIIRR-----SIQI 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
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QVFDKNTCQCKCPNQKPGDTCGNGKDFCPLDCSCKCKNPKPANGCTGVQEWNEEKCQCEC 1179
                                                                                                                              TQCSPRETCVEVASELGKSTNTFFKPPCVNVFR-----CGGCCNEESLICMNTSTSYISK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPKD----LIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SESNVTMQIMRIK-PHQS-QHIGEMSFLQHSRCECR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVVKFMD-VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCAGCCNDEALECVPT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                        unassigned Balbiani ring proteins
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                                                                                                                                                                               43;
                                                                                                                                                                            Score 181.5; DB 2
Pred. No. 1.1e-05;
3; Mismatches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 194; DB 2;
Pred. No. 1.6e-07;
7; Mismatches 65
                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                               105;
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                                                                                                                                                                               Indels 125;
                                                                                                                                                                                                                         Length 1700
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A; Reference number: JC4679; MUID:96183052

A; Morden JC4680

A; Morden JC4680
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C;Accession: JC4680
R;Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.;
                                                        C; Accession: S57956
R; Redmer, D.A.; Dai.
                                                                                      ovine vascular endothelial growth factor
C;Species: Ovis orientalis aries, Ovis
C;Date: 13-Jan-1996 #sequence_revision
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F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-188/Product: vascular endothelial growth factor-related factor #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:U43837; NID:g1314335; PIDN:AAC52553.1; PID:g1314336 C;Comment: This factor is a mitogen, that is selective for endothelial cells, ar endothelial growth factors 167 and VEGF 186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vascular endothelial growth factor-related factor 167 precursor - mouse
N;Alternate names: VRF 167 protein
C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 05-Nov-1999
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                                    submitted to the EMBL Data Library,
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                     A; Reference number:
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A; Residues: 1-188 <TOW>
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 WORTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  42
                                                                                                                                                                                                                          RTCRC-RCRRRFLHCQGRGLELNPDTCRC 183
                                                                                                                                                                                                                                                               KNCSCFECKESLETCCQKHKL-FHPDTCSC
                                                        D.A.; Dai, Y.; Li,
                                                                                                                                                                                                                                                                                                                                    MLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHP 285
                                                                                                                                                                                                                                                                                                                                                                           LMIQYPSSQLGEM---SLEEHSQCECRPKK--
                                                                                                                                                                                                                                                                                                                                                                                                        FEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPID 225
                                                                                                                                                                                                                                                                                                                                                                                                                                               YARATCQPREVVVPLSMELMGNVVKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQI 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTWNSQTCQCS--CP-ATGKCTGAQVWCSKACKCVCPAQKK 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLFHPDTCSCEDRCPFHTRPCASGKTACAKHCR--FPKEKR 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WDSNKCKCVLQE -- ENP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADKAKPASCGDKKSWNDDSCSCQCKSKMPCGGCPPNQQWNEKDC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHLQEPALCGPHMMFDEDRCECVCKTP-----CPKDLIQHPKNCSCFECKESLETCCQKH 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WCDNTCRCVCPKNMEKPADNCKTKWWNDEMCQCVCKPGCPEGGCKGVMKWNANTCSCECP
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                     S57956
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                                                      Jones, S.C.; Moor, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 176.5; DB 2;
Pred. No. 3.2e-06;
                                                                                                            factor - sheep
Ovis ammon ario
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                                                                                            01-Mar-1996
                                      1995
                                                                                                            aries
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                                                                                        #text_change
                                                                                                              (domestic sheep)
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                                                                                            05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69;
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Query Match
Best Local Similarity
""" hes 38; Conserv
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RESULT
A33787
                                                                                                                           J. Virol. 68, 84-92, 1994
A; Title: Homologs of vascular endothelial growth factor are encoded by the A; Reference number: A49530; MUID:94076465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vascular endothelial growth factor (version 1) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 05-Nov-1999
A;Cross-references: GB:S67522; NID:g456900; PIDN:AAB29223.1; A;Note: sequence extracted from NCBI backbone (NCBIN:141422,
                                      A; Molecule type: DNA
A; Residues: 1-148 <LYT>
                                                                       A; Status: preliminary
                                                                                          A; Accession: D49530
                                                                                                            A; Contents: NZ7
                                                                                                                                                                                   R; Lyttle,
                                                                                                                                                                                                      C; Accession: D49530
                                                                                                                                                                                                                      16K vascular endothelial growth factor C;Species: Orf virus C;Date: 07-Apr-1994 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB:M33750; NID:g163810; PIDN:AAA30805.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <TIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Vascular endothelial growth factor: a new member of the platelet-derived gro A;Reference number: A33787; MUID:90121225
A;Accession: A33787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: A33787
R; Tischer, E.; Gospo
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A; Residues: 1-146 < RED>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                D49530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S57956
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Best Local S
Matches 37
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Best Local
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                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                     D.J.;
                                                                                                                                                                                                                                                                                                                                                     EEFNITMQIMRIK-PHQS-QHIGEMSFLQHNKCECRP 105
                                                                                                                                                                                                                                                                                                                                                                                        STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
                                                                                                                                                                                                                                                                                                                                                                                                                            EVVKFMD-VYQRSFCRPIETLVDIFQEYPDEIEFIFKPSCVPLMRCGGCCNDESLECVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEFNITMQIMRIK-PHQS-QHIGEMSFLQHNKCECRP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLP 193
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37; Conser
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37; Conser
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                                                                                                                                                                                     Fraser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                   K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 166.5; DB 2
Pred. No. 1.2e-05;
4; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 167.5; DB 2
Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1198-1206,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                      18-Nov-1994 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                            homolog A2R -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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 PID:g456902
NCBIP:141426)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID:g163811
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Cr

Conservative

12;

Score 164; DB Pred. No. 2.2e 12; Mismatches

DB 2; .2e-05;

Length 148; Indels

40;

26;

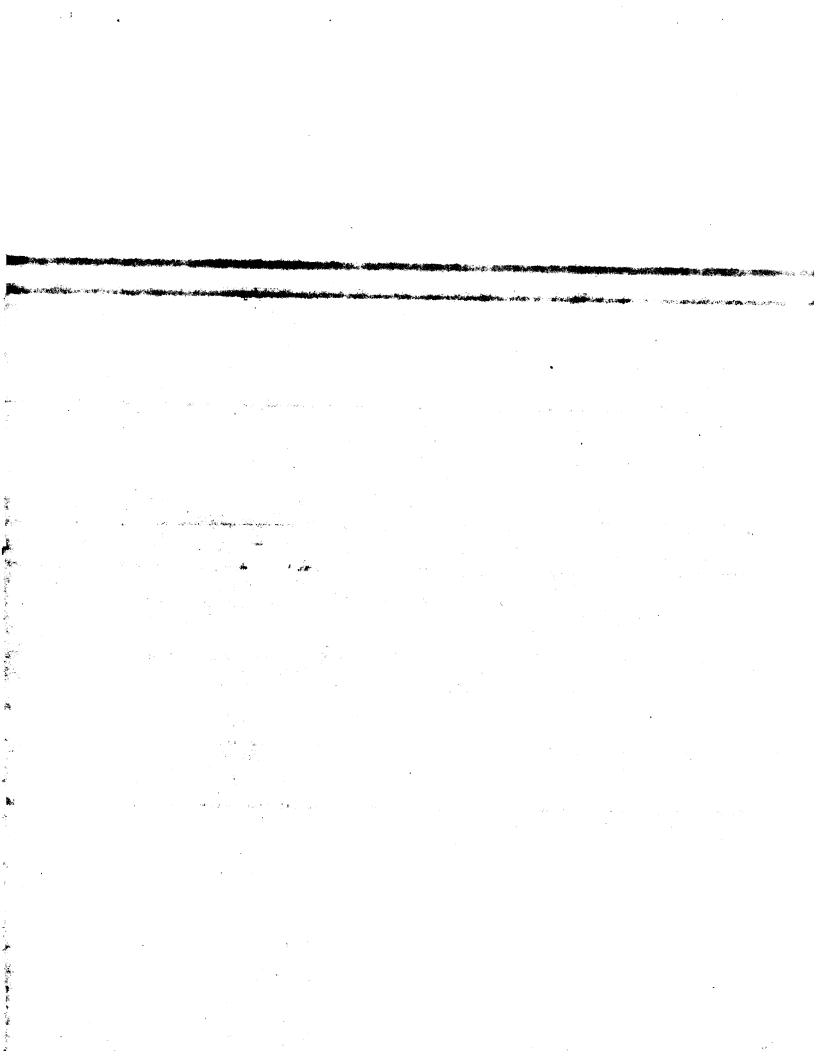
Gaps

4.

8.4%;

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platelet-derived growth factor chain B precursor - cat
N;Alternate names: PDGF-related transforming protein
C;Species: Felis silvestris catus (domestic cat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 31-Mar-
C;Accession: A26402
R;Van den Ouweland, A.M.W.; Van Groningen, J.J.M.; Schalken, J.A.; Van
Nucleic Acids Res. 15, 959-970, 1987
A;Title: Genetic organization of the c-sis transcription unit.
A;Reference number: A26402; MUID:87146463
A;Recession: A26402
A;Molacule type: mRNA
A;Residues: 1-245 <VAN>
C;Genetics:
A;Gene: sis
C;Superfamily: platelet-derived growth factor
C;Reywords: glycoprotein; growth factor
F;21-81/Domain: propeptide #status predicted <SIG>
F;21-81/Domain: propeptide #status predicted <PRO>
F;82-194/Product: platelet-derived growth factor chain B #status predic
F;163-167/Region: receptor binding #status predicted
F;163-167/Region: receptor binding #status predicted
A;Cross-references: GB:X54936; NID:g35521; PIDN:CAA38698.1; C;Genetics: A;Gene: GDB:PGF
                                                                     A; Molecule type: mRNA
A; Residues: 1-149 < MAG>
                                                                                                                                              A; Reference number: A41236; A; Accession: A41236
                                                                                                                                                                                             R:Maglione, D.; Guerriero, V.; Viglietto, G.; Delli-Bovi, Proc. Natl. Acad. Sci. U.S.A. 88, 9267-9271, 1991
A:Title: Isolation of a human placenta CDNA coding for a
                                                                                                                                                                                                                                                                          placental growth factor precursor - human
C;Speciles: Homo sapiens (man)
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 05-Nov-1999
C;Accession: A41236
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                                                                                                                         A; Status: preliminary
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Best Local S
Matches 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Felis silvestris catus (domestic cat)
Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 31-Mar-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKRPVFKKATVTLEDHLACKCETVVAARP---VTRSPGSSQEQR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDR 214
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aham H., Wood W.I.; ad protein: a ligand and receptor Flt4."; 2(1996). J., Greco R., 2(1996). J., Greco R., 2(1996). J., Kovacic S., 20nnessey D., Kovacic S., 20nnessey D., Kovacic S., 20nner K.,	tta; Eutdae; HCdae; HCdae; HCfdae; HCf	R (VEGE-C) (VASCULAR	p54643 dictyosteli Q12986 homo sapien p35555 homo sapien p35555 homo sapien p20033 mus musculu p04412 drosophila Q07954 homo sapien p35440 gallus gall p30432 drosophila Q61555 mus musculu p10039 gallus gall Q9nj15 branchiosto Q9n018 macropus eu

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Pfam; PF00341; PDGF; 1
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PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
                                                                 VASCULAR ENDOTHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitogen;
                                                       FLT4-L).
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U43142;
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AAA85214.1;
AAB02909.1;
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                       Chordata;
Rodentia;
                                                              , Last sequence update)
, Last annotation update)
GROWTH FACTOR C PRECURSOR
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38
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N-LINKED (GLCNAC...) (P
N-LINKED (GLCNAC...) (P
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Pred. No. 2.4
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VASCULAR ENDOTHELIAL GROWTH

4 X 24 AA TANDEM REPEATS.
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                      Craniata; Vertebrata;
Sciurognathi; Muridae;
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) (POTENTIAL).
                       Euteleostomi;
; Murinae; Mus
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REPEAT
CARBOHYD
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SIGNAL
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EMBL; U58112;
HSSP; P15692;
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REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS00278; PDGF_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
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InterPro; IPR002400;
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                                 GPVKRSSQSTLERSEQQIRAASSLEELLRITHSEDWKLWRCRLRLKSFTSMDSRSASHRS
             RSI--QIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQ--
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140; Conservative
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AAB46707.1;
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Pred. No. 1.1e-47
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N-LINKED (GLCNAC. . .) (F
N-LINKED (GLCNAC. . .) (F
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VASCULAR ENDOTHELIAL GROWTH

4 X 24 AA TANDEM REPEATS.
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  Long A., Burgess P., (Kovacic S., Ciarletta R., Beier D.R., Leak I
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Bovidae; E
       EMBL; M32976; AAA30502.1;
EMBL; M31836; AAA30804.1;
EMBL; M33750; AAA30805.1;
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                                                                      use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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                                                                                                                          between
                                                                                                                                                                                                                                                 "Pituitary follicular cells secrete a novel heparin-binding factor specific for vascular endothelial cells.";
Biochem. Biophys. Res. Commun. 161:851-858(1989).
-!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDO
                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 27-31.
                                                                                                                                                                                                                                                                                                                                                                  Tischer E., Gospodarowicz D., Mitchell R.,
Lau K., Crisp T., Fiddes J.C. Naraham J.A.
"Vascular endothelial growth factor: a new
derived growth factor gene family.";
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                                                                                               European Bioinformatics Institute. The by non-profit institutions as long
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SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
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                                                          equires a license agreement (See email to license@isb-sib.ch).
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Best Local
                        MEDLINE-95143284; PubMed=7841203;
Sharma H.S., Tang Z.H., Gho B.C.H., Verdouw P.D.;
Bhochia Blophys. Acta 1260:235-238(1995).

Biochia Blophys. Acta 1260:235-238(1995).

FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL

CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
PERMEABILITY (BY SIMILARITY).

-!- SUBCULIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS

"TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
                                                                                                                                                                                                                                                                                                                                                     VEGF_PIG
P49151;
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SEQUENCE
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01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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PROSITE; PS50278; PDGF_2;
Mitogen; Growth factor; G]
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                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                             Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                     PERMEABILITY FACTOR) (VPF).
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Pfam; PF00341; PDGF;
                                                                                                                                                                                                                     NCBI_TaxID=9823;
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SIMILARITY:
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B40080;
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25.4%;
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            THE PDGF/VEGF FAMILY OF
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INTERCHAIN (BY SIMILARITY).
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EDBF903E46E24789 CRC64;
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No. 4.1e-09;
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            GROWTH FACTORS
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Sus.
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between the Swiss Institute of Bioinf the European Bioinformatics Institute

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Best Local S
Matches 54
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DISULFID
CARBOHYD
SEQUENCE
SEQUENCE FROM N.A. (VEGF-1).
MEDLINE=92355593; PubMed=1644816;
Claffey K.P., Wilkison W.O., Spiegelman B.M.;
"Vascular endothelial growth factor. Regulation
                                                                                                                   Breier G., Albrecht U., Sterrer S., Risau W.; "Expression of vascular endothelial growth factor during embryonic angiogenesis and endothelial cell differentiation."; Development 114:521-532(1992).
                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (Rel. 40, Last annotat: VASCULAR ENDOTHELIAL GROWTH FACTOR PERMEABILITY FACTOR) (VPF).
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                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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PS50278; PDGF_2; 1.
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(Rel. 34, Last sequence update)
(Rel. 40, Last annotation updat
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BY SIMILARITY.
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BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GICNAC. . .) (POTENTIAL).
NO 104040BBD7913047F CRC64;
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Pred. No. 5.9e
24; Mismatches
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WKLWRCRLRL-----KSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSP 113

Query Match Best Local S Matches 63

63; Conser

Conservative

10.1%;

Score 198; DB 1; Pred. No. 6.7e-09; 5; Mismatches 94;

Length 214;

Indels

74;

Gaps

11;

Дb

WVHWTLALLLYLHHAKWSQAAPTTEGEQKSH---

-EVIKEMD-VYQRSYCRP

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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:103178; Vegf.
InterPro; IPR000072;
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J. Biol. Chem. 267:16317-16322(1992).
[3]
                                                                                                                                                                     CARBOHYD
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TISSUE SPECIFICITY: IN DEVELOPING EMBRYOS, EXPRESSED MAINLY IN THE CHOROID PLEXUS, PARAVENTRICULAR NEUROEPITHELIUM, PLACENTA AND KINNEY GLOMERULI. ALSO FOUND IN BRONCHIAL EPITHELIUM, ADRENAL GLAND AND IN SEMINIFEROUS TUBBULES OF TESTIS. HIGH EXPRESSION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEGF CONTINUES IN KIDNEY GLOMERULI AND CHOROID PLEXUS IN ADULTS SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS,
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sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                            Siegel N., Haymore B.L., Leimoruber R., Feder J
"Human vascular permeability factor. Isolation
J. Biol. Chem. 264:20017-20024(1989).
                                                                                                                                                       "AIDS-associated Kaposi's sarcoma cells in culture endothelial growth factor.";
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MEDLINE=90069608; PubMed=2479986;
Leung D.W., Cachianes G., Kuang W.-J.,
"Vascular endothelial growth factor is
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15-JUL-1999 (Rel. 38, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
          MEDLINE-93145946; PubMed=7678805; Fiebich B.L., Jaeger B., Schoelln
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                                    SEQUENCE OF
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[3]
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Mammalia; Eutheria;
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  Marme D.,
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                                                                                    Feder J.;
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                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                        endothelial growth factor.";
Structure 6:637-648(1998).
-i- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS,
CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98298440;
Fairbrother W.J.,
Starovasnik M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Vascular endothelial growth factor: crystal structure mapping of the kinase domain receptor binding site."; proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.; "The crystal structure of vascular endothelial growth factor refined to 1.93-A resolution: multiple copy flexibility and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein Sci.
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Fairbrother W.J., Champe M.A., Christinger H.W.,
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                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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                                                                                                                                                                                                                                                       VEGF-189 AND VEGF-215)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9634701;
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                                                                                                                                                                                                                                                                                                        REMAINS ASSOCIATED RELEASED BY HEPARIN
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Best Local
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DISULFID
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
[1]
                                                                                                                       01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF)
PERMEABILITY FACTOR) (VPF).
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VARSPLIC
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PIR;
PDB;
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                               273
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nes 57; Conserv
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; C40454; C40454.
; JQ1463; JQ1463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
                                                                                                                                                                                                                                                                                                                                                                                             CKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
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S17348; S17348.
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A40079; A40079
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1VPF; 08-APR-98
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PS50278; PDGF_2; 1.
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215 AA;
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MISSING (IN ISOFORM VEGF-121).
; 789759AD5871FF33 CRC64;
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Pred. No. 9.
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K -> N (IN ISOFORM VEGF-121 AND VEGF-165).
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                                      Craniata; Vertebrata; Sciurognathi; Muridae;
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                                        Murinae;
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Best Local :
VEGF_CAVPO STANDARD;
P26617;
01-AUG-1992 (Rel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M32167; AAA41211.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conn G., Bayne M.L., Soderman D.D., Kwok P.W., Sullivan i Palisi T.M., Hope D.A., Thomas K.A.;
"Amino acid and cDNA sequences of a vascular endothelial that is homologous to platelet-derived growth factor.";
Proc. Natl. Acad. Sci. U.S.A. 87:2628-2633(1990).
-!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF MEDLINE=90207249; PubMed=2320579;
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TISSUE SPECIFICITY: EXPRESSED IN THE PITUITARY, IN BRAIN,
PARTICULARLY IN SUPRAOPTIC AND PARAVENTRICULAR NUCLEI AND
CHOROID PLEXUS. ALSO FOUND ABUNDANTLY IN THE CORPUS LUTEUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMODIMER, DISULFIDE-LINKED. SUBCELLULAR LOCATION: SECRETED BUT RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHOROID PLEXUS. ALSO FOUND ABUNDATHE OVARY AND IN KIDNEY GLOMERUL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERMEABILITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
                                                                                                CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD
                                                                                                                        CPKD----LIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE
                                                                                                                                                                              HSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTP
                                                                                                                                                                                                        SESNVTMQIMRIK-PHQS-QHIGEMSFLQHSRCECR-----
                                                                                                                                                                                                                                  STSYISKOLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCS 216
                                                                                                                                                                                                                                                           EVVKFMD-VYQRSYCRDIETLYDIFQEYPDEIBYIFKPSCVPLMRCAGCCNDEALECVPT 96
                                                                                                                                                                                                                                                                                      ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                    l Similarity
53; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00249; PDGF_1;
PS50278; PDGF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000072;
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                                                                                                                                                                                                                                                                                                                 Score 194; DB
Pred. No. 1.2e
Pred. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. ..).
589374010441F377 CRC64;
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INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                        VASCULAR ENDOTHELIAL GROWTH FACTOR. BY SIMILARITY. BY SIMILARITY.
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                             164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
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                                                                                                                                                                                                                                                                                                                               DB 1;
.2e-08;
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                                                                                                  RESULT 9
BAR3_CHITE
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
BAR3_CHITE
Q03376;
01-OCT-1993
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitogen;
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000072; -
Pfam; PF00341; PDGF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M84230; AAA37057.1; -. HSSP; P15692; 2VGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases -i- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) (VASCULAR PERMEABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FACTOR) (VPF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10141;
                                                                                                                                                                                                      119
                                                                                                                                                                                                                                                     272
                                                                                                                                                                                                                                                                                                                                                                                                                                                    157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMODIMER, DISULFIDE-LINKED. SUBCELLULAR LOCATION: SECRETED BUT RETO THE EXTRACELLULAR MATRIX UNLESS RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND PERMEABILITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                  VCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
                                                                                                                                                                                                    -CSERRKHLFVQDPQTCKC-SCRNTDSRCKARQLELNERTCRCD
                                                                                                                                                                                                                                                                                                                                                  HSKKLCPIDMLWDSNKCKC-----VLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCEC 271
                                                                                                                                                                                                                                                                                                                                                                                                EEFNITMQIMRIK-----IGEMSFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                               STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEVKFMD-VYKRSYCRPIEMLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDESLECVPT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00249; PDGF_1; 1.
PS50278; PDGF_2; 1.
Growth factor; Glyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 AA;
(Rel.
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50
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74
                                                                          STANDARD;
27, Created)
27, Last seq
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101
103
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59
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                                                                                                                                                                                                                                                                                                   KCECRPKKEKARQENP
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein.
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 185; DB 1;
Pred. No. 5.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POT);
9EB86A81A9D5DCA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Eute
Hystricognathi; Caviidae;
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                                                                          1700
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                                                                          A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 164;
                                                                                                                                                                                                                                                  315
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chironomus tentans (Midge).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; leukaryota; Neoptera; Endopterygota; Diptera; Nematoces Chironomoidea; Chironomidae; Chironominae; Chironomus
                                                                                                                     1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                       1120 QVFDKNTCQCKCPNQKPGDTCGNGKDFCPLDCSCKCKNPKPANGCTGVQEWNEEKCQCEC 1179
                                                                                                                                                                                                                                                                                                 1073 TKCSDKQKFIESKCECGCETQT----QCKDGFRWSNLECGCLCDDKK--CP-----GK 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X52263; CAA36506.1;
PIR; S08167; S08167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Salivary gland; MEDLINE=90172404; PubMed=1689777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1994 (Rel. 30, Last annotation update) BALBIANI RING PROTEIN 3 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P18055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7153;
                                                                                                                                                                                                                                                                                                                                 109
                             305
                                                                                                                                                                                                                                                                       164
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                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: SECRETED.
TISSUE SPECIFICITY: SALIVARY GLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: HAS 82 APPROXIMATE REPEATS OF CYS-X-CYS-X-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM FORMING WATER-INSOLUBLE FIBERS TOO EARLY.
QTWNSQTCQCS--CP-ATGKCTGAQVWCSKACKCVCPAQKK 1394
                            KLFHPDTCSCEDRCPFHTRPCASGKTACAKHCR--FPKEKR 343
                                                                                                                                                 WDSNKCKCVLQE - - ENP - -
                                                                                                                                                                                                                                                                     QLFEISVPLTSVPELVPVKVANH------TGCKCLPTAPRHPYSIIRR-----SIQI 209
                                                                                                                                                                                                                                                                                                                               TQCSPRETCVEVASELGKSTNTFFKPPCVNVFR-----CGGCCNEESLICMNTSTSYISK 163
                                                         ADKAKPASCGDKKSWNDDSCSCQCKSKMPCGGCPPNQQWNEKDC--
                                                                                      SHLQEPALCGPHMMFDEDRCECVCKTP-----CPKDLIQHPKNCSCFECKESLETCCQKH 304
                                                                                                                   WCDNTCRCVCPKNMEKPADNCKTKWWNDEMCQCVCKPGCPEGGCKGVMKWNANTCSCECP
                                                                                                                                                                               PKDKPKKQCPGGQDWNNHQCQCGCPTPAPTCSNNQKYSNVSCSCGCNPGKPKNGCPGNQI 1239
                                                                                                                                                                                                             PEE-----
                                                                                                                                                                                                                                                                                                                                                             l Similarity
68; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR00876; MTNEMATODE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000853;
                                                                                                                                                                                                                                                                                                                                                                                                                                       1700
                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                           1700
                                                                                                                                                                                                                                                                                                                                                                        9.2%;
19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       186145
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                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                       WW;
                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.16
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Score 181.5; Db 1
                                                                                                                                                                                                                                                                                                                                                                                                                                     BALBIANI RING PROTEIN 3.
W; 34202B28521B0815 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                               105;
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                                                                                                                                                                                                                                                                                                                                                                                        Length 1700;
                                                        ECKCSATGNCPAG 1356
                                                                                                                                                                                                                                                                                                                                                               125;
                                                                                                                                                LAGTEDH 249
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RESULT

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Qy
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                                                              В
                                                                                            QΥ
                                                                                                                                                                                                            VEGB_MOUSE
                                                                                                                           Query Match
Best Local Similarity
Matches 49; Conser
                                                                                                                                                                                                                                                                                                               EMBL; U48800; AAB06273
EMBL; U43837; AAC52553
HSSP; P15692; ZVGH,
MGC); MGI:10619; Vegfb
InterPro; IPR000072;
                                                                                                                                                                                                                                       Mitogen;
SIGNAL
                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of the murine VEGF-related factor gene.";
Biochem. Biophys. Res. Commun. 220:922-928(1996).
-!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96197355; PubMed=8637916;
Olofsson B., Pajusola K., Kaipainen A.
Saksela O., Orpana A., Pettersson R.F.
"Vascular endothelial growth factor B,
endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VASCULAR
                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P49766;
                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Townson S., Lagercrantz J., Grimmond S., Nordenskjoeld M., Weber G., Hayward N.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96183052; PubMed=8607868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGFB OR VRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEGB_MOUSE
                                                                                              106
 102
                                 166
                                                              42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS C
TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN HEART, BRAIN, KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WITH VEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                            WQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQL 165
LMIQYPSSQLGEM--
                               FEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPID
                                                             YARATCQPREVVVPLSMELMGNVVKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQI 101
                                                                                                                                                                                                                                                                                                       PF00341; PDGF; 1.
                                                                                                                                                       J0341; PDGF; 1,

PS00249; PDGF 1; 1.

PS50278; PDGF_2; 1.

PS50278; PDGF_2; 1.

PS50278; PDGF_2; 1.

PS50278; PDGF_2; 1.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL GROWTH FACTOR DS2A055FB995E9CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKELETAL MUSCLE
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                      AAC52553.1;
                                                                                                                                                                                                                                                                                                                                                                                   AAB06273.1;
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                                                                                                                                                                                                                                                                                                                                   Vegfb.
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Rodentia;
                                                                                                                                            9.0%;
23.3%;
 SLEEHSQCECRPKK - - -
                                                                                                                             22;
                                                                                                                           Score 176.5; DB:
Pred. No. 2.9e-07
2; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93:2576-2581(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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, Alitalo K., Eriksson U.;
a novel growth factor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Silins G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽Ã
KESAVKPDSPRI - - - - LCP - -
                                                                                                                             Indels
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                                                                                                                             69;
                                                                                                                          Gaps
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RESULT 11
VEGB_HUMAN
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MEDLINE-97077124; PubMed-8919691;
Grimmond S., Lagercrantz J., Drinkwater C., Silins G.,
Pollock P., Gotley D., Carson E., Rakar S., Nordenskjo
Hayward N., Weber G.;
"Cloning and characterization of a novel human gene re
vascular endothelial growth factor.";
Genome Res. 6:124-131(1996).
-i- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BII
-i- SUBBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FOR
                                        InterPro; IPR000072; -.

pfam; PF00341; PDGF; 1.

PROSITE; PS00249; PDGF_1; 1.

PROSITE; PS0278; PDGF_2; 1.

Mitogen; Growth factor; Signal; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996
01-OCT-1996
01-OCT-2000
                                                                                                                         MIM:
                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of hisinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEGB_HUMAN
P49765;
                                                                                                                                     EMBL; U48801; AAB06274.1; -. EMBL; U43369; AAA91463.1; -. HSSP; P15692; 1VPF.
                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELL!
TO THE EXTRACELLULAR MARRIX UNLESS RELEASED BY HEPARIN.
-!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.
HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.
-!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olofsson B., Pajusola K., Kaipainen A., von Euler G. Saksela O., Orpana A., Pettersson R.F., Alitalo K., "Vascular endothelial growth factor B, a novel growth endothelial cells.";
       SEQUENCE
                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad.
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MEDLINE=96197355; PubMed=8637916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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(Rel.
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Primates;
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         MW.
                     VASCULAR ENDOTHELIAL GROWTH FACTOR
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       F04654D5A3727194
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       CRC64;
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K., Eriksson
Factor
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MBL outstation -
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Query Match

8.9%;

Score 175.5;

DB

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Length 188;

Local

24.0%;

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DISULFID
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                                                        PROSITE;
PROSITE;
Mitogen;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEGF_SHEEP
P50412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR
PERMEABILITY FACTOR) (VPF).
                                                                                                           InterPro; IPR000072; -
Pfam; PF00341; PDGF; 1
                                                                                                                                   EMBL; X89506; CAA61677.1; -. HSSP; P15692; 1VPF.
                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                          between
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Reynolds L.P., Moor R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ovis aries (Sheep).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97117958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                   factor (VEGF) in the ovine corpus luteum.";
J. Reprod. Fertil. 108:157-165(1996).
-!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS,
                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization and expression of vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163
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  P800249; PDGF_1; 1.
; PS50778; PDGF_2; 1.
; Growth factor; Glycol
1 26
27 146
D 51 93
D 82 127
D 86 129
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Cetartiodactyla;
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Glycoprotein; Signal.
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3; Mismatches
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actyla; Ruminantia; Pe
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73;
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                                            FACTOR
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Best Local :
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P52585;
01-OCT-1996 (Rel.
01-OCT-1996 (Rel.
15-JUL-1999 (Rel.
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CARBOHYD
SEQUENCE
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SIGNAL
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CARBOHYD
SEQUENCE
                                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                         J. Virol. 68:84-92(1994).
-!- FUNCTION: INDUCES ENDOTHELIAL
-!- SUBUNIT: HOMODIMER, DISULFIDE-
                                                                                                                                                                                                                                                                                                                      MEDLINE=94076465; PubMed=8254780; Lyttle D.J., Fraser K.M., Fleming "Homologs of vascular endothelial poxvirus of virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORFN7
                                                                                    CHAIN
                                                                                                                                       Pfam; PF00341; PDGF;
                                                                                                                                                            EMBL; S67522; HSSP; P15692;
                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                   PROSITE;
                                                                                                                              PROSITE;
                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=73495;
                                                                                                                                                                                                                                                                                                                                                                                                  Parapoxvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                      Orf virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEFNITMQIMRIK-PHQS-QHIGEMSFLQHNKCECRP 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVMKFMD-VYQRSFCRPIETLVDIFQEYPDEIEFIFKPSCVPLMRCGGCCNDESLECVPT 96
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37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                           996 (Rel. 34, Created)
996 (Rel. 34, Last sequence up
999 (Rel. 38, Last annotation
ENDOTHELIAL GROWTH FACTOR HON
                                                                                                                                                                                                                                              the Swiss Institute of Bioinformatics and the
                                                                                                          Growth
                                                                                                                             PS00249;
                                                                                                                                                                                                                                                                                                                                                                                                            dsDNA viruses,
                                                                                                                   PS50278;
                                                                                                                                                                                                                         non-profit institutions as long
                                                                                                                                                  IPR000072;
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                                                                                                         factor;
                                                                                             PDGF_2; 1.
PDGF_2; 1.
PDGF_2; 1.
POTENTIA
                                                                                                                             PDGF_1;
           88
130
132
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38.1%;
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                                                                                                                             FALSE_NEG
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                                                                                                                                                                                                                                                                                                                                                                                                           RNA stage;
                                       HOMOLOG.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY)
INTERCHAIN (BY SIMILARITY)
IN-LINKED (GLCNAC. .) (PO'
N-LINKED (GLCNAC. .) (PO'
F0E13BA104CC73F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (P
; 4E792CB557F91760 CRC64;
                                                                                   VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 167.5;
Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN INTERCHAIN
                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                 S.B., Mercer A.A., Robinson A.J.; growth factor are encoded by the
                                                                                                                                                                                                                                                                                                   PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMOLOG PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148
                                                                                    ENDOTHELIAL
                                                                                                        Signal
                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                           Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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There are no restrictions on it
ing as its content is in no wa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
SIMILARITY).
AC. . . ) (POTENTIAL).
                                                                                                                                                                                                              Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
                                                                                    GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                               Ьy
           (POTENTIAL)
                                                                                                                                                                                                                and
                                                                                    FACTOR
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                                                                                                                                                                                                               in no way commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156
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Query Match Best Local S Matches 38

18; Conser

8.4%; nilarity 32.8%; Conservative 1

12;

Score 164; DB 1; Pred. No. 2.1e-06; 2; Mismatches 40

40;

Indels

26;

Gaps

4

Length 148

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RESULT
PDGB_FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρ
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SEQUENCE FROM N.A.

MEDLINE=87146463; PubMed=3822831;

Wan den Ouweland A.M.W., van Groningen J.J.M., Schalken J

van Neck H.W., Bloemers H.P.J., van de Ven W.J.M.;

"Genetic organization of the c-sis transcription unit.";

"Genetic organization of the c-sis transcription unit.";
                                                                                                                                                                                                                                                                                                                                                                                                           Van den Ouweland A.M.W.;

van den Ouweland A.M.W.;

Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.

-i- SUBUNT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONLOENTICAL (A AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CHAIN
PROPEP
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LT 14
_FELCA
                                                                                            SIGNAL
                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                 PROPEP
                                                                                                            Mitogen;
                                                                                                                                                               InterPro; IPR000072; -.
InterPro; IPR002400; -.
Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDGFB OR 515.
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Fissipedia; Felidae;
                                                                                                                                      PROSITE;
                                                                                                                                                                                                         HSSP; P01127; 1PDG
                                                                                                                                                                                                                      PIR; A26402; TVCTSS.
                                                                                                                                                                                                                                     EMBL; X05112; CAA28758.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN) (PDGFB) (C-SIS) (PDGF-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P12919;
                                                                                                                                                  PRINTS; PR00438; GFCYSKNOT.
                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDGB_FELCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161
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                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISKQLFEISVPLTSV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EWQRT----QCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSY 160
                                                                                                                                                                                                                                                                                         non-profit institutions as long and this statement is not removed.
                                                                                                            Growth
                                                                                                                       PS00249; PDGF_1; 1. PS50278; PDGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                          RECEPTOR
 1
82
195
101
134
138
128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -VTVSVTGVSSSSGTNSGVSTNLQRISVTEHTKCDCIGRTTTTPTTTREP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                            factor;
 20
81
194
245
145
182
184
                                                                                                                                                                                                                                                                                                                                                                                                     A-A AND B-B;
                                                                                              Proto-oncogene; Platelet;
BY SIMILARITY.
                                                                                                                                                                                                                                  ALT_SEQ.
INTERCHAIN (BY SIMILARITY).
                                                                   PLATELET-DERIVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -PELVPVKVANHTGCKCL-----PTAPRHP
            C SIMILARITY.
C SIMILARITY.
C SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                     AS WELL AS A-B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245
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                                                                                                                                                                                                                                                                                                       as its content
                                                                    GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schalken J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                     DIMERS
                                                                                                         Signal.
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Felis.
                                                                   FACTOR,
                                                                                                                                                                                                                                                                                                                                                                                                     CAN BIND TO THE
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                                                                   B
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CRETT REFERENCE REPORT OF THE PROPERTY OF THE 
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01-OCT-1996 (Rel. 34, Las
01-OCT-2000 (Rel. 40, Las
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                     "Placenta growth factor. Potentiation of factor bloactivity, in vitro and in vivo, to Flt-1 but not to Flk-1,KDR.";
J. Biol. Chem. 269:25646-25654(1994).
                                                                                                                    CHARACTERIZATION, AND SEQUENCE OF 19-24.
MEDLINE=95014370; PubMed=7929268;
Park J.E., Chen H.H., Winer J., Houck K.
                                                                                                                                                                                                                                                                         Maglione D., Guerriero V., Viglietto G., Ferraro M.G., Ap
Alitalo K., del Vecchio S., Lei K.-J., Chou J.Y., Persico
"Two alternative mRNAs coding for the angiogenic factor,
growth factor (PIGF), are transcribed from a single gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92021031; PubMed=1924389;
Maglione D., Guerriero G., Viglietto G., Delli-Bovi P., Persico M.G
"Isolation of a human placenta cDNA coding for a protein related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGF OR ruse: Human).
Homo sapiens (Human).
Chordata;
                                                                                                                                                                                                         Oncogene
[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        placenta."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the vascular permeability fact Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93205407; PubMed=7681160;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth Factors 9:259-268(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hauser S., Weich H.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94198032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (PLGF-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (PLGF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLGF_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A heparin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 RKRPVFKKATVTLEDHLACKCETVVAARP---VTRSPGSSQEQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50
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FUNCTION: GROWTH FACTOR OF UNKNOWN FUNCTION. BINDS TO RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNRCWA---LFLSLCCYLRLV---SAEGDPIPEELYKML--SDHSIR---SFDDLQRLLH 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTEVFEVSRRLIDRTNANFLVWPPCVEVQRCSGCCNNRNVQCRPTQVQLRLVQVRKIEIV
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34, Last sequence update)
40, Last annotation update)
40, PAGECURSOR (PLGF-1/PLGF-2).
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                                                                                                                                                                                                                                                                                                                                                                                                              (PLGF-2)
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Pred. No. 6.1e-06;
4; Mismatches 103
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E7715291D9837512 CRC64;
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                                                                                          A., Ferrara N.;
vascular endothelial growth
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Search completed: October 17, 2001, 14:51:47 Job time: 473 sec
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Best Local Similarity 28.3
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heparin-binding.
SIGNAL 1
CHAIN 19
DISULFID 52
DISULFID 83
DISULFID 77
DISULFID 77
DISULFID 77
DISULFID 33
CARBOHYD 101
VARSPLIC 142
CONFLICT 91
SEQUENCE 170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000072; -. Pfam; PF00341; PDGF; 1. PR0SITE; PS00249; PDGF_1; 1. PROSITE; PS50278; PDGF_2; 1. Mitogen; Growth factor; Glyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X54936; CAA38698.1; -.
EMBL; A18411; CAA01393.1; -.
EMBL; S72960; AAB30462.2; -.
HSSP; P15692; 1VPF.
MIM; 601121; -.
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                                                                                                                               115 PSYVELTFSQHVRCECRP 132
                                                                                                                                                                                   176 PELVPVKVANHTGCKCLP 193
                                                                                                                                                                                                                                                                                       116 TCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSV 175
                                                                                                                                                                                                                                                                                                                                                                                              63 KLWRCRLRLKSFTSMD-----SRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRE 115
                                                                                                                                                                                                                                     57 RLVDVVSEYPSEVEHMFSPSCVSLLRCTGCCGDEDLHCVPVETANVTMQLLKIR--SGDR 114
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SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
SUBCELLULAR LOCATION: BOTH FORMS ARE SECRETED BUT THE LONGER FORM APPEARS TO REMAIN CELL ATTACHED UNLESS RELEASED BY HEPARIN.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; PLGF-1 AND PLGF-2 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. PLGF-1 DIFFERS FROM PLGF-2 IN LACKING A 21 RESIDUES SEGMENT IN THE C-TERMINAL SECTION WHICH ACTS AS A CELL RETENTION SIGNAL.
TISSUE SPECIFICITY: WHILE BOTH FORMS ARE PRESENT IN MOST PLACENTAL AND ONLY THE SHORTER FORM IS SPECIFIC TO EARLY (8 WEEK) PLACENTA AND ONLY THE SHORTER FORM IS FOUND IN THE COLON AND MAMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: N-CLYCOSYLATED.
SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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Pred. No. 5.6e-06;
5; Mismatches 57;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
MISSING (IN ISOFORM PLGF-1).
D -> N (IN REF. 1).
; E47639AC59C0963F CRC64;
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BY SIMILARITY.
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BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
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Perfect score:
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Maximum DB seq length: 2000000000
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     SPTREMBL_16:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungl:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:
12: sp_unclass:
13: sp_vertebra
14: sp_virus:**
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Gapop 10.0 , Gapext 0.5
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1963
1 MYREWYVVNVFMMLYVQLVQ......HCRFPKEKRAAQGPHSRKNP 354
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sp_organelle:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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191	208	190	190	1704	194	190	232	209	190	190	254	126	122	420	418	326	358	354	Query Match Length
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075875	Q9XSF4	Q9QX39	Q9GL52	Q94446	042572	Q9XSF3	Q9H1W9	060720	077643	Q9GKR0	Q16889	035757	Q9GLX1	Q9XS50	057352	035251	P97946	043915	ij
075875 homo sapien	Q9xsf4 canis famil	Q9qx39 spalax leuc	Q9g152 sus scrofa	Q94446 chironomus	O42572 xenopus lae	Q9xsf3 canis famil	Q9h1w9 homo sapien	060720 homo sapien	077643 ovis aries		Q16889 homo sapien	035757 rattus norv	Q9glxl bos taurus	Q9xs50 bos taurus	057352 coturnix co	035251 rattus norv	P97946 mus musculu	043915 homo sapien	Description

ALIGNMENTS

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P97946
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DT 01
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EMBL; D89630; BAA24264.1; ---
EMBL; AJ000185; CAA03942.1; ---
EMBL; Y12863; CAA73370.1; ---
HSSP; P15692; 1VPP.
InterPro; IPR000072; ---
Pfam; PF00341; PDGF; 1.
PrODOm; PD001629; --; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS00249; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                           STRAIN-C57BL/6J;
MEDLINE-97030254; PubMed-8876195;
Ordandini M., Marconcini L., Ferruzzi R., Oliviero S.;
"Identification of a c-fos-induced gene that is related platelet-derived growth factor/vascular endothelial grow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P97946 PRELIMINARY; PRT; 358 AA. P97946; Ol-MAY-1997 (TrEMBLrel. 03, Created) Ol-MAY-1997 (TrEMBLrel. 03, Last sequence update) Ol-MAY-1997 (TrEMBLrel. 16, Last annotation update) VASCULAR ENDOTHELIAL GROWTH FACTOR D (C-FOS INDUCED
MEDLINE=97349118; PubMed=9205122;
Yamada Y., Nezu J., Shimane M., Hirata Y.;
"Molecular cloning of a novel vascular endothelial growth
VEGF-D.";
                                                                                             TISSUE-LUNG;
                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF-D OR FIGF.
Mus musculus (Mouse).
                                                                                                                                                                                      family."
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Sciurognathi; Muridae;
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Pred. No. 1.8e-175;
                                                                                                                                                              93:11675-11675(1996).
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GROWTH
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Best Local (
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                                                                                                                                                                                                                                                        O35251 PRELIMINARY;
O35251;
O1-JAN-1998 (TrEMBLrel. 05, C.
O1-JAN-1998 (TrEMBLrel. 16, L.
O1-MAR-2001 (TrEMBLrel. 16, L.
VASCULAR ENDOTHELIAL GROWTH F.
         HSSP: p15692: 1VPP.
InterPro: IPR000072; -.
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; -; 1.
PROSITE; PS00249; PDGF-1: 1.
PROSITE; PS002749; PDGF-2: 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics 42:483-488(1997).

EMBL; X99572; CAA67892.1; -.

EMBL; D89628; BAA14002.1; -.

HSSP; P15692; 1VPP.

MGD; MGI:108037; Figf.

InterPro; IPR00072; -.

Pfam; PF00341; PDGF; 1.

PROSITE; PS00249; PDGF—1; 1.

PROSITE; PS00278; PDGF—1; 1.

PROSITE; PS00278; PDGF—1; 1.

SMART; SM0141; PDGF; 1.
                                                                   Genomics 42:483-488(1997).

EMBL; AF014827; AAB66557.1;

HSSP; P15692; 1VPP.

InterPro; IPR000072; -.
                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                           STRAIN-SPRAGUE DAWLEY;
MEDLINE-97349118; PubMed-9205122;
Yamada Y., Nezu J., Shimane M., Hirata
"Molecular cloning of a novel vascular
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                               VEGF-D.
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                                                                                                                                                                                                                                                                                                                                                                                          SLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PELVPVKIANHTGCKCLPTGPRHPYSIIRRSIQTPEEDECPHSKKLCPIDMLWDNTKCKC
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Last annotation
FACTOR D.
                                                                                                                                                                                                                                                                                             Created)
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Pred.
1261AFA373596C00 CRC64;
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No. 1.4e-148;
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                                                                                                                            endothelial growth factor,
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on update)
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Query Match
Best Local Similarity
Matches 140; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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01-JUN-1998
01-JUN-1998
01-MAR-2001
                                                                                                                                                             Signal.
                                                                                                                   CHAIN
SEQUENCE
                                                                                                                                                                                                         PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eichmann A., Corbel C., Jaffredo T., Breant V., Joukov V., Kumar V., Alitalo K., Le Douarin N.M.; "Avian VEGF-C: cloning, embryonic expression pattern and stimulation of the differentiation of VEGFR2-expressing endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2001 (TrEMBLrel. 16, VASCULAR ENDOTHELIAL GROWTH
                                                                                                                                                                                                                                                                                                                               InterPro; IPR000072; -.
InterPro; IPR002400; -.
Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                                   PRINTS; PRO0438; GFCYSKNOT. ProDom; PD001629; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; V15837; CAA75799.1;
HSSP; P15692; IVPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Development 125:743-752(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precursors."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98167900; PubMed=9435294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 057352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAHSEDWKLWRCRLKLKSLANVDSRSTSHRSTRFAATFYDTETLKVIDEEWQRTQCSPRE
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111
418
  Conservative
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                                                                                                                      AA;
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418
46839
                      35.3%;
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16,
                                                                                                                      WW.
  52;
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Last annotation updat
FACTOR C PRECURSOR.
Score 692; DB
Pred. No. 1.1e
52; Mismatches
                                                                                                              POTENTIAL.

VASCULAR ENDOTHELIAL GROWTH

; 099BFCC79151BF2B CRC64;
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                      DB 13;
.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                            Length
Indels
                                                                                                                                         FACTOR
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62;
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Gaps
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Best Local S
Matches 133
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Q9X550;
Q1-NOV-1999 (TrEMBLrel. 12, Cr
Q1-NOV-1999 (TrEMBLrel. 16, Le
Q1-MAR-2001 (TrEMBLrel. 16, Le
VASCULAR ENDOTHELIAL GROWTH FR
                                                                                                                                                                                                                                           Signal.
                                                                                                                                                                                                                      CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                         PROSITE; PS00249; PDGF_1; PROSITE; PS50278; PDGF_2; SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                    Liu X., Yonekura H., Yamagishi S., Yamamoto Y., "Structure and expression of bovine VEGF family Submitted (MAY-1997) to the EMBL/GenBank/DDBJ de EMBL, AB004275; BAA77687.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                             InterPro; IPR000072; -
Pfam; PF00341; PDGF; 1
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
                                                                                                                                                                                                                                                                       SMART; SM00141;
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Bovinae; Bos.
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 178
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                                                                                                                                                      Local Similarity 37.7 hes 133; Conservative
                                                                            97
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                                                                                                                 EQQIRAASSLEELLRITHSEDWKLWRCRLRLKSFTSMDSRSASHRST----RFAATFYDI 96
                                                 EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHSTEQANTNIRTGETLKFAAAHYNT 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSIQIPEE
STSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPAALPQ-
                        STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAP--RHPYSIIRRSI--QIPEE
                                                                ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NISTNYISKTLFEITVPLSHGPKPVTVSFANHTSCRCMSKLDVYRQVHSIIRRSLP-ATQ
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Last annotation update)
FACTOR C PRECURSOR.
                                                                                                                                                                  Score 682.5; DB 6
Pred. No. 8.4e-56;
                                                                                                                                                                                                                      POTENTIAL.

VASCULAR ENDOTHELIAL GROWTH FACTOR
; 58BA84317A3C8E2D CRC64;
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                                                                                                                                                      Indels
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                                                                                                                                                                                420;
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Best Local Similarity 91.8%;
Matches 112; Conservative
                                                                                                                                                                                                    O35757 PRELIMINARY; PRT; 126 AA. 035757; 01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) VASCULAR ENDOTHELIAL GROWTH FACTOR-C (FRAGMENT).
SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-LUNG;
Mandriota S.J., Pepper M.S.;
Submitted (JUN-1997) to the EMBL/Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mandriota S.J., Pepper M.S.;
Submitted (OCT-1998) to the EM
EMBL; AF099135; AAG29747.1; -.
NON_TER 122 122
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
VASCULAR ENDOTHELIAL GROWTH
                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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Mammalia; Eutheria;
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122 AA;
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Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13820 MW;
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Last annotation update)
FACTOR-D (FRAGMENT).
       EMBL/GenBank/DDBJ
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Sciurognathi;
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actyla; Ruminantia;
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thi; Muridae; Murinae; Rat
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.6e-53;
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EMBL; 885192; AAC63102.1; -.
EMBL; S85224; AAC63101.1; -.
EMBL; S8529; AAC63101.1; JOINED.
EMBL; S85291; AAC63101.1; JOINED.
EMBL; S85219; AAC63101.1; JOINED.
EMBL; S85221; AAC63101.1; JOINED.
EMBL; S85222; AAC63101.1; JOINED.
EMBL; S85222; AAC63101.1; JOINED.
EMBL; S85222; AAC63101.1; JOINED.
EMBL; S8522; AAC63101.1; JOINED.
EMBL; S8522; AAC63101.1; JOINED.
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Q16889;
Q1-NOV-1996
Q1-NOV-1998
Q1-MAR-2001
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SEQUENCE
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Pfam; PF00341; PDGF; 1.
PROSITE; PS00249; PDGF_1;
PROSITE; PS50278; PDGF_2;
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PROSITE; PS50278; PDGF_2;
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of RNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92168017; PubMed=1791831; Houck K.A., Ferrara N., Winer J., Cachianes G., Li B., Leung D. "The vascular endothelial growth factor family: identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000072;
Pfam; PF00341; PDGF;
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[1]
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RASETMNFLL - - - -
                                                                  RAASSLEELLRITHSEDWKLWRCRLRLKSFTSMDSRSA-----SHRSTRFAATFYDI
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                                                                                                                                     70;
                                                                                                                                                                 Similarity
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   --SWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHH----
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                                                                                                                                 Score 204; DB
Pred. No. 2.5e
31; Mismatches
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Last annotation update)
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Catarrhini; Hominidae;
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No. 2.2e-19;
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.5e-11;
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Best Local S
Matches 60
                          077643;
01-NOV-1998 (
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01-MAR-2001 )
     VASCULAR
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Miura N., Misumi K., Kawahara K., Nakashima M., Fukumitsu S.,

Kawabata H., Uto N., Oka T., Maruyama I., Sakamoto H.;

"Cloning of cDNA and High-Level Expression of Equine Vascular

"Cloning of cDNA and High-Level Expression of Equine Vascular

Endotherial Growth Factor (VEGF).";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR 165.
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01-MAR-2001
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTAEFNITMQIMRIK-PHQS-QH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WVHWSLALLLYLHHAKWSQAAPMAEGEHKTHEVVKFMDV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRARQEKKSVRGKGKGQKRKRKKSRYKSWSVYVGARCCLMPWS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EESNITMQIMRIK-----PHQGQHIGEMSFLQHNKCECR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVVKFMD-VYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT 119
1998 (TrEMBLrel. 08, 1998 (TrEMBLrel. 08, 2001 (TrEMBLrel. 16, R ENDOTHELIAL GROWTH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22312 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.3%;
23.3%;
                    16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
Created)
Last sequence update)
Last annotation update
FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 203; DB Pred. No. 2.3e 29; Mismatches
                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         -PKKDKA-
                                                                                                                             190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6,
2.3e-11;
87;
                                                                                                                                                                                                                                                                                                                                                        CSERRKHLFVQDPQTCKC-SCKNTD
                                                                                                                          AΑ
                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----YQRSYCRPIETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PKK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LPGPHPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82;
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RESULT
060720
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P15692, 1VGH.
Interpro; IPRO00072; -.
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; -; 1.
PROSITE; PS00249; PDGF_1; 1
PROSITE; PS50278; PDGF_2; 1
SMART; SM00141; PDGF; 1.
SEQUENCE 190 AA; 22342 M
                                                                                                                                                                                                                                                                                                                                              060720
060720;
                                                                                                                                                                                                                                                                  01-AUG-1998 (TrembLrel. 07, Created)
01-MAY-1999 (TrembLrel. 10, Last sequence update)
01-MAR-2001 (TrembLrel. 16, Last annotation update)
VEGF183 PROTEIN PRECURSOR (VASCULAR ENDOTHELIAL GROWTH FACTOR 183)
(DJ261G23.6.6) (VASCULAR ENDOTHELIAL GROWTH FACTOR).
                                                                     Lei J. Jiang A., Pei D.;
Lei J. Jiang A., Pei D.;
"Identification and characterization of a new splicing variant
"ascular endothelial growth factor: VEGF183.";
vascular endothelial growth factor: Expr. 1443:400-406(1998).
            Jingjing L., Roque R.S.; Submitted (MAY-1998) to
                                        TISSUE=RETINA;
                                                      SEQUENCE OF 114-209 FROM N.A.
                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
                                                                                                                                     MEDLINE=99096474; PubMed=9878851;
                                                                                                                                                       TISSUE-KIDNEY;
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF071015; AAC23608.1; -. HSSP; P15692; 1VGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheung C.Y., Brace R.A.;
"Ovine vascular endothelial growth
expression in fetal tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=COLUMBIA-RAMBOULLIET;
                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth Factors 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                     145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSKKLCPIDMLWDSNKCKC-----VLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEFNITMQIMRIK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVMKFMD-VYQRSFCRPIETLVDIFQEYPDEIEFIFKPSCVPLMRCGGCCNDESLECVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                     -CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -NKCECRPKKDKARQENP---
                                                                                                                                                                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22342 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.2%;
            the
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            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                               Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -------PHQSQH-----IGEMSFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0D5E3B3E5C53E739 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201; DB 6;
No. 3.6e-11;
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                                                                                                                                                                                                                                                                                                                                                              209
                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                 Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66;
            databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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AC Q1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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Pfam; PP00341; PDGF; 1.
ProDom; PD001629; -: 1.
PROSITE; PS00249; PDGF_1; 1
PROSITE; PS50278; PDGF_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9HIW9 PRELIMINARY; PRT; 232 AA. Q9HIW9; 01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) 01-MAR-2001 (TREMBLREL ENDOTHELIAL GROWTH FACTOR).
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL136131; CAC19512.1; . . SEQUENCE 232 AA; 27042 MW; FB49F364446F4D01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-2000) to the EMEL; AJ010438; CAA09179.1; --
EMBL; AF062645; AAC16730.1; --
EMBL; AL136131; CAC19514.1; --
HSSP; P15692; 2VPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Williams S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Williams S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
213
                                                                                                 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
DRCSHSKKLCPIDMLWDSNK - -
                                                                                                                                                   EVVKEMD-VYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD
                                                                                                 STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
                                                                                                                                                                                                     ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EESNITMQIMRIK-----PHQGQHIGEMSFLQHNKCECR-----PKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVVKFMD-VYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT
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27
209
                                                                                                                                                                                                                                                       Conservative
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209 V
24422 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
                                                                                                                                                                                                                                                                                  10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVRGK--
                                                  -PHQGQHIGEMSFLQHNKCECR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>--</u> --
                                                                                                                                                                                                                                                          24;
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                                                                                                                                                                                                                                                       Score 200.5; DB 4;
Pred. No. 4.8e-11;
4; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
VEGF183 PROTEIN.
; F01CCEACD945D6CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 201;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GKGQKRKRKKSRPCGP
-CKCVLQEENPLAGTEDHSHLQEPALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                  -----PKK 134
                                                                                                                                                                                                                                                                                                         232;
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                                                                                                                                                                                                                                                       Gaps
258
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RESULT
042572
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AC 04
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Q9XSF3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                            042572 PRELIMINARY;
042572;
01-JAN-1998 (TrEMBLrel. 05, C
01-JAN-1998 (TrEMBLrel. 05, L
01-MAR-2001 (TrEMBLrel. 16, L
VASCULAR ENDOTHELIAL GROWTH F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jingjing L., Roque R.S.;
Submitted (MAR-1999) to the EMEMEL; AF133248; ADD29682.1; -.
HSSP; P15692; 1VGH.
InterPro: IPRO00072; -.
Pfam; PF00341; PDGF; 1.
PRODOM; PD001629; -; 1.
PROSITE; PS502749; PDGF_1; 1.
PROSITE; PS502749; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
           Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniat
Amphibia; Batrachia; Anura; Mesobatra
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Eukaryota; Metazoa; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9XSF3 PRELIMINARY; PRT; 190 AA.
Q9XSF3;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR 164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEGF.
                                                                                  VEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       145
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                                                                                                                                                                                                                                       CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD
                                                                                                                                                                                                                                                                 CKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE
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                                                                                                                                                                                                                                                                                                                       DRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECV
                                                                                                                                                                                                                                                                                                                                                                           STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEE 212
                                                                                                                                                                                                                                                                                                                                                                                                      EVVKFMD-VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPHMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRARQEKKSVRGKGKGQKRKRKKSRYKSWSVYVGARCCLMPWS-----LPGPHPC
                                                                                                                                                                                                                                                                                                                                                 EEFNITMQIMRIK-----PHQGQHIGEMSFLQHSKCECR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -CSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNERTCRCD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22292 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                          Mesobatrachia;
                                                                                              Last sequence update)
Last annotation updat
FACTOR 196.
                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 199; DB 6; Pred. No. 5.5e-11;
                                                      Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2053500BC9085CE0 CRC64;
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                                                                                                                                                                    194
                                                                                                                                                                    A
                                        Pipoidea;
                                                                                                            update)
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                                        Pipidae;
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SEQUENCE FROM N.A.

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Best Local S
Matches 57
                                                             Query Match
Best Local :
                                               Matches
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ProDom; PD001629; -; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
SEQUENCE 194 AA; 22672 MW;
                                                                                                                                                                                                                                                                                                           Chironomus thummi thummi (Midge).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q94446;
Q94446;
                                                                                                                   InterPro; IPR000561; -.
InterPro; IPR000853; -.
PRINTS; PR00876; MINEMATODE.
PROSITE; PS00002; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
SEQUENCE 1704 AA; 185745 MW; 3A3F20247C8F1E28 CRC64;
                                                                                                                                                                                                         TISSUE-SALIVARY GLAND; TISSUE-SALIVARY GLAND; Case S.T., Cox C., Bell W.C., Hoffman R.T., Martin J., Hamilton Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U54641; AAA99804.1; -.
                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TIEMBLIEL 02, 01-FEB-1997 (TIEMBLIEL 02, 01-OCT-2000 (TIEMBLIEL 15, 220 KDA SILK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF008594; AA:
HSSP; P15692; IVGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cleaver O., Tonissen Submitted (JUN-1997)
                                                                                                                                                                                                                                                                                                NCBI_TaxID=7155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000072; -.
109 TOCSPRETCVEVASELGKSTNTFFKPPCVNVFR-----CGGCCNEESLICMNTSTSYISK 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 C-SCKNTDSRCKTRQLEINERTCRCE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 CFECKESLETCCQKHKLFHPDTCSCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 VPLTSVPELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWD 229
                                            Local Similarity nes 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QCSPRETCVEVASELGKSTNIFFKAPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEIS 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHPKNCS 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHISQ--HIMDMSFQQHSQCECRP-----KKEVKSKQENHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAVLLYIPHAQ-----LSGAAPMPG-EGDHKPTEV----VKFLKV----YERS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCQVREILVDIFQEYPDEVEYIFKPSCVPLMRCAGCCNDESLECVPTECYNITMQIMKIK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
57; Conserv
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JUN-1997) to the EM
594; AAB63680.1; -.
                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                          10.1%;
21.7%;
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                                              42;
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e EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                          Score 198.5; DB 5;
Pred. No. 5.4e-10;
2; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 198.5; DB
Pred. No. 6.2e-11
4; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                              Indels 129;
                                                                         Length
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                                            Gaps
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                                                                                                                           287
                                                                                                                                                                                                                                                                                                  212
QTCPAGQSWDSQTCQCSCPATGKCTGAQFWCAKQCK 1392
                                         RPCASGKT--
                                                                                                                                                                                                                                                                                                                                        QIFDKNTCKCKCPNEKPGDSCGKGKDFCPVDCS----CKCKSPKPANGCP----GVQEWN 1177
                                                                                                                                                                                                                                                                                                                                                                                  QLFEISVPLTSVP-------ELVPVKVANHTGCKCLPTAPRHPYSIIRRSIQIPE 211
                                                                                                                         N-CSCFECKESLET--CCQKHKLFHPDTCSCEDR-----CPFH----
                                                                                                                                                                   KGCPGNQVWCENSCQCVCPKNMEKPADNCGNKWWNDKACECECKPGCPEAGCKGVQKWNK 1297
                                                                                                                                                                                                                                                    EDKCKCECPKDKSKTTCEGGQKWNDNQCQCGCPTPAPTCSASQKYSNVTCSCGCNPGMPA 1237
                                                                                                                                                                                                                                                                                              EDRC - - - - - SHSKKLCPIDMLWDSNKCKCVLQEENP-LAGTEDHSHLQEPALCGPHM - -
                                                                                 NTCAC-ECPPGKATPASCGDKKSWNPDSCSCQCKSKMPGGGCPSNQQWNCETCKCECSGT 1356
                                                                                                                                                                                                            -----KDLIQHPK 286
                                       --ACAKHCR 337
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Search completed: October 17, Job time: 422 sec 2001, 14:50:56

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Minimum DB seq
Maximum DB seq
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                        A_Geneseq_0601:*
1: /SIDSB/gcgdata,
2: /SIDSB/gcgdata,
3: /SIDSB/gcgdata,
4: /SIDSB/gcgdata,
5: /SIDSB/gcgdata,
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
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48.110 Million cell updates/sec
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Hullidii C. FOS Tuduce	#CC hTMWW	TO	040	20.9	4	ŀ
	7 7 I I I I I	10	200	90	2	
Human vascular end	AAB70685	22	354	98.9	463	10
Human VEGF-D. Hom	AAB37606	22	354	100.0	468	٠
Human VEGF-D1 prot	AAY97573	22	354	100.0	468	, α
Human vascular end	AAY70983	21	354	100.0	468	7
Human prepro-vascu	AAY70750	21	354	100.0	468	10
Human VEGF-D prote	AAB29049	21	354	100.0	468	. О
Human VEGD protein	AAB10649	21	354	100.0	468	4.
Human vascular end	AAW44293	19	354	100.0	468	· Lu
Homo sapiens vascu	AAW53241	19	354	100.0	468	N
Human zvegf2 growt	AAW49036	19	354	100.0	468	,
Description	ID	DB	Query Match Length DB	Query Match	Score	Result No.

45	44	43	42	41	40	39	38	37	36		3 4	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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21	14	16	20	22	22	21	21	21	21	21	20	20	20	19	19	18	18	18	18	20	19	18	19	18	20	20	22	19	19	18	19	19	19
AAG27882	AAR33180	AAR76076	AAY20148	AAB37605	AAY97570	AAY70982	AAY70749	AAY97144	AAB29048	AAB10648	AAW86203	AAY22320	AAY30518	AAW75740	AAW75751	AAW11478	AAW13833	AAW00932	AAW17837	AAW86237	AAW75742	AAW00933	AAW75743	AAW00934	AAY08286	AAY08287	AAY97572	AAW53240		AAW14992	AAW44295	AAW53242	AAW53243
idopsis thali	L3T4 mutant M1. S	pacteri	B. burgdorferi ant	Human VEGF-C. Hom			Human prepro-vascu	Vascular endotheli				Full length human	Vascular endotheli	Human vascular end	Vascular endotheli			Flt4 re	foetal	VEGF-C fu	e vascu	Œ	l vascu	Flt4 re	growth	ד			Rat vascular endot	Murine c-Fos induc	Mouse vascular end	Mus musculus vascu	Mus musculus vascu

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AAW49036
ID AAW4
                                                                  RESULT
                                                                 Region
                                                                                                                                                                                                      Human zvegf2 growth factor; mitogen; fibroblast; smooth muscle cell; venous stasis ulcer; diabetic ulcer; skin wound; chemotactic effect; anglogenic effect; tumour; diabetic retinopathy; psoriasis; arthritis;
WO9824811-A2.
                           Region
                                                                                      Region
                                                                                                         Binding-site
                                                                                                                                                           Key
                                                                                                                                                                                                scleroderma.
                                                                                                                                                                                                                                               Human zvegf2 growth factor.
                                                                                                                                                                                                                                                                                        AAW49036;
                                              Region
                                                                                                                           Peptide
                                                                                                                                                Peptide
                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                          AAW49036 standard; Protein;
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109..197
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206..256
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275..2
                                                                 /note= "C
257..274
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                           /note=
295..3
                                                                                                                                                Location/Qualifiers
1..23
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                            ...354
                                              ..294
                                    "Balbiani ring motif"
                                                       "Balbiani ring motif"
                                                                                              "Receptor binding domain"
                "Cysteine-rich domain""
                                                                            "Cysteine-rich domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a human zvegf2 growth factor encoded by the zvegf2 cDNA which was isolated from a human heart cDNA library. It is zvegf2 protein in a dimeric form acts as a mitogen for fibroblasts or smooth muscle cells. zvegf2 is claimed to be useful for stimulating the revascularisation of tissue or the re-endothelialisation of vascular tissue. zvefg2 is particularly claimed to be useful for the treatment of full-thickness skin wounds, including venous stasis ulcers and diabetic ulcers. The zvegf2 protein is also claimed to be useful as an additive in tissue adhesives for promoting revascularisation of the healing tissue. Antagonists against zvegf2 can be used to block its mitogenic, chemotactic and angiogenic effects. The antagonists may therefore be useful for reducing growth of solid tumours by inhibiting neovascularisation of the developing tumour or by directly blocking through the treatment of diabetic retinopathy, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 92
Homo sapiens
                            diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive airway disease; intestinal malabsorptive syndrome; blopsy; metastatic risdetection; diagnosis; congestive heart failure.
                                                                                          vascular endothelial growth factor; VEGF-D; angiogenesis; modification; acceleration; wound healing; tissue; organ; transplants; collateral circulation; infarction; arterial stenosis; coronary artery disease; inhibition; cancer; treatment;
                                                                                                                                                                      Homo sapiens vascular endothelial growth factor D (VEGF-D)
                                                                                                                                                                                                         03-AUG-1998
                                                                                                                                                                                                                                       AAW53241;
                                                                                                                                                                                                                                                                       AAW53241 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated vascular endothelial growth factor - used to develop products for treating e.g. wounds, burns, myocardial infarction, tumours, psoriasis, arthritis, restenosis or organ transplants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-1998
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06-DEC-1996;
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С
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96US-0759657.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 468; DB 19;
Pred. No. 8.3e-48;
; Mismatches 0;
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                                              metastatic risk;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        collateral circulation in tissue infarction or arterial stenosis, such as coronary artery disease, and inhibition of angiogenesis in the treatment of cancer or of diabetic retinopathy. It can also be used in the treatment of lung disorders to improve blood circulation in the lung and/or gaseous exchange between the lungs and the blood stream or to improve blood circulation to the heart and O2 gas permeability in cases of cardiac insufficiency, to improve blood flow and gaseous exchange in chronic obstructive airway disease, or to treat malabsorptive syndromes in the intestinal tract. Quantitation of VEGF-D in cancer biopsy specimens may be useful as an indicator of future metastatic risk. Antagonists can be used for treating or conditions such as concertive heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-1996;
23-AUG-1996;
11-NOV-1996;
                                                                        AAW44293
                                           AAW44293;
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 for treating e.g. conditions such as congestive heart failure, involving accumulations of fluid in the lung resulting from increases in vascular permeability. The products can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of human lung vascular endothelial growth factor D (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis in wound healing, tissue or organ transplantation, or to establish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16; Pages 60-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated vascular endothelial opposition for use in e.g. modifying heart or intestinal disorders
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10-FEB-1997;
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                                                                                                                                                                  61 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAAT
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                                                                                                                                                                                                            myrewvvvnvfmmlyvqlvqgssnehgpvkrssqstlerseqqiraassleellrithse 60
                                                                                                                                                                                                                            MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
                                                                                                                                                   dwklwrcrlrlksftsmdsrsashrstrfaat
                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                       354 AA;
                                                                                                                                                                                                                                                                         100.0%; ilarity 100.0%; Conservative
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96US-0031097.
97AU-0004954.
97US-0038814.
97AU-0007435.
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96AU-0001825.
96US-0023751.
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                                                                        Protein;
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Pred. No. 8.3e-48;
); Mismatches 0;
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lung,
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22-JUN-1998

(first entry)

Human vascular

endothelial growth factor D.

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RESULT
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Best Local :
                                                                              VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth; VEGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents human vascular endothelial growth factor D (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind the protein, may be useful in, e.g. gene therapy and in treatment of inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGF-D DNA sequences may be used for screening for the compounds which bind to the VEGF-D protein.
          29-JUN-2000
                                  WO200037641-A2
                                                                                                                                                                    Human VEGD protein.
                                                                                                                                                                                                                       AAB10649;
                                                                                                                                                                                                                                             AAB10649 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF-D protein encoded by DNA - useful for,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; vascular endothelial growth factor D; VEGF-D; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammation;
                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                         61 dwklwrcrlrlksftsmdsrsashrstrfaat 92
                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                      DWKLWRCRLRLKSFTSMDSRSASHRSTRFAAT 92
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV15156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 18-20; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oedema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nezu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96JP-0185216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-JP02456
                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 468; DB 19; 100.0%; Pred. No. 8.3e-48; tive 0; Mismatches 0;
                                                                                                                                                                                                                                              354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has CC vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and CC antidiabetic activity and acts as an angiogenesis and vascularization CC regulator. An antisense molecule of the invention is useful for treating CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic cetinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood CC vessels, growth and development of tissues, tissue regeneration and organ CC or preparing medicaments for treating wounds such as dermal ulcers, comparing the products of the invention are useful CC pressure sores, venous sores, diabetic ulcers and burns and to promote Skin graft growth, tissue repair, proliferation of new blood vessels, ctissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGD protein used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-DEC-1998;
18-MAR-1999;
08-NOV-1999;
                                            WO200058511-A1
                                                                                                        Milroy-Nonne syndrome;
vascular endothelial g
                                                                                                                                      Human; Flt4; fms-like tyrosine kinase 4; lymphoedema;
vascular endothelial growth factor receptor 3; VEGFR-
                                                                                                                                                                                      Human
                                                                                                                                                                                                                                                                                   AAB29049 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds - \frac{1}{2}
                                                                         Homo sapiens.
                                                                                                                                                                                                                     31-JAN-2001
                                                                                                                                                                                                                                                    AAB29049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 11; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gordon RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JANC ) JANSSEN PHARM NV
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                                                                                                                                                                                                                                                                                                                                                                               61 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAAT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MYREWVVVNVEMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
                                                                                                                                                                                                                                                                                                                                                                                                                           1 myrewvvvnvfmmlyvqlvqgssnehgpvkrssqstlerseqqiraassleellrithse
                                                                                                                                                                                                                                                                                                                 G
                                                                                                                                                                                                                                                                                                                                                                dwklwrcrlrlksftsmdsrsashrstrfaat 92
                                                                                                                                                                                      VEGF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SN,
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I, Xu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                      protein sequence.
                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98GB-0028377
99US-0124967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0164131
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                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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JJ,
                                                                                                        lymphoedema praecox; VEGF-D;
rowth factor D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yon
                                                                                                                                                                                                                                                                            354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 468; DB 21;
Pred. No. 8.3e-48;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dijkmans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JJH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gosiewska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                          09-OCT-1998;
                                                                                                                                                                          Human; receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase; VEGFR-3; vascular endothelial growth factor receptor 3; Chromosome 5q; cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis; neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the protein sequence of the human vascular endothelial growth factor D (VEGF-D). It was used to demonstrate the methods of the invention, which involve the screening of individuals to determine which vascular endothelial growth factor receptor 3 (VEGFR-3, also known as Flt4 or fms-like tyrosine kinase 4) alleles they possess and thus their likelihood of developing hereditary lymphoedema. Conditions associated with lymphoedema include Milroy-Nonne syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening a human subject for increased risk of developing a disorder, comprises assaying a nucleic acid to determine a muraltering the sequence of a vascular endothelial growth factor receptor-3 -
(LUDW-) LUDWIG
                                                    08-OCT-1999;
                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                             Human prepro-vascular endothelial growth factor D.
                                                                                                                                                                                                                                                                                                                              AAY70750 standard;
                                                                               20-APR-2000
                                                                                                          WO200021560-A1
                                                                                                                                                                                                                                                                         17-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING (UYPI-) UNIV PITTSBURGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferrell RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
                                                                                                                                                                                                                                                                                                                                                                                               dwklwrcrlrlksftsmdsrsashrstrfaat 92
                                                                                                                                                                                                                                                                                                                                                                                                                        DWKLWRCRLRLKSFTSMDSRSASHRSTRFAAT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                  myrewvvvnvfmmlyvqlvqgssnehgpvkrssqstlerseqqiraassleellrithse 60
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                                                                                                                                                               malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 64-65; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alitalo K,
INST CANCER RES
                        98US-0169079
                                                    99WO-US23525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                onset lymphoedema and lymphoedema praecox, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US06133
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                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                               VEGF-D; vascular endothelial growth factor D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Finegold DN,
                                                                                                                                                                                                                                                                                                                              354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 468; DB 21;
Pred. No. 8.3e-48;
O. Mismatches 0;
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                                                                                                                                                                                                                                                                                                                              AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a lymphatic mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                           melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                     5q35;
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RESULT
AAY70983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ligand to Fild thereby inhibiting Filt4 mediated proliferation of vascular cendothelial cells. The compound is useful for treating neoplastic disease such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas and sarcomas. Filt4 receptor tyrosine kinase binding compounds can be used for manufacturing medicament useful for diagnostic screening, imaging and treatment of malignancles characterised by Filt4-expressing blood cells. The Filt4 gene maps to chromosomal region 5935 and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in their 3' sequences and are differentially expressed in HEL and DAMI cell lines. Filt4 delights a subfamily of class III receptor tyrosine kinases (RTKs). It is used as a target for tumour imaging and anti-tumour therapy. The present sequence is a human prepro-vascular endothelial growth factor D (VEGF-D), a specific example of Filt4 binding compound. A recombinantly matured VEGF-D lacking residues 1-92 and 202-354 retains the ability to activate VEGFR-3 and VEGFR-3 receptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 92
                                                                                                                                                                               Vascular endothelial growth factor-D; VEGF; human; re-endothelialisation; vascular endothelial growth factor receptor; VEGFR; vascular trauma; blood vessel; cardiovascular surgery; anti-restenosis agent; prevention:
Peptide
                                                                       Peptide
                                                                                                                                                                                                                                                           Human vascular
                                                                                                                                                                                                                                                                                            09-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                  AAY70983 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      referred as vascular endothelial growth factor receptor-3, VEGFR-3 endothelial cells of blood vessels adjacent to malignant neoplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating neoplastic diseases such as lymphoma, carcinomas, melanomas and sarcomas, involves administering a compound capable of inhibiting binding of ligand proteins to fms-like tyrosine kinase-4 receptor -
                                                                                                                          Homo sapiens
                                                                                                                                                                  restenosis; stenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method involves administering a compound that inhibits binding of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The patent discloses a method to treat neoplastic disease characterised by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYHE-) UNIV HELSINKI LICENSING LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DWKLWRCRLRLKSFTSMDSRSASHRSTRFAAT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myrewvvvnvfmmlyvqlvqgssnehgpvkrssqstlerseqqiraassleellrithse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-17; Page 142-143; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as non-covalently linked dimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                              cardiovascular surgery; anti-restenosis ag
tenosis; percutaneous transluminal coronary
                                                                                                                                                                                                                                                       endothelial growth factor (VEGF)-D protein.
 protein"
22..92
                                 /label= Signal_peptide
/note= "Cleavage results
                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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Pred. No. 8.3e-48;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                    AA
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                                 in
                                 partially-processed VEGF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                               AAY97573
                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                              The present amino acid sequence is the complete human prepro-vascular endothelial growth factor (VEGF)-D. VEGF-D has the ability to stimulate re-endothelialisation of an injured blood vessel, without significant stimulation of smooth muscle cell proliferation. It can bind to and stimulate VEGFR-2 (vascular endothelial growth factor receptor) and/or VEGFR-3 phosphorylation in cells that express such receptors. An anti-restenosis agent comprising either a VEGF-D gene or protein is used in a method to reduce or prevent restenosis and stenosis of a blood vessel following vascular trauma e.g., cardiovascular surgery and percutaneous transluminal coronary angioplasty.
            Human; angiogenic protein; wound healing; vascular tissue repair;
peripheral arterial disease; critical limb ischaemia; coronary di
                                                    Human VEGF-D1
                                                                              05-APR-2001
                                                                                                                                 AAY97573 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preventing stenosis and restenosis in mammals using vascular endothelial growth factor proteins or the nucleic acids encoding % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYHE-)
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                                                                                                                                                                                                                                                 MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
                                                                                                                                                                                                 dwklwrcrlrlksftsmdsrsashrstrfaat
                                                                                                                                                                                                                           DWKLWRCRLRLKSFTSMDSRSASHRSTRFAAT 92
                                                                                                                                                                                                                                                                                                          l Similarity
92; Conser
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YLA-HERTTUALA S.
                                                                                                                                                                                                                                                                                                                                                                           354 AA;
                                                                                                                                                                                                                                                                                                          Conservative
                                                                              (first entry)
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                                                   protein sequence
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/note= "Processed vascular epithelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Carboxy_terminal_peptide
/note= "Cleavage results in partially-processed VEGF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Amino_terminal_peptide
/note= "Cleavage results in fully-processed mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alitalo
                                                                                                                                                                                                                                                                                                                    100.0%;
inflammation; diabetic retinopathy;
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                                                                                                                                 354
                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                       Score 468; DB 21;
Pred. No. 8.3e-48;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English:
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             disease;
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RESULT
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AC AAB3
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                                                                                                                                                                                                                                                                                                                                                                    CC ameliorate disease and to detect diseases, or succeptibility, by detecting mutations or the presence or amount of angiogenic protein cc expression. Particularly they are used to stimulate wound healing, CC growth of damaged bone and tissue, and for repair of vascular tissue, CC especially peripheral arterial disease, critical limb ischaemia or CC coronary disease. Antagonists of the sequences are used to inhibit any coronary disease in tumours and to treat inflammation (where associated with CC increased vascular permeability), diabetic retinopathy, rheumatoid CC arthitis or psoriasis. Agonists are also useful for stimulating CC (lymph)angiogenesis. The proteins are also useful for stimulating CC (lymph)angiogenesis. The proteins are also useful for raise antibodies. The antibodies are useful as therapeutic agents) and to raise antibodies. CC The antibodies are useful as therapeutic (ant)agonists; for detection, CC purification and targeting of proteins for in vivo or in vitro diagnosis (c including imaging) or for therapy (including when linked to e.g. a label CC or cytotoxin); and for immunotyping of cells, e.g. for detecting minimal CC reseases or haematopoietic progenitor/stem cells. It is also CC contemplated that the sequences might be useful for treating a very wide range of other disorders, e.g. autoimmne diseases; allergy; cancer; infectious diseases (viral, bacterial, fungal or parasitic); recentration, of the norvous system atc.
                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                            Matches
   AAB37606;
                                     AAB37606 standard; Protein; 354 AA
                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is vascular endothelial growth factor-D1 (VEGF-D1), which is an angiogenic protein of the invention. The angiogenic pand the DNA sequences encoding them, are used to prevent, treat c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 228-229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  critical limb ischaemia or coronary disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding angiogenic proteins, useful e.g. for promoting healing of wounds and treating peripheral arterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAA91007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infectious disease; meurodegeneration
                                                                                                                                                                61
                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                61
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                                                                                                                                                                                              MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-071057/08
                                                                                                                                                                DWKLWRCRLRLKSFTSMDSRSASHRSTRFAAT 92
                                                                                                                                                                                                                                                                                                                                                                   354 AA;
                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     nervous system
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                                                                                                                                                                                                                                                                            0;
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Pred. No. 8.3e-48;
0; Mismatches 0;
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RESULT 10
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                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                          Matches
AAB70685;
                             AAB70685 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening a human for an increased risk of developing lymphatic disorder comprises assaying nucleic acid for alterations in the sequences expressing vascular endothelial growth factor receptor-3
                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Pages 66-67; 99pp; English
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(UYHE-) UNIV HELSINKI LICENSING
(LUDW-) LUDWIG INST CANCER RES.
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16-AUG-1999;
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                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                          61 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAAT
                                                                                                                                                                           <u>بـــ</u>
                                                                                                                                                                                        1 MYREWVVVNVEMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
                                                                                                          dwklwrcrlrlksftsmdsrsashrstrfaat
                                                                                                                                                                        myrewvvvnvfmmlyvqlvqgssnehgpvkrssqstlerseqqiraassleellrithse 60
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                                                                                                                                                                                                                                                                                                                       354 AA;
                                                                                                                                                                                                                                          Conservative
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99US-0375248.
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                            protein;
                                                                                                                                                                                                                                                      100.0%;
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                               354
                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                     Score 468; DB 22;
Pred. No. 8.3e-48;
A. Mismatches 0;
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RESULT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for inducing angiogenesis in a tissue, or area, in need of angiogenesis, in a mammal. The method comprises administering recombinant vascular endothelial growth factor D (VEGF-D) or its angiogenically active fragment or mutant (I). The present sequence represents the human VEGF-D protein, which can be used in the method of the invention. (I) has cardiant and vasotropic activities, and is an angiogenesis inducer. The method can be used for inducing angiogenesis in a tissue in need of angiogenesis, or in an area in need of angiogenesis in a mammal. (I) is useful for treating various is chaemic conditions manifested by vascular insufficiency such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             angiogenesis; c:fos induced growth factor D; VEGF-D; angiog ischaemic condition; ischaemia; vascular insufficiency; peripheral vascular disease; coronary artery disease; myocardial infarction.
c-Fos induced frowth factor; FIGF; Fos regulated gene;
                              Human c-Fos induced growth factor (clone HF175 ORF2 product).
                                                               05-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of recombinant vascular endothelial growth factor or its unjudgenically active fragment or mutant, for inducing angiogenes vivo or in vitro and for treating myocardial infarction, coronary artery disease
                                                                                                                            AAW14994 standard;
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          peripheral vascular disease, coronary artery disease or myocardial
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                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                              354 AA;
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                             (first entry)
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                                                                                                                            Protein;
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98.9%;
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                                                                                                                                                                                                                                                                                                                                               Score 463; DB 22; Pred. No. 3.3e-47;
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                                                                                                                                                                                                                                                                                                                                                             Length 354;
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Misc-difference
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antibody; transgenic animal.
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/note=
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/note=
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       "residue 592 corresponds to an stop codon in reading frame 2
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                                            "residue 579
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                                                                                                                                "residue 553
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                                                                                                                                                         "residue 541 corresponds
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AAW53243 ID AAW5

AAW53243 standard; Protein; 321 AA

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61 DWKLWRCRLRLKSFTSMDSRSASHRSTRFAAT 92

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 Polypeptide sequences (AAW1493-95) are the respective translated sequences of reading frames 1, 2 and 3 of clone HF175 (AAT62961), the human homologue of murine clone F0401 (AAT62960), which codes for a novel c-Fos induced growth factor (FIGF) (see also AAW14992). Examination of the 3 polypeptides indicates that reading frame 2 has the longest region free of nonsense codons. FIGF is a c-fos-dependent autocrine growth factor able to induce cell division entry and, when over-expressed, a transformed phenotype in
                                                                                                                                                                                                                                                                                                                       Recombinant FIGF can be produced in tumours and development. Recombinant FIGF can be produced in transformed host (e.g. CHO) cells. It can be used to identify its receptors and in an assay for the identification of agonists and antagonists. Antibodies raised against FIGF can be used to block the function of the protein and thereby inhibit or suppress tumour growth. Transgen animals expressing FIGF can be generated for use e.g. as models
                                                                                                                                                                                                                                                Sequence
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29-SEP-1995;
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03-AUG-1998

(first entry)

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Query Match
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10-FEB-1997;
19-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         flow and gaseous exchange in chronic obstructive airway disease, or to treat malabsorptive syndromes in the intestinal tract. Quantitation of VEGF-D in cancer biopsy specimens may be useful as an indicator of future metastatic risk. Antagonists can be used for treating e.g. conditions such as congestive heart failure, involving accumulations of fluid in the lung resulting from increases in vascular permeability. The products can also be used for account of the congestive heart failure increases in vascular permeability.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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23-AUG-1996;
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                                                                                                                                                                                                                                                                                             Local Similarity
nes 73; Conserv
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                                                                                                                                                      \vdash
                                                            MYREWVVVNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE 60
mygewgmgnilmmfhvylvqgfrsehgpvkrssrsmlerseqqiraassleellqiahse 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96AU-0003554.
96US-0031097.
97AU-0004954.
97US-0038814.
97AU-0007435.
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96US-0023751
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                                                                                                                                                                                                                                                                                                                                                         79.7%;
79.3%;
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                                                                                                                                                                                                                                                                                                                                                 Score 373;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                         DB 19;
.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 321;
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RESULT 13
AAW53242
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collateral circulation in tissue infarction or arterial stenosis,
couch as coronary artery disease, and inhibition of angiogenesis in
the treatment of cancer or of diabetic retinopathy. It can also be
used in the treatment of lung disorders to improve blood circulation
in the lung and/or gaseous exchange between the lungs and the blood
stream or to improve blood circulation to the heart and O2 gas
permeability in cases of cardiac insufficiency, to improve blood
flow and gaseous exchange in chronic obstructive airway disease,
or to treat malabsorptive syndromes in the intestinal tract.
Quantitation of FUGF-D in cancer biopsy specimens may be useful
for treating e.g. conditions such as congestive heart failure,
involving accumulations of fluid in the lung resulting from
increases in vascular permeability. The products can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1997;
23-AUG-1996;
23-AUG-1996;
                                                                                                                                                                                                                                                                     The sequence is that of mouse lung vascular endothelial growth factor D1 (VEGF-D1). VEGF-D1 can be used for e.g. acceleration of angiogenesis in wound healing, tissue or organ transplantation, or to establish
                                                                                                                                                                                                                                                                                                                                                                                      New isolated vascular endothelial growth factor-D - used to products for use in e.g. modifying angiogenesis or treating heart or intestinal disorders \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modification; acceleration; wound healing; tissue; organ; transplants; collateral circulation; infarction; arterial s coronary artery disease; inhibition; cancer; treatment; diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive airway disease; intestinal malabsorptive syndrome; blopsy; metastatic risk; intestinal malabsorptive syndrome; blopsy; metastatic risk;
                                                                                                                                                                                                                                                                                                                                                  Claim 16; Pages 63-64; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-179057/16.
N-PSDB; AAV20808.
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10-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection; diagnosis; congestive heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9807832-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vascular endothelial growth factor; VEGF-D; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus vascular endothelial growth factor D1 (VEGF-D1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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96US-0023751.
96AU-0003554.
96AU-031097.
97AU-0004954.
97AU-0007435.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stacker SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilks AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stenosis;
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Best Local S
Matches 73
                                                                               Matches
                                                                                                   Query Match
                                                                                          Best
                                                                                                                                    Sequence
                                                                                                                                                                   D (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind the protein, may be useful in, e.g. gene therapy and in treatment of inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGF-D DNA sequences may be used for screening for the compounds which bind to
                                                                                                                                                                                                      The present sequence represents mouse vascular endothelial growth factor D (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind
                                                                                                                                                                                                                                       Example 7; Page 32-35;
                                                                                                                                                                                                                                                            VEGF-D protein encoded by DNA - useful for, e.g. gene therapy treating oedema \,
                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; vascular endothelial growth factor D; VEGF-D; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW44295;
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                                                                                                                                                                                                                                                                                                                                                     (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammation;
56 ITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 73; Conserv
                                   \vdash
                                             1 MYREWVVVNVEMMLYVQLVQGSSNEHGPVK-----RSSQSTLERSEQQIRAASSLEELLR 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MYREWVVNVFMMLYVQLVQGSSNEHGPVK----RSSQSTLERSEQQIRAASSLEELLR 55
                                  mygewgmgnilmmfhvylvqgfrsehgpvkdfsferssrsmlerseqqiraassleellq 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFAAT
                                                                                         Similarity
                                                                                                                                                                                                                                                                                              AAV15177
                                                                                                                                                                                                                                                                                                                               Nezu J;
                                                                                                                                      358
                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358
                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oedema
                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                           96JP-0185216.
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75.3%;
                                                                                          77.0%;
75.3%;
                                                                                                                                                                                                                                    52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358
                                                                                         Score 360.5; DB : Pred. No. 5.6e-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 360.5;
Pred. No. 5.
                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6e-35;
                                                                                                   DB 19;
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                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                   Length
                                                                                                     358;
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RESULT 1
AAW14992
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AC AAW1
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                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                 Novel murine c-Fos induced growth factor (FIGF) (AAW14992) shows homology to the growth factor VEGF. It is encoded by the F0401 gene (AAT62960) obtd. from mouse fibroblast cells. FIGF is a c-fos-dependent autocrine growth factor able to induce cell division entry and, when over-expressed, a transformed phenotype in fibroblasts. It could be implicated in tumours and development. Recombinant FIGF can be produced in transformed host (e.g. CHO) cells. It can be used to identify its receptors and in an assay for the identification of agonists and antagonists. Antibodies raised against FIGF can be used to block the function of the protein and thereby inhibit or suppress tumour growth. Transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide molecule encoding c-Fos induced growth factor protein useful in therapy, in manufacture of compositions for treatment developmental disorders and in generation of transgenic animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c-Fos induced frowth factor; FIGF; Fos proto-oncogene; lung disorder; cancer; antibody; transgenic animal.
                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                      animals expressing FIGF can be generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 1; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT62960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oliviero
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                                                                                                                                                                                                                                                        research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-226216/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUN-1996;
29-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine c-Fos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW14992 standard; Protein; 358
61
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                                                              mygewgmgnilmmfhvylvqgfrsehgpvkdfsferssrsmlerseqqiraassleellq 60
                              ITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFAAT
                                                                                MYREWVVVNVFMMLYVQLVQGSSNEHGPVK-----RSSQSTLERSEQQIRAASSLEELLR 55
                                                                                                                                  l Similarity
72; Conserv
                                                                                                                                                                                                                    358 AA;
                                                                                                                                    Conservative
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95GB-0019928.
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74.2%;
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Pred. No. 1.7e-34;
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Search completed: October 17, 2001, 14:46:03 Job time: 129 sec

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Maximum Match 100%
Listing first 45 summaries
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3: /cgn2_6/ptodata/2
4: /cgn2_6/ptodata/2
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
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PCT-US96-09001-2
US-08-95-734-2
US-08-444-623-2
US-08-4471-869-2
PCT-US94-08267-2
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	Sequence 8, Appli Sequence 7, Appli Sequence 7, Appli Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 16, Appl Sequence 16, Appl Sequence 2, Appli Sequence 2, Appli Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 68, Appl Sequence 68, Appl Sequence 68, Appl Sequence 68, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli	

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US-08-915-795-5
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                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANG, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                              TELEX: N/A INFORMATION FOR SEQ ID NO:
ORIGINAL SOURCE: TISSUE TYPE:
                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                   MOLECULE TYPE: PI
                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSEE: Evenson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: KAT1 ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                              TELEPHONE:
                                                                       TOPOLOGY:
                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20005
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                                                                                                                                                                                                : (202) 628-8800
(202) 628-8844
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                                                                    ss: single
linear
Human Lung
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Score 468; DB 4; Pred. No. 9.8e-52;

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RESULT 3
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US-08-915-795-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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CITY: Washington
                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                         DWKLWRCRLRLKSFTSMDSRSASHRSTRFAAT 92
                                                                                                                                     MYGEWGMGNILMMFHVYLVQGFRSEHGPVKRSSRSMLERSEQQIRAASSLEELLQIAHSE 60
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1200 G Street, NW., Suite 700
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                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andrew F. WILKS
Steven A. STACKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marc G.
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79.3%;
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                                                                                                                                                                                                      Score 373; DB 4; Length 321; Pred. No. 1.1e-39; Mismatches 12; Indels
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                                                                                                                                                                                    Sequence 3, Application US/08915795 Patent No. 6235713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                GENERAL INFORMATION:
APPLICANT: MATC G. ACHEN
APPLICANT: ANDREW F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: KATI ALITALO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 628-884
TELEX: N/A
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 1064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                TITLE OF INVENTION: GH
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
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MEDIUM TYPE: Floppy
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APPLICANT: ANDTHEW F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: KARI ALITALO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GROWTH FACTOR
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STREET: 1200 G St:
CITY: Washington
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                                                                                                                                                                                                                                                                                                           56 ITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFAAT 92
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OPERATING SYSTEM: PC-DOS/MS-DOS
                 STREET:
                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                         61 IAHSEDWKLWRCRLKLKSLASMDSRSASHRSTRFAAT
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
mes 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                               1 MYREWVVVNVFMMLYYQLVQGSSNEHGPVK-----RSSQSTLERSEQQIRAASSLEELLR 55
                                                                                                                                                                                                                                                                                                                                                             1 MYGEWGMGNILMMFHVYLVQGFRSEHGPVKDFSFERSSRSMLERSEQQIRAASSLEELLQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                3: Evenson, McKeown, Edwards & Lenahan P.L.L.C. 1200 G Street, NW, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                              77.0%;
75.3%;
                                                                  GROWTH FACTOR: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 360.5;
Pred. No. 5e
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                                                                                                                                                                                                                                                                                                                                                                                                                                               5e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy disk

COUNTRY:

United States of America

20005 R

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                                                                                                                                                                                                                                                                                                                                                                                                               US-08-795-430-13
                                                                                                                                                                                                                                                                                                                                                                         sequence 13, Application US/08795430 Patent No. 6130071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: N/A
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/795,430
                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                              APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladdmir
TITLE OF INVENTION: Vascular
TITLE OF INVENTION: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: a....
STRANDEDNESS: SING
CLASSIFICATION: 435
                                                                                                                                                                COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                FILING DATE:
                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 RSSQSTLERSEQQIRAASSLEELLRITHSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFA 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 628-8844
TELEFAX: (202) 628-8844
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Too
STREET: 6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 AT 92
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                                                                                                                                                                                                                Chicago
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                                                                                                                                                                                                                                                                               Vascular Endothelial Growth Factor C (VEGF-C) Protein and Gene, Mutants Thereof, and Uses T 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.0%;
                                                                                                                                                                                                                               O'Toole,
fower, 233
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South Wacker Drive
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RESULT 6
US-08-795-430-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
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APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 01-AUG-1996
                                                                                                                                                           COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 01-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3
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                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                              CITY: Chicago
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TOPOLOGY: linear
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                                                                                                                                                                                                                            Illinois
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                                                                                                                                                                                                                                                                                                                         Vascular Endothelial Growth Factor C (VEGF-C)
Protein and Gene, Mutants Thereof, and Uses Thereof
                  PCT/FI96/00427
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South Wack
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Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 418
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PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

FILING DATE: APPLICATION NUMBER:

28-JUN-1996

APPLICATION NUMBER:

14-FEB-1996

08/601,132

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US-08-999-811-2
; Sequence 2, A
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: VA
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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LENGTH: 415 amino acid
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APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/207,550 FILING DATE: 8-MAR-1994
                                                 CLASSIFICATION:
                                                                  FILING DATE:
                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 GEVKAFEGKDL---EEQLRSVSSVDELMSVLYPDYWKMYKCQLRKGGWQQPTLNTRTGDS 102
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                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 GPVKRSSQSTLERSEQQIRAASSLEELLRITHSEDWKLWRCRLRLKSFTSMDSRSASHRS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                            WASHINGTON
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ROSEN, CRAIG A.
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                                                                  HEREWITH
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01-AUG-1995
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12-JAN-1996
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                                                                               us/08/999,811
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Pred. No. 0.00091;
"" wismatches 25;
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Best Local Similarity 31.6
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REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN 6 FOX
STREET: 1100 NEW YORK AVENUE
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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OR OBJECT OF THE PRIOR OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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NAME: MARKOWICZ, KAREN F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                   APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1995
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(702)371-2540
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INFORMATION FOR SEQ ID NO:

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SEQUENCE CHARACTERISTICS

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MOLECULE TYPE: -09-042-105-18
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Best Local Similarity
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                                                                                       TELEFAX: (202)371-2540
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                         REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                         CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/465,968
APPLICATION EN 06-JUN-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: FLOPPY DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.30
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APPLICANT:
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NAME: ERIC K. STEFFE
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                            TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 24-DE
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US FILING DATE: 8-MAR-1994
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                              TOPOLOGY:
                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                              419 amino acids
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ROSEN, CRAIG A.
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31.6%;
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                                                                                                                                                                                                                                                                           TO BE ASSIGNED
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                                                                                                                                                                                          36,688
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                                                                                                                                                                            1488.1000003/EKS
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; TOPOLOGY: 1i; MOLECULE TYPE: US-08-795-430-8
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Patent No. 6130071
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/671
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               FILING DATE: 12-JAN-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                   TELEFAX: JI.,
TELEFAX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/
FTT.ING DATE: 01-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                               NAME: Gass, David A REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 EQQIRAASSLEELLRITHSEDWKLWRCRLRL-----KSFTSMDSRSASHRSTRFAA 91
                                                                                                                                              TELEPHONE:
                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAA 111
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                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60606-6402
                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08795430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Illinois
                                                           419 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Marshall, O'Toole, 6300 Sears Tower, 233
                                                                                                                                312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                      14-NOV-1994
             protein
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31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein and Gene, Mutants Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vascular Endothelial Growth Factor C (VEGF-C)
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                                                                                                                                                                             28967/33691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerstein, Murray & Borun
South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.30
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Query Match Best Local Similarity Thes 18; Conserve

Conservative

19;

Mismatches

12;

Indels

8

Gaps

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19.2%;

Score 90; DB 4; Length 419; Pred. No. 0.0019;

41

EQQIRAASSLEELLRITHSEDWKLWRCRLRL-----KSFTSMDSRSASHRSTRFAA

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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-08-510-133A-35
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                                                                                                                                                                                                                  Sequence 2, Application PC/TUS9609001 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  Màtches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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            STREET: 0 L-
STREET: NOSELAND
CTATE: NEW JERSEY
TISA
                                                                                                                                    TITLE OF INVENTION: Human Vascular EndothelialGrowth Factor 2 NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                  APPLICANT:
                                                                                             ADDRESSEE:
COUNTRY: UZIP: 07068
                                                                                                                                                                                                                                                                                                                                  57 EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAA 111
                                                                                                                                                                                                                                                                                                                                                                         41 EQQIRAASSLEELLRITHSEDWKLWRCRLRL-----KSFTSMDSRSASHRSTRFAA 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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Joukov, Vladomir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Receptor Ligand NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSR--TEETIKFAA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/510,133A FILING DATE: 01-Aug-1995 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States of America ZIP: 60606-6402
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 419 amino acids
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                                                                       6 BECKER FARM ROAD
                                                                                                                                                                                              HU, ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                             CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6300 Sears Tower,
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31.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.0019;
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Best Local :
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/465
FILING DATE: 6 JUN 95
APPLICATION NUMBER: 08/207
FILING DATE: 8 MAR 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
                                              APPLICATION NUMBER: US/08/095,734
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REGERENCY/COURTER 32,227
                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ANDITCATION NUMBER: UR /08/005 724
                                                                                                                                                                                                                               ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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LENGTH: 419 AMINO ACIDS
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MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Hamilion Drive
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                                     REFERENCE/DOCKET NUMBER:
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nes 18; Conserv
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 TELEPHONE:
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WORD PERFECT 5.1
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617-861-6240
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                                                                                                                                                                                                                                                                                                                                                                                                                 Homologously Recombinant Slow Growing Mycobacteria and Uses Therefor
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US-08-444-623-2
; Sequence 2, Application US/08444623
; Patent No. 5866403
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US-08-095-734-2
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-JUL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 130
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              NAME: Granahan, Patricia REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0; Version #1.25
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STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                APPLICATION NUMBER: 07/10
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WHI93-11MZ
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Pred. No.
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Best Local
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US94/08267
FILING DATE: 22-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/095,734
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,334
FILING DATE: 06-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Aldovi
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APPLICATION NUMBER: I
FILING DATE: 18-JUN-
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                               APPLICATION NUMBER: US 0 FILING DATE: 05-JUN-1989
                                                                                                                                APPLICATION NUMBER: PCT/US89/02962 FILING DATE: 07-JUL-1989
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nes 16; Conserv
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STRANDEDNESS: si
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19-JUN-1989
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                               JMBER: US 07/223,089
22-JUL-1988
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US 07/216,390
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Pred. No.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen
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submitted to the EMBL Data Library,
A; Reference number: H01557
A; Accession: G02659
A; Status: preliminary; translated fi
A;Cross-references: GDB:3890883; OMIM:601528 F;1-12/Domain: signal sequence #status predicted F;13-102/Domain: propeptide #status predicted <PF
                                                                                 A;Cross-references: EMBL:U58111; NID:g1373426; PIDN:AAB02909.1; PID:g1373427 C;Genetics:
                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 'X',104-120 <JOUZ>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein
A;Reference number: S69208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vascular endothelial growth factor C precursor - human
N;Alternate names: FLT4 ligand DHM
C;Species: HOmo sapiens (man)
C;Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 08-Oct-1999
C;Accession: S69207; S61795; S71443; S69208; G02659
R,JOukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel
EMBO J. 15, 1751, 1996
A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand
A;Reference number: S69207; MUID:96203094
A;Accession: S69207
                                                                 A; Gene: GDB: VEGFC; VRP
                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-419 < MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:JONKOV, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtii EMBO J. 15, 290-298, 1996 A;Title: A novel vascular endothelial growth factor, VEGF-C, A;Reference number: S61795; MUID:96178224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X94216; NID:g1177488; PIDN:CAA63907.1; PID:e221096; PID:g118 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995 A;Note: only a part of the translation is shown
A;Note: this is a revision to the sequence from reference S61795
B;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel
                                                                                                                                                                                                                                             A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989
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A; Residues: 1-419 <LEE>
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A; Residues: 70-419 <JOUL>
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A; Residues: 1-419 < JOU>
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Score

Match Query

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S64540

A32495 B71405 JC4019

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Minimum DB Maximum DB

seq length: 0 seq length: 2000000000

Total number of

Searched

219241 seqs,

Post-processing: Minimum Match 0%
Maximum Match 10

Listing

Match 100% first 45 summaries

Database

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Title: Perfect score:

US-09-427-657-4_COPY_1_92 468

MYREWVVVNVFMMLYVQLVQ...

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 ,

Gapext 0.

Run

on:

OM protein - protein search, using sw model

October 17,

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probable calcium channel protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein R8501; protein YGR217w
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 23-Mar-2001
C;Accession: $64540; $64541; $57680; $63896
R;Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
A:Experimental source: strain S288C
R;van der Aart, Q.J.M.; Kleine, K.; Steensma, H.Y.
submitted to the EMBL Data Library, June 1995
A;Description: Sequence analysis of the 43 KB CRM1-YLM9-PET54-SMI1-PH081-YHB4-PFK1 regic
A;Reference number: S57680
A;Accession: S57680
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                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-1359 <RIE>
A; Cross-references: EMBL: Z73002; MIPS: YGR217w
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                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1184-2039 <VAN>
                                                                                                                                                                                                   A; Accession: S64541
                                                                                                                                                                                                                   A; Reference number: S64541
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A; Accession: T48839
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Pred. No. 0.
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F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>
A;Cross-references: GB:M23021; NID:g511859; PIDN:AAA46565.1; C;Superfamily: potato leaf roll virus RNA-directed RNA polymometric references: nucleotidyltransferase; RNA biosynthesis
                                                                                                                                                                   probable RNA-directed RNA polymerase (EC 2.7.7.48) - southern bean mosaic virus (stra C;Species: southern bean mosaic virus, SBMV C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 11-Jun-1999 C;Accession: B3739 R;Wu, S.; Rinehart, C.A.; Kaesberg, P. Virology 161, 73-80, 1987
                                                                                                      A;Title: Sequence and organization of southern bean mosaic virus genomic RNA A;Reference number: A33739; MUID:88044510 A;Accession: B33739
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C; Keywords: transmembrane
F; 347-363/Domain: transmen
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A;Reference number: S63896; MUID:96267763
A;Accession: S63896
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                                                               A; Molecule type: genomic RNA
A; Residues: 1-956 <WUS>
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F;1281-1297/Domain:
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F;904-920/Domain:
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F;1753-1769/Domain:
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A; Residues: 1184,'Q',1186-1202,'N',1204-2039 <VA3>
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A; Residues: 1184,'Q'
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32.6%;
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Pred. No. 13;
L6; Mismatches
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                       polymerase
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Query Match

15.2%;

Score

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Length

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RESULT
C49930
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C;Date:
C;Access
                                                                                                                                                                                                                                                             J. Bacteriol. 175, 7282-7289, 1993
A;Title: The uraA locus and homologous recombination in A;Reference number: A49930; MUID:94042902
A;Accession: C49930
                                                                                                                                                                                                                                                                                                                                             hypothetical protein (uraA 3' region) - Mycobacterium bovis (strain BCG) (fragment) c;Species: Mycobacterium bovis (c;Species: Mycobacterium bovis (c;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 19-May-1995 C;Accession: C49930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: rnc; RP117
C;Superfamily: ribonuclease III; double-stranded RNA-binding repeat homology
                                                                             Qy
                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-501 <ALD>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                   R; Aldovini, A.;
J. Bacteriol. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
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RESULT
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A;Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499
A;Accession: C71721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribonuclease III (rnc) RP117 - Rickettsia
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Best Local :
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Best Local
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Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
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                                              GPMLISATQNGELSAQYAEAASEVEELLGVVASEGWQ 101
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                                                                                                                                                                                                                                                                                                              sson, R.N.; Young, R.A.
7282-7289, 1993
                                                                                                                                                                                                 GB: U01072
                                                                                                                              14.5%;
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                                                                                                            Score 68; DB
Pred. No. 8.5;
5; Mismatches
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Pred. No. 2
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hypothetical protein TZL5.4 - Arabidopsis thaliana c;Specles: Arabidopsis thaliana (mouse-ear cress) C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 C;Accession: T01950
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(;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C;Accession: A70899

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete

A;Reference number: A70500; MUID:98295987
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
"hehes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: prfB
C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:Z80108; GB:AL123456;
A;Experimental source: strain H37Rv
C:Genetics:
A;Gene: PPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE000758; NID:g2984111; PIDN:AAC07656.1; A;Experimental source: strain VF5
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A; Residues: 1-373 <AQF>
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R;Geisel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: The complete genome of the hyperthermophilic bacterium A; Reference number: A70300; MUID:98196666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 392, 353-358, 1998
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Best Local Similarity
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  c.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G.; Warren, P.V.; Gaasterland, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation releasing
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A.; Le,
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Pred. No.
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Pred. No. 8
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9.2;
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                                            #text_change 24-Mar-1999
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C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change,31-Mar-2001
C:Accession: D85749
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Ap Nature 409, 529-533, 2001
A; Reference number: A; Accession: D85749
                               A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, September 1997 A; Reference number: Z21749 A; Accession: T38457 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          putatve sensory transduction histidine kinase - fission yeast (Schizosaccharomyces C;Speciles: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T38457
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
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A; Map position: 1
                                                                                                                                                                          hypothetical protein 22421 [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z98978; PIDN:CAB11683.1; A;Experimental source: strain 972h-; cosmid c27E2
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A; Residues: 1-2310 < MUR>
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Best Local
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                                                                                                                                                                                                                                                                              1261 YKLWVCLLEGLRQRNLGNYMEALRLFEKVTSMGAS
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                                                                                                                                                                                                                                                                                                                     62 WKLWRCRLR-----
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                A85480;
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24.7%; Pred.
                  MUID:21074935;
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                                                                                                                                                                          Escherichia coli (strain 0157:H7)
                  PMID: 11206551
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21;
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probable DNA repair protein - human (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 02-Jun-2000 (C;Accession: T02244 R;Lamerdin, J.E.; McCready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhart-Schultz, Christensen, M.; Georgescu, A.; Avila, J.; Liu, S.; Attix, C.; Andreise, T.; Tre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein b1341 - Escherichia coli C,Species: Escherichia coli C,Species: Escherichia coli C;Species: Escherichia coli C;Date: 112-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999 C;Accession: H64883
R,Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; F.R.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: H64883
A;Accession: H64883
A;Scatus: nucleic acid sequence not shown; translation not shown
A; Cross-references: EMBL: AC004472; NID: g2984582; PIDN: AAC07981.1; PID: g2984583
                           A; Molecule type: DNA
A; Residues: 1-622 <LAM>
                                                                                A; Status: translated from GB/EMBL/DDBJ
                                                                                                      A; Reference number: Z14637
A; Accession: T02244
                                                                                                                                                        submitted to the EMBL Data Library, March 1998 A; Authors: Duarte, S.; Lucas, S.; Bruce, R.; Thomas, A; Description: Sequence analysis of a human Pl clone
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A;Molecule type: DNA
A;Residuss: 1-430 <STO>
A;Residuss: 1-430 <STO>
A;Cross-references: GB:AE005174; NID:g12515414; PIDN:AAG56456.1; GSPDB:GN00145; UWGP:
A;Cross-references: Strain O157:H7, substrain EDL933
C;Genetics:
C;Genetics:
A;Gene: Z2421
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WVV------VNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQRKEEETALSCRLVLRKLTETEPVIIFEGIEAPATLGLKASRSANYQ 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --VNVFMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLR 55
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22.2%; Pred. No. 23;
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A;Title: Isolation and sequence of L3T4 complementary DNA clones: expression A;Reference number: A02110; MUID:87018845
A;Accession: A02110
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A;Title: Unusual intron in the immunoglobulin A;Reference number: A26038; MUID:87115821
                                  A;Cross-references: GB:M13816; NID:g192070; R;Littman, D.R.; Gettner, S.N. Nature 325, 453-455, 1987
                                                                                                                                                                                    R; Tourvieille, B.; Gor
Science 234, 610-614,
                                                                                                                                                                                                                                                                           T-cell surface glycoprotein CD4 precursor - mouse N; Alternate names: T-cell differentiation antigen L3T4; T-cell surface antigen
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C;Genetics:
A;Gene: At2g14140
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                                                                                         A; Molecule type: mRNA
A; Residues: 1-457 <TOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map
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A; Residues: 1-783 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome
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Matches 24
                                                                                                                                                                                                  Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999; Accession: A02110; A26038; A39893; A39955; I54564; I69018; A47642; Tourvieille, B.; Gorman, S.D.; Field, E.H.; Hunkapiller, T.; Parnes, J.R.
                                                                                                                                                                                                                                                              Species: Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       position:
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                                                                                                                                                                                                                                                                                                                                                                                              724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    664 EITQGQSNLQTPLTPVMLSQEVMEEIDLKVKKWAKNKLIRDLLSSLEEILWPDSKWQKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 CLLPELLSALH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                          IWDMWDEKKYKLALKKATLLIHPDKLPRAHPEVKYLA 760
                                                                                                                                                                                                                                                                                                                                                                                                                               DWKLW----RCRLRLKSFTSM----DSRSASHRSTRFAA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELTVTCNFIILRASLAQGFTEDQAQDIQRSLERVLETQEQQGPRLEQGLRELWDSVLRAS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLVQGSSNEHGPVK--RSSQSTLERSEQQIR-----AASSLEELL----RITHSE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EWVVVNVFMMLYVQLVQGSSNEHG-PVKRSSQSTLERSEQQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaul,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F84514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fuji
fat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; T
n, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:AE002093; NID:g4587683; PIDN:AAD25853.1;
                                                                                                                                                                                    1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 63; DB Pred. No. 39; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
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                                                                       PIDN: AAA37267.1;
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                 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the plant Arabidopsis thaliana
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                   of.
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                 the
                 newly isolated murine
                                                                     PID:g309112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
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L.; Tallon, L
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CLLSEGDKVKMDSR CRLRLKSFTSMDSR

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F;321-372/Domain: immunoglobulin homology <IM4>
F;395-419/Domain: transmembrane #status predicted
F;496-477/Domain: intracellular #status predicted
F;420-457/Domain: intracellular #status predicted
F;42-112,159-188,328-370/Disulfide bonds: #status
F;187,298,323,392/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                               F;139-190/Domain: immunoglobulin homology *status atypical F;220-301/Domain: immunoglobulin homology <IM3>F;241-457/Product: CD4, brain-specific short form *status |
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 18/1; 74/1; 128/1; 207/1; 319/1; 386/1; 425/3; 448/2 C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: alternative initiators; duplication; glycoprotein; T-cell; F;1-26/Domain: signal sequence #status predicted <SIG> F;27-457/Product: T-cell surface glycoprotein CD4 #status experimental F;35-114/Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Classon, B.J.; Tsagaratos, J.; Kirszbaum, Immunogenetics 23, 129-132, 1986
A;Title: The L3T4 antigen in mouse and the A;Reference number: A47642; MUID:86186694
A;Accession: A47642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-25, E;,27-457 <GOR>
A; Residues: 1-25, E;,27-457 <GOR>
A; Cross references: GB:M17080; GB:J03003; NID:g192515; PII
A; Cross references: GB:M17080; GB:J03003; NID:g192515; PII
R; Maddon, P.J.; Molineaux, S.M.; Maddon, D.E.; Zimmerman,
Proc. Natl. Acad. Sci. U.S.A. 84, 9155-9199, 1987
A; Title: Structure and expression of the human and mouse:
A; Reference number: A39955; MUID:88097446
A; Accession: A39955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 27-43 <CLA>
C;Comment: This protein is expressed on most thymocytes, on a subset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 208-318 < RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: A; Accession: I69018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: L3T4 and the immunoglobulin gene A; Reference number: I54564; MUID: 88152875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Gorman, S.D.; Tourvieille, B.; Parnes, J.R.
Proc. Natl. Acad. Sci. U.S.A. 244-7648, 1987
A;Title: Structure of the mouse gene encoding CD4
A;Reference number: A39893; MUID:88041159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M36851; NID:g198672; R;Classon, B.J.; Tsagaratos, J.; Kirszbaum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Parnes, J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: the cited GenBank accession number,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 25-457 <M
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A; Cross-references: GB: X04836; NID: g50353; PIDN: CAA28539.1; PID: g50354
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                                                                                                                              Query Match
Best Local Similarity
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312
                                                    8
                                              VNVFMMLYVQLVQGSSNE-HGPVKRSSQSTLERSEQQIRAASSLEELLRITHSEDWKLWR 66
VNLVVMKVAQLNNTLTCEVMGPTSPKMRLTLKQENQEAR-VSEEQKVVQVVAPET-GLWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hunkapiller, T.
00, 109-127, 1987
                                                                                                  Conservative
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29.7%;
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                                                                                                                              Score
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L.; Maddox, J.; I
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                                                                                                     Indels
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Mackay, C.R.;
                                                                                                                                                                                                                                   #status predicted
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Search completed: October 17, 2001, 14:48:44 Job time: 290 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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     Match
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Y46B_MYCGE
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ALIGNMENTS

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EMBL; U73620; AAC52984 1; EMBL; U58112; AAB46707.1; HSSP; P15692; IVPF. MGD; MGI-109124; Vegfc. InterPro; IPR002400; InterPro; IPR002400; Pfam; PF00341; PDGF; 1. PRINTS; PR00438; GFCYSKNOT. PROSITE; PS00249; PDGF_1; 1. PROSITE; PS00249; PDGF_2; 1.	his SWISS-PROT entry is copyright. It is produced through a coll etween the Swiss Institute of Bioinformatics and the EMBL out he European Bloinformatics Institute. There are no restriction se by non-profit institutions as long as its content is in odified and this statement is not removed. Usage by and for contities requires a license agreement (See http://www.isb-sib.ch/r.send an email to license@isb-sib.ch).	Characterization of mutine Fit4 ligand/YEGF-C."; Oncogene 15:613-618(1997)i- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTHi- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY)i- SIMILARITY: BELONGS TO THE PDGF/YEGF FAMILY OF GROWTH FACTORS.	47316; ler P., Long A., Bu ler B., Kovacic S., Zollner R., Beier [SEQUENCE FROM N.A. STRAIN-BALB/C; MEDLINE-97164697; PubMed-9012504; KUKK E., Lymboussaki A., Taira S., Kaipainen A., Jeltsch M., Joukov V., Alitalo K.; "VEGF-C receptor binding and pattern of expression with VEGFR-3 suggests a role in lymphatic vascular development."; Development 122:3829-3837(1996).	VEGFC. Mus musculus (Mouse). Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. MCBI_TaxID=10090;	VEGC_MOUSE STANDARD; PRT; 415 AA. P97953; P97953; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (FLT4 LIGAND) (FLT4-L).	RESULT 1

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 Submitted (JU - ! - FUNCTION:
                                    Zollner R., Wood C.R.;
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P49767;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR
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Fitzgerald M.,
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Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                 MEDILINE-96312526; PubMed=8700872;
Lee J., Gray A., Yuan J., Luch S.-M., Avraham H., Wood W.I.;
"Vascular endothelial growth factor-related protein: a ligand
specific activator of the tyrosine kinase receptor Flt4.";
Proc. Natl. Acad. Sci. U.S.A. 93:1988-1992(1996).
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                                                  Towler P.S., Long A.J., Greco R.,
J., Ciarletta A., Hennessey D., Kova
eto H., Weich N., Neben S., Finnerty
Nickbarg E., Gassaway R., Turner K.,
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                                                     chromosome
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
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                                                                          Rieger M., Brueckner
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-!- PTM: PROBABLY PROTEOLITICALLY PROCESSED IN THE C-TERMINUS.
-!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
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                       SEQUENCE
                                                     "Sequence analysis chromosome VII.";
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Growth factor; G1
                      OF 1184-2039 FROM
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00341; PDGF; 1.
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ner M., Schaefer M
s of 203 kilobases
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35, Last annotation update)
CHANNEL PROTEIN.
   PubMed=8701610
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Pfam; PF00520; ion_trans; 1.
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"Sequence analysis of the 43 kb CRM1-YLM9-PET54-DIE2-SMI1-PHO81-YHB4-
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ELSYLPRIMHSFDGPLSFKIWEGRLTIKS 1836
                                SLEELLRITHSED----WKLWRCRLRLKS
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IPR000636; -.
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CAA97245.1; -.
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                                                                                                                                        Score 72.5; D
Pred. No. 5.3;
6; Mismatches
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800B3825D6C6E527 CRC64;
                                  73
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                                                                                                                                                                            Length 2039;
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PIR; B33739; RRBWSC.
InterPro; IPR001795; -...
Pfam; PF02123; Luteo_ORR3; 1.
PRINTS; PR00914; LVIRUSRNAPOL.
Transferase; RNA-directed RNA po.
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30-MAY-2000 (Rel. 3

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P21405;
01-MAY-1991
01-MAY-1991
15-DEC-1998
SEQUENCE FROM N.A.
STRAIR-MADRID 5;
MEDLINE-9903949; PubMed-9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M.
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and i
                                                                                                                                                                                             Rickettsiaceae; Rickettsiaae; Rickettsia.

NCBL_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and institutions are not removed.
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01-MAY-1991 (Rel. 18, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PROBABLE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48).
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. 39, Last sequence update)
. 39, Last annotation update)
(EC 3.1.26.3) (RNASE III).
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24.4%;
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Matches 17
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067695;
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                                                                                                                                                                                                                                                                                                                                                                Deckert G., Warren P.V., Gaasterland T., Young W.G., Le Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PSS0137; DS_RBD; 1.

PROSITE: PS00517; RNASE_3_2; 1.

PROSITE: PS50142; RNASE_3_2; 1.

Hydrolase; Nuclease; Endonuclease; RNA-binding DOMAIN 208 224 DREM.
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SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: CONTAINS 1 DRBM (DOUB)
                              SUBCELLULAR LOCATION: CYTOPLASMIC. SIMILARITY: BELONGS TO THE PROKARYOTIC FACTORS FAMILY.
                                                                                                                                                     FUNCTION: PEPTIDE CHAIN RELEASE FACTOR TRANSLATION IN RESPONSE TO THE PROCESS OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
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Last annotation update)
FACTOR 2 (RF-2).
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Pred. No. 0.85
18; Mismatches
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HE PEPTIDE
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                                                                          AND MITOCHONDRIAL RELEASE
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ay M., Huber
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RESULT 7
FACG_HUMAN STANDARD; PRT; 622 AA.
AC O15287;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FANCONI ANEMIA GROUP G PROTEIN (FACG PROTEIN)
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Best Local S
Matches 18
                       TISSUE-Fibroblast, and Foreskin;
Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwage
Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,
Christensen M., Georgescu A., Avila J., Liu S., Attix C., And
Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas
Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,
Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olser
                                                                                                                                                                                                                                                                                                                                            MEDLINE=97404378; PubMed=9256465;
Liu N., Lamerdin J.E., Tucker J.D., Zhou Z.-Q., Walter C.A.,
Albala J.S., Busch D.B., Thompson L.H.;
"The human XRCC9 gene corrects chromosomal instability and mutagen
sensitivities in CHO UV40 cells.";
                                                                                                                                                                                                                    Bosnoyan-Collins L., Alon N., Car
Schindler D., Pronk J.C., Arwert
Buchwald M., Joenje H.;
            Submitted
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                          "The
                                                                                                                                                                                                                                                   MEDLINE=99021385; PubMed=9806548;
De Winter J.P., Waisfisz Q., Rooimans
Bosnoyan-Collins L., Alon N., Carreau
                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute or BIOLINICAL There are no restrictions on the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer modified and this statement is not removed. Usage by and for commer modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000352; -.
Pfam; PF00472; RF-1; 1.
PROSITE; PS00745; RF_PROK_I;
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              (MAR-1998)
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20:281-283(1998)
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28.1%;
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          EMBL/GenBank/DDBJ databases
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Catarrhini; Hominidae
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H
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No. 3:4;
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Best Local S
Matches 21
                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
T-CELL SURFACE GLYCOPROTEIN CD4 PRECURSOR (T-CELL SURFACE T4/LEU-3) (T-CELL DIFFERENTIATION ANTIGEN L3T4).
 MEDLINE=87018845; PubMed=Tourvieille B., Gorman S. "Isolation and sequence c in T cells and brain.";
                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                            P06332;
                                                                                                                                                                                                                                                          CD4_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                         SEQUENCE FROM N.A.
                                                                                         NCBI_TaxID=10090;
                                                                                                        Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U70310; AAB80802.1; -. EMBL; AJ007669; CAA07602.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
MEDLINE=99303779; PubMed=10373536;
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                                                                                                                                                                                                                                                                                                                                    130 CLLPELLSALH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISEASE: DEFECTS IN FANCG ARE THE CAUSE OF ONE OF THE 8
COMPLEMENTATION GROUPS OF FANCONI ANEMIA (FA), AN AUTOSOMAL
RECESSIVE DISORDER CHARACTERIZED BY PROGRESSIVE PANCYTOPAENIA, A
DIVERSE ASSORTMENT OF CONGENITAL MALFORMATIONS, AND A
PREDISPOSITION TO THE DEVELOPMENT OF MALIGNANCIES. AT THE CELLULAR
LEVEL IT IS ASSOCIATED WITH HYPERSENSITIVITY TO DNA-DAMAGING
AGENTS, CHROMOSOMAL INSTABILITY (INCREASED CHROMOSOME BREAKAGE),
                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Cell. Biol. 19:4866-4873(1999).
FUNCTION: DNA REPAIR PROTEIN THAT MAY OPERATE IN A POSTREPLICATION REPAIR OR A CELL CYCLE CHECKPOINT FUNCTION. MAY BE IMPLICATED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND DEFECTIVE DNA REPAIR.
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                                                                                                        Eutheria;
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                                                                                                                                                                                                                                                          STANDARD;
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                                             PubMed=3094146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
68553 MW;
                                                                                                        Rodentia;
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               S.D., Fie of L3T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63; DB Pred. No. 15; 9; Mismatches
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            Field E.H., Hunkapiller T., Parnes J.R., 3T4 complementary DNA clones: expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Naf D., Wasik J., D'Andrea A.D.; CA, FANCC, and FANCG/XRCC9 interact in a
                                                                                                    Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                            PRT;
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15;
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A02110; A26038;

RWMST4. A26038.

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EMBL; M36850; AAA39401.1; -.
EMBL; M3816; AAA37267.1; -.
EMBL; M3816; CAA28539.1; -.
EMBL; M36851; AAA39402.1; -.
EMBL; M17078; AAA37403.1; JOINED.
EMBL; M17079; AAA37403.1; JOINED.
EMBL; M17079; AAA37403.1; JOINED.
EMBL; AC002397; AAC36010.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                "Partial primary structure of the T4 antigens of mouse and sheep: assignment of intrachain disulfide bonds.";
Proc. Natl. Acad. Sci. U.S.A. 83:4499-4503(1986).
-!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.
-!- SUBURIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE V-LIKE AND 3 C2-LIKE DOMAINS.
                                                                                                                                                                                                                                    or send
                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                              entities requires
                                                                                                                                                                                                                                                                                    modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Classon B.J., Tsagaratos J., McKenzie I.F.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Classon B.J., Tsagaratos J., Brandon M., McKenzie I.F.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Comparative sequence analysis of a gene chromosome 12p13 and its syntenic region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86166694; PubMed=3082751;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gorman S.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The L3T4 antigen in mouse and the sheep equivalent are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3enome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87115821; PubMed=3027575;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD4 (L3T4) gene.";
325:453-455(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gorrell J.H.,
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                                                                                                                                                                                                                                 email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8:29-40(1998).
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                                                                                                                                                                                                                                                         a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=3086886;
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Oeltjen J.C., Schwartz
H., Chinault A.C., Belmc
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Belmont J.W., N
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of mouse and sheep:
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
INTERLEURIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
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  between
             This
                                                                                                    Lakkis F.G., Cruet E.N.;
"Cloning of rat interleukin-13 (IL-13) cDNA and analysis gene expression in experimental glomerulonephritis.";
                                                                                                                                      MEDLINE=94092138; PubMed=7916615;
                                                                                                                                                 STRAIN-SPRAGUE-DAWLEY; TISSUE-Kidney
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                             P42203;
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                                                                                                                                                                                                                                                                                                                                                                                 312
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InterPro; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                             67
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                                                            e expression in experimental glomerulonephritis.";
chem. Biophys. Res. Commun. 197:12-618 (1993).
FUNCTION. CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
SYNERGIZES WITH IL2 IN REGULATING INFERFERON-GAMMA SYNTHESIS.
MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSE
                              SUBCELLULAR LOCATION: SECRETED. SIMILARITY: BELONGS TO THE IL-4 /
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           SWISS-PROT entry is
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IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
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CYTOPLASMIC
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EXTRACELLULAR
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ght. It is produced through a collaborati
Bioinformatics and the EMBL outstation
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(GLCNAC. . .)
                               IL-13 FAMILY
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STRAIN-S288C / AB972;
STRAIN-S288C / AB972;
Johnston M., Andrews S., Brinkman R., Cooper J., Lington J.,
Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
Mardis E., Menezes S., Miller N., Whan M., Pauley A., Peluso
Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,
Rifken L., Riles L., Taich M., Wilson R., Waterston R.;

""" "" " Wohldman P., Vaudin M., Wilson R., Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                               YL92_YEAST STAND
P18633;
01-NOV-1990 (Rel. 16,
01-NOV-1997 (Rel. 35,
15-DEC-1998 (Rel. 37,
15-DEC-1998 (Rel. 37,
YLR392C OR L8084.13;
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                                                              This
                                                                                     Ackerman S.H., Tzagoloff A.;
"ATP 10, a yeast nuclear gene required mitochondrial F1-F0 complex.";
J. Biol. Chem. 265:9952-9959(1990).
                                                                                                                                         SEQUENCE OF 1-210 FROM N.A. MEDLINE=90277691; PubMed=2141026;
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; i
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
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l Similarity 28.4%;
27; Conservative
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01-JAN-1990
            EMBL;
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01-NOV-1997
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                                                                                                                                                                                                                                      SEQUENCE OF 1-917 FROM N.A.
MEDLINE=89384567; PubMed=2674679;
Linton J.P., Yen J.-Y.J., Selby E.,
                                                                                                                                                                                                                                                                                 MEDLINE=95011610; PubMed=7926796;
Liu K., Niu L., Linton J.P., Crouse G.F.;
"Characterization of the mouse Rep-3 gene: sequence similarities bacterial and yeast mismatch-repair proteins.";
Gene 147:169-177(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
Mammalia; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA MISMATCH REPAIR PROTEIN MSH3
                                                                                      entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSH3 OR REP-3
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                                                                                                                                                              . Cell. Biol. 9:3058-3072(1989).
FUNCTION: NOT KNOWN. PROBABLE DNA-REPAIR PROTEIN.
SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
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                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                         musculus (Mouse).
                                                                                                                               SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EM
M80360;
L10319;
L10295;
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(Rel. 35, Last ann
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AAA40052.1;
AAB60711.1;
AAB60711.1;
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AAB60711.1;
AAB60711.1;
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Best Local
Yaque E., Mehak-Zunic M., Wood D.A., Thurston C.F.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: SUCCINYL-COA + GLYCINE = 5-AMINOLEVULINATE
COA + CO(2).
-!- COPACTOR: PYRIDOXAL PHOSPHATE.
-!- COPACTOR: PYRIDOXAL PHOSPHATE.
-!- PATHWAY: FIRST AND RATE-LIMITING STEP IN HEME BIOSYNTHESIS.
-!- SUBGUIT: HOMODIMER (BY SIMILARITY).
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                              HEM1_AGABI STANDARD; PRT; 621 AA. 092403; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) 5-AMINOLEVULINIC ACID SYNTHASE, MITOCHONDRIAL (DELTA-AMINOLEVULINATE SYNTHASE) (DELTA-ALA SY
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TE; PS00486; DNA_MISMATCH_REPAIR_2;
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                                                                                                                                                                                                                                                         Basidiomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.9%;
27.3%;
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Pred.
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MV -> IL (IN REF.
T -> A (IN REF. 2)
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                                                                                                                                                                                                                                                         Hymenomycetes;
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No. 58;
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                                                                                                                                                                                                                                                                                                                AL PRECURSOR (EC SYNTHETASE).
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RESULT
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Best Local
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01-FEB-1995
01-FEB-1995
01-FEB-1995
             EMBL; M81087;
HSSP; P00829;
                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THIFE
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TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as not removed. modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                  Thiobacillus ferrooxidans complement Escherichia coli Fl unc
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 33020;
MEDLINE-95047244; PubMed-7958772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATPB_THIFE
                                                                                                                                                                                                                                                                                                                                                  Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thiobacillus ferrooxidans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                Brown L.D., Dennehy M.E., Rawlings D.E.;
"The F1 genes of the F1F0 ATP synthase from the acidophilic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          468 IYVQAINYPTVARGEERLRITVTPRHTMEQMEGLIRSLNQVFEELNINRLSDWKL 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 LYVQLVQ----GSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSEDWKL 64
                                                                                                European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                  SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CORE - AND CF(0) - THE MEMBRANE PROTON CHAPS SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTHAS THREE MAIN SUBUNITS: A, B AND C.
                                                                                                                                                                                                                                                          FUNCTION: PRODUC
GRADIENT ACROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYNTHASE
                                                                                                                                                                      SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
                                                                                                                                                                                                                                              ALS.";
Microbiol. Lett. 122:19-26(1994).
FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
TOWN ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMINOTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osynthesis; Transferase; Acyltransferase; Mitochondrion; peptide; Pyridoxal phosphate.
                                                                                                                           the Swiss Institute of Bioinformatics
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PS00599; AA_TRANSFER_CLASS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteobacteria; gamma subdivision; Acidithiobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362
621 AA;
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(Rel. 31, Last seq
(Rel. 31, Last ann
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                            AAA53127.1;
                1COM
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31, Last annotation update)
CHAIN (EC 3.6.1.34).
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362 P
67426 MW;
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29.1%;
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Pred.
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PYRIDOXAL PHOSPHATE (PROBABLE).; A335C3268FAE1AA3 CRC64;
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                                                                                              There are no restrictions ong as its content is in
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NNEL. CF(1) HAS FIVE
TA(1), EPSILON(1). CF(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 621
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RESULT 14
CYAA_PODAN
ID CYAA_P
AC Q01513
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Best Local
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Q01513;
01-NOV-1997
01-NOV-1997
01-OCT-2000
           REPEAT
REPEAT
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                                                                                             Lyase;
REPEAT
                                                                                                                                                                                                                                                                                      This
                                                                                                                    PRINTS; PR00019; LEURICHRPT.
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
                                                                                                                                            Pfam; PF00560; LRR; 13. Pfam; PF00481; PP2C; 1.
                                                                                                                                                                            EMBL; L43413; AAB05642.1; InterPro; IPR001611; -.
                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      Loubradou G., Begueret J., Turcq B.;
"An additional copy of the ademylate cyclase-encoding gene rel
developmental defects produced by a mutation in a vegetative
incompatibility-controlling gene in Podospora anserina.";
Gene 170:119-123(1996).
Gene 170:119-123(1996).
HETABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENG
                                                                                                                                                                 InterPro; IPR001932;
                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADENYLATE CYCLASE CYCLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrogen ion transport.
NP_BIND 155 162
SEQUENCE 468 AA; 5061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00006; ATP-synt_ab; 1.
Pfam; PF00306; ATP-synt_ab_C; 1.
PROSITE; PS00152; ATPASE_ALPHA_BETA;
Hydrolase; ATP synthesis; CF(1): ATP-
                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=96200867; PubMed=8621071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Podospora anserina.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 EHGPVKRSSQSTLERSE--QQIRAASSLEELLRITHSEDWKLWRCRLR
                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYI SIMILARITY: BELONGS TO ADENYLYL CLASS-3 SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LI SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EHYDVARSCQKTLQRYKELQDIIAILGMDEL----SEDDKLLVSRAR
                                                                                                         Repeat;
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Pred. No. 27;
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; A6039491D4390574 CRC64;
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Matches 17
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SP17_MOUSE
Q62252;
                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                        Splī.";
Biol. Reprod. 53:579-590(1995).
-i- FUNCTION: SPERM SURFACE ZONA PELLUCIDA BINDING PROTEIN. HELPS TO BIND SPERMATOZOA TO THE ZONA PELLUCIDA WITH HIGH AFFINITY. MIGHT FUNCTION IN BINDING ZONA PELLUCIDA AND CARBOHYDRATES (BY
                                                                                                                                                                                                                                                         STRAIN-BALB/C; TISSUE-Testis;
MEDLINE-96039129; PubMed=7578682;
Kong M., Richardson R.T., Widgren E.E., O'Rand M.G.;
"Sequence and localization of the mouse sperm autoantigenic protein,
"Sep17.";
                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
SPERM SUFFACE PROTEIN SP17 (SPERM AUTOANTIGENIC PROTEIN 17).
SPA17 OR SP17.
EMBL; Z46299; CAA86455.1; MGD; MGI:1333778; Sp17. InterPro; IPR000048; -. Pfam; PF00612; IQ; 1.
                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1988 LYPHALSGRIETHSKHEKEQAQDLREIRPAILSPGS---ELSVEPDDIWSLWRVALRIEM 2044
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                                                                                                                                                   SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (POTENTIAL).
TISSUE SPECIFICITY: TESTIS- AND SPERM-SPECIFIC.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
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Pred. No. 1.7e+02;
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Search completed: October 17, 2001, 14:51:49 Job time: 475 sec
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Matches 14; Conserv
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149 AA; 17296 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyright
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sp_vertebrate:*
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096699 borrelia bu
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ALIGNMENTS

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RESULT
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01-JUN-1998 (TrEMBLTel. 0
01-JUN-1998 (TREMBLTEL. 0
01-MAR-2001 (TREMBLTEL. 1
GROWTH FACTOR FIGF.
"Vascular endothelial growth factor D (VEGF-D) is a ligand for the tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4)."; Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).

EMBL; Y12864; CAA73371.1; -
EMBL; Y12865; CAA73371.1; JOINED.
EMBL; Y12865; CAA73371.1; JOINED.
EMBL; Y12867; CAA73371.1; JOINED.
EMBL; Y12867; CAA73371.1; JOINED.
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MEDLINE-98140120; PubMed-9479493;

ROCCHIGIANI M., Lestingi M., Luddi A., Orlandini M., Franco B.,

Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,

Rossi E., Ballabio A., Zuffardi O., Oliviero S.;

"Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1

between the PIGA and the GRPR genes.";

Genomics 47:207-216(1998).
                                                                                                                                                                                                                     Yamada Y., Nezu J., Shimane M., Hirata "Molecular cloning of a novel vascular VEGF-D.";
                                                                                                                            MEDLINE=98118549; PubMed=9435229; Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F., Alitalo K., Stacker S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIGF OR VEGF-D.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Q9NQX0 Q9RR39 Q9S069 P71657

Q44806 Q44816 P70443 082601 014002

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InterPro; IPRO00072; -.
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; -; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
PROSITE; PS50278; PDGF_2; 1.
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PROSITE; PS50278
SMART; SM00141; |
SEQUENCE 358 A
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STRAIN-C57BL/6J;
MEDLINE=9730254; PubMed=8876195;
MEDLINE=9730254; PubMed=8876195;
Ordandini M., Marconcini L., Ferruzzi R., Oliviero S.;
"Identification of a c-fos-induced gene that is related platelet-derived growth factor/vascular endothelial grow family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TIEMBLIEL 03,
01-MAY-1997 (TIEMBLIEL 03,
01-MAR-2001 (TIEMBLIEL 16,
VASCULAR ENDOTHELIAL GROWTH
VEGF-D OR FIGF.
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97349118; PubMed=9205122;
Yamada Y., Nezu J., Shimane M., Hirata
"Molecular cloning of a novel vascular
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HSSP; P15692;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                 SL; X99572; CAA67892.1; -
SL; D89628; BAA14002.1; -
SP; P15692; 1VPP.
); MGI:108037; Figf.
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L; Y12870; CAA73371.1; JOII

L; D89630; BAA24264.1; -...

L; AJ000185; CAA03942.1; -...

L; Y12863; CAA73370.1; -...

P15662; 1VPP...
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                                                                                       6636B17FBF07037C
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No. 6.5e-46;
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RESULT O57352
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VASCULAR ENDOTHELIAL GROWTH FE
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Matches 69
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035251;
01-JAN-1998
01-JAN-1998
01-MAR-2001
                                                        Coturnix coturnix japonica (Japanese quail). Eukaryota; Metazoa; Chordata; Craniata; Vert Archosauria; Aves; Neognathae; Galliformes;
SEQUENCE FROM N.A. MEDLINE=98167900;
                                             Coturnix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEGF-D.
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MEDLINE-97349118; PubMed=9205122;
Yamada Y., Nezu J., Shimane M., Hirata
"Molecular cloning of a novel vascular
"Molecular cloning of a novel vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116;
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01-JAN-1998 (Tremblrel. 05,
01-MAR-2001 (Tremblrel. 16,
VASCULAR ENDOTHELIAL GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF014827; AAI
HSSP; P15692; 1VPP
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EMBL; AF014827; AAB66557.1;
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Eukaryota; Metazoa; Chor
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                                                                                                                                                                                                                       VAHSEDWKLWRCRLKLKSLANVDSRSTSHRSTRFAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
 PubMed=9435294;
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Rodentia;
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71.1%;
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FACTOR
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Pred. No. 1.3e
8; Mismatches
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FACTOR D.
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annotation updat
OR C PRECURSOR.
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                                                                                                                 update)
                                                        Phasianidae;
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SEQUENCE
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SIGNAL
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                                                                                                                                           SMART; SM00141; PDGF; 1
                                                                                                                                                                                               "Structure and expression of bovine VEGF famil submitted (MAY-1997) to the EMBL/GenBank/DDBJ EMBL; AB004275; BA377687.1; -. HSSP; P15692; 1VPP.
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                     Q9XS50
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EMBL; Y15837; CAA75799.1; -.
HSSP; P15692; 1VPP.
                                                                                                                                                   PROSITE; PS00249; PDGF_1; PROSITE; PS50278; PDGF_2;
                                                                                                                                                                           InterPro; IPR000072; -. Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                       TISSUE=HEART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eichmann A.,
                                                                                                                                                                                                                                Liu X., Yonekura H., Yamagishi S.,
"Structure and expression of boving
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00141; PDGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursors."
 58
                     41 EQQIRAASSLEELLRITHSEDWKLWRCRLR 70
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                                                                                                                                                                                                                                                                                                                                  taurus (Bovine).
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EEQLRSVSSVDELMTVLYPEYWKMYKCQLR
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                                           l Similarity
13; Conserv
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420 /
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                                                                                                 AA;
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420 V
46681 MW;
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                                          Score 87; DB
Pred. No. 0.05
12; Mismatches
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Last annotation updat
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VASCULAR ENDOTHELIAL GROWTH FACTOR
; 58BA84317A3C8E2D CRC64;
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Pred.
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bovine VEGF family
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VASCULAR ENDOTHELIAL GROWTH FACTOR

; 099BFCC79151BF2B CRC64;
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0.0029;
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0.054;
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Q9S0H7;
01-MAY-2000
01-MAY-2000
01-MAY-2000
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068470;
01-AUG-1998
01-NOV-1999
                                                             Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Lathigra R., White O., Dodson R., Hickey E.K., Gwinn M., Peterson J., van-Vugt i Palmer N., Haft D., Rosa P., Stevenson B.; Palmer N. Haft D., Rosa P., Stevenson B.; "A bacterial genome in flux: The twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yang X., Popova T.G., Hagman K.E., Wikel S.K., Schoeler G.B., Caimano M.J., Radolf J.D., Norgard M.V.; "Identification, Characterization and Expression of Three New Members of the Borrelia burgdorferi Mlp (2.9) Lipoprotein Gene Family."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                       spirochete Borrelia burgdorferi.";
Mol. Microbiol. 0:0-0(1999).
EMBL; AE001576; AAF07449.1; -.
                                                                                                                                                       Bacteria; Spirochaetales; NCBI_TaxID=139;
                                                                                                                                                                       Plasmid cp32-3
Bacteria; Spiro
           Lipoprotein;
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                Borrelia burgdorferi (Lyme
                                                                                                                                                                                                                BBS30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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01-NOV-1999 (TYEMBLIEL 12, Last sequence update)
01-NOV-1999 (TYEMBLIEL 12, Last annotation update)
01-NOV-1999 (TYEMBLIEL 12, Last annotation update)
MLP8 (2.9-8) LIPOPROTEIN (FRAGMENT)
                                                                                                                                                                                                                          LIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipoprotein; Plasmid NON_TER 149 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96236048; PubMed=8655511;
Porcella S.F., Popova T.G., Akins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi supercoiled plasmids pen reading frames and a lipoprotein gene . Bacteriol. 178:3293-3307(1996).
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                                                                                                                                                                                                                                                                                                                                                                                       58 HSEDWK 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                            7 VVNVFMMLYVQLVQG-SSNEHGPVKRSSQST-----LERSEQQIRAASSLEELLRIT
                                                                                                                                                                                                                                                                                                                                                             LSDDQK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity
19; Conserv
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148
                                                                                                                                                                                                                                       (TrEMBLrel. 13, ) (TrEMBLrel. 13, ) (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 AA;
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           Plasmia
                                                                                                                                                                                                                                                                                             PRELIMINARY;
AA;
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16731 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.7%;
                                                                                                                                                                        Spirochaetaceae; Borrelia
                                                                                                                                                                                                disease spirochete)
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                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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Pred. No. 0.
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1D406F6BC310895C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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family.";
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CRC64;
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Matches 18
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Best Local
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Q9S0B7;
Q1-MAY-2000
01-MAY-2000
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01-JUL-1997
01-MAR-2001
                       01-MAY-2000
LIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Lathigra R., White O., Dodson R., Hickey E.K., Gwinn M., Peterson J., van-V Palmer N., Haft D., Rosa P., Stevenson B.;

"A bacterial genome in flux: The twelve linear and nine circulextrachromosomal DNAs in an infectious isolate of the Lyme disspirochete Borrella burgdorferi.";

Mol. Microbiol. 0:0-0(1999).

EMBL; AF000270; AAC46120.1; -
EMBL; AF000270; AAC46120.1; -
Lipoprotein; Plasmid.

SEQUENCE 148 AA; 16413 MW; 97C9ACAA3026EAFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gilmore R.D., Mbow M.L.;
"A monoclonal antibody generated by antigen inoculation via tick bite is reactive to the Borrelia burgdorferi Rev protein, a member of the 2.9 gene family locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLASMID=CP32-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Infect. Immun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98147709; PubMed=9488385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-B31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVNVFMMLYVQLVQG-SSNEHGPVKRSSQSTLERSEQQI-----
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18; Conserv
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                                       ) (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.
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                                                                                                                                       PRELIMINARY;
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29.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 72; DB 2
Pred. No. 0.96;
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Pred. No. 0.74;
7; Mismatches
                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                       149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 148;
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Best Local Similarity
Matches 19; Conser
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Best Local
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Q9Y787;
Q1-NOV-1999
01-NOV-1999
01-MAR-2001
Q9NQX0 PRELIMINARY;
Q9NQX0;
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                        Costanzo M.C., Bonnefoy N., Williams E.H., Fox T.D.;
"Orthologs of Saccharomyces cerevisiae mitochondrial mRNA-specific
translational activators exist in other budding yeasts.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF120714; AAD29121.1; -.
SEQUENCE 791 AA; 94812 MW; BBD54A6924EF4BA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
COX2 MRNA-SPECIFIC TRANSLATIONAL ACTIVATOR PET111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spirochete Borrelia burgdorferi.";
Mol. Microbiol. 0:0-0(1999).
EMBL; AE001578; AAF07539.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....eria; Spirochaetales;
NCBI_TaxID=139;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PET111
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                                                                                                                                                                                                                                                                                                                                                        STRAIN=CBS2359;
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=28985;
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                                                                                                                                                                                                                    15.2%;
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                                                                                                                                                                               SSQSTLERSEQQIRAASSLEELLRITHSEDW-KLWRCR 68
                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                         Score 71; DB
Pred. No. 7.2;
L1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 72; DB 2
Pred. No. 0.97;
                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycotina; Saccharomycetes; cetaceae; Kluyveromyces.
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                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                 Length 791
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PRESIDENT PRESID
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A family of novel Pk suppressors.";
                                                        MEDLINE-20002587; PubMed-10531261; Yang X., Popova T.G., Hagman K.E., Wikel S.K., Sch Caimano M.J., Radolf J.D., Norgard M.V.; "Identification, characterization, and expression of the Borrelia burgdorferi M.p (2.9) lipoprotein Infect. Immun. 67:6008-6018(1999).
EMBL; AF047000; AAC36593.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                           open
                        Lipoprotein;
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid cp3
Bacteria; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrelia burgdorferi (Lyme disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9RR39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9RR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deng Q.-D., Yang X.-H., Huan Submitted (MAY-2000) to the EMBL; AF272898; AAF78078.1;
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      Porcella S.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TREMBLIEGL 15, 01-MAR-2001 (TREMBLIEGL 16, PR-DOMAIN ZINC FINGER PROTE
                                                                                                                                                                                                                                                                        Norgard M.V.;
"Borrelia burgdorferi supercoiled plasmids open reading frames and a lipoprotein gene pen reading frames 3307(1996).
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96236048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000822; -.
InterPro; IPR001214; -.
Pfam; PF00096; zf-C2H2; 4.
PROSITE; PS00028; ZINC_FINGER_C2H2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding; Metal-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .9-10 LIPOPROTEIN (FRAGMENT).
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15; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spirochaetales; Spirochaetaceae;
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                                           Plasmid
                        66
    AΑ;
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                                                                                                                                                                                                                                                                                                                                                        PubMed=8655511;
pova T.G., Akins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huang S.;
PR-domain
  7636
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27
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    W.
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the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 70; DB
Pred. No. 7.1;
14; Mismatches
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  69E5D29D5B34A085 CRC64;
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                                                                                                                                                                                                                                                                                                                                                      D.R.,
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                                                                                                                                                                   Schoeler G.
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Best Local (
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                                                                                                                         P71657; PRELIMINARY; PRT; 539 AA.
P71657; O1-JAN 1998 (TrEMBLrel. 05, Created)
O1-JAN 1998 (TrEMBLrel. 05, Last sequence update)
O1-JUN 2000 (TrEMBLrel. 14, Last annotation updat)
HYPOTHETICAL 55,4 KDA PROTEIN CY21B4.04.
RV1387 OR MTCY21B4.04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                  extrachromosomal DNAs in an infectious spirochete Borrelia burgdorferi."; Mol. Microbiol. 0:0-0(1999).
EMBL; AE001580; AAF07641.1; -.
Lipoprotein; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser C.M., Casjens S., Huang W.M., White O., Dodson R., Hickey E.K., Gw. Palmer N., Haft D., Rosa P., Stevenso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9S069;
Murphy L., Harris D., Barrell B.G., Rajandream M.A.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POT
-i- SIMILARITY: BELONGS TO THE MTCY31.06C / MTCY251.15
                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Spirochaetales;
NCBI_TaxID=139;
                                             STRAIN-H37RV;
                                                         SEQUENCE
                                                                                                                  Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                          Lipoprotein;
SEQUENCE 1
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                                                                              NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palmer N., Haft D., Rosa P., Stevenson B.; "A bacterial genome in flux: The twelve linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                               l Similarity 26.:
17; Conservative
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                                                       FROM N.A.
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28.6%;
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                                                                                                                                                                                                                                                                                                                                                18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.1;
8; Mismatches
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Gwinn M.,
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                                                                                                     Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                       Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               and nine cir
of the Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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 .15 / MTCY02
                                                                                           Mycobacterium
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RESULT 15.
044806
AC 044806
AC 044806
DT 01-NO
DT 01-NO
DT 01-NO
CO DE LIPO
GE LIPO
GE LIPO
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RC STF
RX MEI
RA NO
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Best Local Similarity 24.6
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 43...
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 280108; CAB02192.1
TubercuList; Rv1387; -.
InterPro; IPR000030; -.
InterPro; IPR001899; -.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                          Q44806;
Q44806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                 Lipoprotein.
SEQUENCE 145 AA;
                                                                                                                                                  "Borrelia burgdorferi supercoiled plasmids encode multicopy tandem open reading frames and a lipoprotein gene family.";
J. Bacteriol. 178:3293-3307(1996).
EMBL; U45422; AAB07830.1; -.
                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
TRANSMEM
                                                                                                                                                                                           MEDLINE-96236048; PubMed-8655511;
Porcella S.F., Popova T.G., Akins D.R., Li M., Radolf J.D.,
Morgard M.V.;
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=297;
                                                                                                                                                                                                                                                                  Borrelia burgdorferi (Lyme disease spirochete).
Bacteria: Spirochaetales: Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00823; PPE; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                          NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; TRANSMEM 8 28
                                                                                                                                                                                                                                                                                                 LIPOPROTEIN
63 NDDQK 67
                   59 SEDWK 63
                                                                                                                                                                                                                                                                                                                                                                                                   ω
                                                  IINILFCLFLLMLNGCNSNDNDTLKNNAQQTKSRGKRDLTQKELTQEKPKSKEELLKEKL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391
539 AA;
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117
279
312
347
368
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55403 MW;
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83
137
299
332
367
388
                                                                                                                                  16210 MW;
                                                                                        14.3%;
24.6%;
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                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                           score 68; DB; Pred. No. 11; 5; Mismatches
                                                                              Score 67; DB 2
Pred. No. 3.5;
19; Mismatches
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Last sequence update)
Last annotation update)
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, 7FE63A9BAC6FBEB5 CRC64;
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11;
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                                                                               Indels
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Search completed: October 17, 2001, 14:50:58 Job time: 424 sec

GenCore version Copyright (c) 1993 - 2000

4.5 Compugen Ltd

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Title:
Perfect score:
 Minimum DB
Maximum DB
                                             Total number of hits satisfying chosen parameters:
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seq
length: 2000000000
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                                                                              412676 seqs,
                                                                                                              Gapop 10.0 ,
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897
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                                                                                                                                                              IIRRSIQIPEEDRCSHSKKL....HCRFPKEKRAAQGPHSRKNP 153
                                                                                 60623988 residues
                                                                                                              Gapext 0.5
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80.009 Million cell updates/sec
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_0601:*
1: /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*

hase: A_Geneseq_0601:*

1: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*

2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*

3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*

4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*

5: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*

6: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*

7: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*

9: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*

10: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*

11: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*

12: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*

13: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*

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24: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*

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26: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*

27: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*

28: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*

29: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*

20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		% Query				
No.	Score	Match Length DB	ength	DB	ID	Description
1	897	100.0	325	19	AAW53240	Homo sapiens vascu
2	897	100.0	325	22	AAY97572	Human VEGF-D prote
ω	897	100.0	354	19	AAW4 9036	Human zveqf2 growt
4	897	100.0	354	19	AAW53241	Homo sapiens vascu
ъ	897	100.0	354	19	AAW44293	Human vascular end
6	897	100.0	354	21	AAB10649	
7	897	100.0	354	21	AAB29049	Human VEGF-D prote
8	897	100.0	354	21	AAY70750	
9	897	100.0	354	21	AAY70983	_
10	897	100.0	354	22	AAY97573	Human VEGF-D1 prot
11	897	100.0	354	22	AAB37606	_

	AAY97570	22	419	•	244.5	5
	AAY70982	21	419		244.5	4
Human prepro-vascu	AAY70749	21	419	•	244.5	ω
Vascular endotheli	AAY97144	21	419	•	244.5	N
	AAB29048	21	419	•	244.5	-4
Human VEGC protein	AAB10648	21	419	•	244.5	0
Human vascular end	AAW86203	20	419	•	244.5	ø
Full length human	AAY22320	20	419	•	244.5	œ
Vascular endotheli	AAY30518	20	419		244.5	7
Human vascular end	AAW75740	19	419	•	244.5	6
	AAW75751	19	419		244.5	Ġ
Human vascular end	AAW13833	18	419	•	244.5	4
Flt4 re	AAW00932	18	419		244.5	ũ
foetal	AAW17837	18	419	•	244.5	Ñ
VEGF-C	AAW86237	20	399		244.5	Ë
Human VEGF-2 prote	AAY97577	22	350		244.5	Õ
Truncated vascular	AAY97145	21	350		244.5	ق
Truncated human VE	AAY22321	20	350		244.5	æ
A truncated vascul	AAY30519	20	350	•	244.5	7
ar endo	AAR82686	16	350		244.5	õ
growth	AAY08284	20	318		244.5	Ğ
VEGF-C	AAW86222	20	307		244.5	4
VEGF-C	AAW86223	20	302	•	244.5	ω̈
VEGF-C	AAW86224	20	297		244.5	Ñ
	AAW86225	20	292		244.5	ï
an vascula	AAW11478	18	419		246.5	õ
	AAW53243	19	321		7	ف
Rat vascular endot	AAW44296	19	326		595	œ
Mouse vascular end	AAW44295	19	358		•	7
Mus musculus vascu	AAW53242	19	358			Ġ
	AAW14992	18	358		•	'n
5	28	20	337		•	4
c-Fos inc	49	18	620	97.2	872	w
Human vascular end	AAB70685	22	354		881	2

ALIGNMENTS

AAW53240 ID AAW5 RESULT vascular endothelial growth factor; VEGF-D; angiogenesis; modification; acceleration; wound healing; tissue; organ; transplants; collateral circulation; infarction; arterial stenosis; coronary artery disease; inhibition; cancer; treatment; diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive airway disease; intestinal malabsorptive syndrome; blopsy; metastatic risk; Region 21-AUG-1997; 26-FEB-1998. WO9807832-A1. Region Key detection; diagnosis; congestive heart failure. 03-AUG-1998 Homo sapiens. Homo sapiens vascular endothelial growth factor D (VEGF-D). AAW53240; AAW53240 standard; Protein; Region _ (first entry) 97WO-US14696 /note= "potential N-linked glycosylation site" 156..158/note= "potential N-linked glycosylation site"
258..260 Location/Qualifiers 126..128 /note= "potential N-linked glycosylation site" 325 ĄΑ

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X DE X D X A X I D
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AAY97572
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Best Local Similarity
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11-NOV-1996;
14-NOV-1996;
05-FEB-1997;
10-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                such as coronary artery disease, and inhibition of angiogenesis in the treatment of cancer or of diabetic retinopathy. It can also be used in the treatment of lung disorders to improve blood circulation in the lung and/or gaseous exchange between the lungs and the blood stream or to improve blood circulation to the heart and 02 gas permeability in cases of cardiac insufficiency, to improve blood flow and gaseous exchange in chronic obstructive airway disease, or to treat malabsorptive syndromes in the intestinal tract. Quantitation of VEGF-D in cancer biopsy specimens may be useful as an indicator of future metastatic risk. Antagonists can be used for treating e.g. conditions such as congestive heart fallure, involving accumulations of fluid in the lung resulting from increases in vascular permeability. The products can also be used for datection and diagnosis
       Human VEGF-D protein sequence
                                         05-APR-2001
                                                                                                    AAY97572 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated vascular endothelial growth factor-D - used to devel products for use in e.g. modifying angiogenesis or treating lung, heart or intestinal disorders {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in wound healing, tissue or organ transplantation, or to establish collateral circulation in tissue infarction or arterial stenosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1997;
23-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-1997;
                                                                                                                                                                                                                                            233
                                                                                                                                                                                  293
                                                                                                                                                                                                                                                                                                       173
                                                                                                                                                                                                              121 TRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 153
                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis
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                                                                                                                                  N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection and diagnosis.
                                                                                                                                                                                                                                                                                                                    IIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPH
                                                                                                                                                                                                                                                          MMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFH 120
                                                                                                                                                                                                                                                                                                    iirrsiqipeedrcshskklcpidmlwdsnkckcvlqeenplagtedhshlqepalcgph
                                                                                                                                                                               trpcasgktacakhcrfpkekraaggphsrknp
                                                                                                                                                                                                                                          mmfdedrcecvcktpcpkdliqhpkncscfeckesletccqkhklfhpdtcscedrcpfh
                                                                                                                                                                                                                                                                                                                                                                    153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                       (first entry)
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97AU-0004954.
97US-0038814.
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96AU-0001825.
96US-0023751.
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                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                             Score 897;
Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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2.5e-70;
s 0;
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유 2

121 TRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP

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                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                          (lymph)angiogenesis. The proteins are also used to identify specific binding agents (potential therapeutic agents) and to raise antibodies. The antibodies are useful as therapeutic (ant)agonists; for detection, purification and targeting of proteins for in vivo or in vitro diagnosis (including imaging) or for therapy (including when linked to e.g. a label or cytotoxin); and for immunotyping of cells, e.g. for detecting minimal residual disease or haematopoietic progenitor/stem cells. It is also contemplated that the sequences might be useful for treating a very wide range of other disorders, e.g. autoimmune diseases; altergy; cancer; infectious diseases (viral, bacterial, fungal or parasitic); neurodegeneration, also as chemotactic agents or for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is vascular endothelial growth factor-D (VEGF-D), which is an angiogenic protein of the invention. The angiogenic proteins and the DNA sequences encoding them, are used to prevent, treat or ameliorate disease and to detect diseases, or susceptibility, by detecting mutations or the presence or amount of angiogenic protein expression. Particularly they are used to stimulate wound healing, growth of damaged bone and tissue, and for repair of vascular tissue, especially peripheral arterial disease, critical limb ischaemia or coronary disease. Antagonists of the sequences are used to inhibit angiogenesis in tumours and to treat inflammation (where associated with increased wascular permeability) dishatic retipocathy.
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          increased vascular permeability), diabetic retinopathy, rheumatoid arthritis or psoriasis. Agonists are also useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 226-227; 244pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis;
rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy;
infectious disease; neurodegeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        critical limb ischaemia or coronary disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding angiogenic proteins, useful e. promoting healing of wounds and treating peripheral arts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA91006
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                                                                                                                                                                                                                                                                                                             regeneration of the nervous system etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vascular endothelial growth factor-D; VEGF-D:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; angiogenic protein; wound healing; vascular tissue repair; peripheral arterial disease; critical limb ischaemia; coronary di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
  233
                                                                                    173
                                        61
                                                                             MMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFH 120
mmfdedrcecvcktpcpkdliqhpkncscfeckesletccqkhklfhpdtcscedrcpfh
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                                                                                                                                                                   100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                                                                                                                                         AA;
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Pred. No. 2.5e-70;
D; Mismatches 0;
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                                                                                                                                                                   Gaps
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RESULT
AAW49036
                The present sequence represents a human zvegf2 growth factor encoded by the zvegf2 cDNA which was isolated from a human heart cDNA library. Zvegf2 protein in a dimeric form acts as a mitogen for fibroblasts or smooth muscle cells. zvegf2 is claimed to be useful for stimulating the revascularisation of tissue or the re-endothelialisation of vascular tissue. zvegf2 is particularly claimed to be useful for the treatment of full-thickness skin wounds, including venous stasis ulcers and claimed to be useful as an additive in tissue adhesives for protein is also claimed to be useful as an additive in tissue adhesives for promoting revascularisation of the healing tissue. Antagonists against zvegf2 can be used to block its mitogenic, chemotactic and angiogenic effects. The antagonists may therefore be useful for reducing growth of solid tumours by inhibiting neovascularisation of the developing tumour or by directly blocking through the treatment of diabetic retinopathy, psoriasis,
                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                    New isolated vascular endothelial growth factor - used to develop products for treating e.g. wounds, burns, myocardial infarction, tumours, psoriasis, arthritis, restenosis or organ transplants
                                                                                                                                                                                                                                                                                                                                                                                                           18-SEP-1997;
06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human zvegf2 growth factor; mitogen; fibroblast; venous stasis ulcer; diabetic ulcer; skin wound; angiogenic effect; tumour; diabetic retinopathy;
                                                                                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9824811-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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                                                                                                                                                                                                                                                                                                               1998-333256/29.
DB; AAV32823.
                                                                                                                                                                                                                                                                                                                                                      DC,
                                                                                                                                                                                                                            Pages 53-54; 77pp; English.
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           scieroderma.
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96US-0759657
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275..294
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257..27
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206..256
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295..3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cysteine-rich domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Balbiani ring motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Balbiani ring motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cysteine-rich domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Pro-region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                      Hart
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                                                                                                                                                                                                                                                                                                                                                     Nygaard S,
                                                                                                                                                                                                                                                                                                                                                  Sheppard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           psoriasis; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        smooth muscle cell;
chemotactic effect;
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RESULT
AAW53241
ID AAW5
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Best Local Sin
Matches 153;
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10-FEB-1997;
19-JUN-1997;
                                                                                                                                                                                                                                                                                     01-JUL-1997;
23-AUG-1996;
23-AUG-1996;
                                               Claim 16;
                                                                     New isolated vascular endothelial growth factor-D - used to products for use in e.g. modifying angiogenesis or treating heart or intestinal disorders \,
                                                                                                                         N-PSDB;
                                                                                                                                                            Achen MG, Alitalo K,
                                                                                                                                                                                    (LUDW-) LUDWIG INST CANCER RES (UYHE-) UNIV HELSINKI LICENSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       modification; acceleration; wound healing; tissue; organ; transplants; collateral circulation; infarction; arterial s coronary artery disease; inhibition; cancer; treatment; diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive airway disease; intestinal malabsorptive syndrome; blopsy; metastatic risk; detection; diagnosis; congestive heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                       21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                       WO9807832-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW53241;
                                                                                                                                                                                                                                                               14-NOV-1996;
                                                                                                                                                                                                                                                                          11-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vascular endothelial growth factor; VEGF-D; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens vascular endothelial growth factor D (VEGF-D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW53241 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPH
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                                                                                                                                     1998-179057/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFH 120
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                                                                                                                         AAV20807
                                               Pages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                        96AU-0003554.
96US-0031097.
97AU-0004954.
97US-0038814.
97AU-0007435.
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                                                                                                                                                                                                                                                                                      96AU-0001825
96US-0023751
                                                                                                                                                                                                                                                                                                               97US-0051426
                                                                                                                                                                                                                                                                                                                                       97WO-US14696
                                              60-61; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 897; DB 19; 100.0%; Pred. No. 2.7e-70; tive 0; Mismatches 0;
                                                                                                                                                                                     LICENSING LTD.
                                                                                                                                                            Stacker SA,
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                                                                                                                                                            Wilks
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                                                                                  lung,
                                                                                               develop
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The sequence is that of human lung vascular endothelial growth factor D (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis

healing, tissue or organ transplantation,

or

to establish

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        collateral circulation in tissue infarction or arterial stenosis,
Such as coronary artery disease, and inhibition of angiogenesis in
the treatment of cancer or of diabetic retinopathy. It can also be
used in the treatment of lung disorders to improve blood circulation
cin the lung and/or gaseous exchange between the lungs and the blood
stream or to improve blood circulation to the heart and O2 gas
permeability in cases of cardiac insufficiency, to improve blood
flow and gaseous exchange in chronic obstructive airway disease,
or to treat malabsorptive syndromes in the intestinal tract.
Countitation of VEGF-D in cancer biopsy specimens may be useful
as an indicator of future metastatic risk. Antagonists can be used
for treating e.g. conditions such as congestive heart failure,
involving accumulations of fluid in the lung resulting from
increases in vascular permeability. The products can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
            The
                                   Claim 1; Page 18-20; 52pp; Japanese.
                                                                        VEGF-D protein encoded by DNA - useful
                                                                                                                                                                                                                                                            WO9802543-A1
                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                               Human vascular
                                                                                                                                                             (CHUG-) CHUGAI
                                                                                                                                                                                     15-JUL-1996;
                                                                                                                                                                                                            15-JUL-1997;
                                                                                                                                                                                                                                    22-JAN-1998
                                                                                                                                                                                                                                                                                                            inflammation;
                                                                                                                                                                                                                                                                                                                                                                        22-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                       AAW44293 standard; Protein; 354
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Ne present sequence represents
(VEGF-D). The VEGF-D protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection and diagnosis.
                                                                                                 1998-110591/10
DB; AAV15156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             trpcasgktacakhcrfpkekraaggphsrknp 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153;
                                                                                                                                    ,×
                                                                                                                                                                                                                                                                                                                        vascular
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                                                                                                                                    Nezu J;
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                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                             RES
                                                                                                                                                                                                                                                                                                                                             endothelial growth factor D.
                                                                                                                                                                                     96JP-0185216
                                                                                                                                                                                                            97WO-JP02456
                                                                                                                                                                                                                                                                                                                      endothelial growth factor D;
                                                                                                                                                             INST MOLECULAR MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No. 2.7
0; Mismatches
human vascular compounds and a
                                                                                                                                                                                                                                                                                                                                                                                                                       ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e 897; DB 19;
. No. 2.7e-70;
smatches 0;
                                                                        for,
                                                                       e.g.
                                                                                                                                                                                                                                                                                                                      VEGF-D;
                                                                      gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                      gene therapy;
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antibodies, endothelial

which growth

can factor an bind

or preventing

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psoriasis

and diabetic

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PR PR XX PR 
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AAB10649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-1998;
18-MAR-1999;
08-NOV-1999;
             This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an anglogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating
                                                                                                                                                                                                                                 New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                WPI; 2000-442669/38
                                                                                                                                                                                                                                                                                                                                                                                                                              Gordon RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antifrheumatic; antiarhritic; antipscriatic; antidiabetic; treatment; anglogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulter; pressure sore; tissue regeneration; tissue repair; wound; dermal ulter; pressure sore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human VEGD protein
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VEGF-D protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sprengel
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                                                                                                                                                                                                                                                                                                                                                                                                     č
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98GB-0028377.
99US-0124967.
99US-0164131.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ulcer; burns; skin graft growth; VEGD.
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ich bind to
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RESULT AAB29049 ID AAB29049 ID AAB29049 ID AAB2 XX AB2 XX AB2 XX Huma 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                     (LUDW-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGD protein used to illustrate the method of the invention.
                                                                                                                                                                                                  Screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vascular endothelial growth factor
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Milroy-Nonne syndrome; lymphoedema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Flt4; fms-like tyrosine kinase 4; lymphoedema;
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DB; AAC62407.
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UNIV HELSINKI LICENSING
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                                                                                                                                           a human subject for increased risk of developing a lymphatic comprises assaying a nucleic acid to determine a mutation the sequence of a vascular endothelial growth factor
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Pred. No. 2.7e-70;
Mismatches 0;
                                                         English
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                                                                                                                                                                                                                                                                                                                                                   Karkkainen
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present sequence is

the protein sequence

of the

human

The patent discloses a method to treat neoplastic disease characte by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also referred as vascular endothelial growth factor receptor-3, VEGFR-3 endothelial cells of blood vessels adjacent to malignant neoplasm. method involves administering a compound that inhibits binding of

characterised VEGFR-3) in

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Best Local
                                                                                                Treating neoplastic diseases such as lymphoma, carcinomas, melanomas and sarcomas, involves administering a compound capable of inhibiting binding of ligand proteins to fms-like tyrosine kinase-4 receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endothelial growth factor D (VEGF-D). It was used to demonstrate the methods of the invention, which involve the screening of individuals to determine which vascular endothelial growth factor receptor 3 (VEGFR-3, also known as F114 or fms-like tyrosine kinase 4) alleles they possess and thus their likelihood of developing hereditary lymphoedema. Conditions associated with lymphoedema include Milroy-Nonne syndrome, which is early onset lymphoedema and lymphoedema praecox, which is late
                                                                       Example 15-17; Page 142-143; 148pp; English
                                                                                                                                                                               Alitalo K,
                                                                                                                                                                                                                                               09-OCT-1998;
                                                                                                                                                                                                                                                                        08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                        Human; receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4; VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35; cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis; neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma
                                                                                                                                                                                                       (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prepro-vascular endothelial
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                                                                                                                                                                                                                                                                        99WO-US23525
                                                                                                                                                                                                                                               98US-0169079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                            VEGF-D;
                                                                                                                                                                               Valltola R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354
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                                                                                                                                                                                                                                                                                                                                                                            vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 897; DB 21; Pred. No. 2.7e-70;
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Best Local Similarity
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                                                                                                                                                                                                                                                   Key
Peptide
                                                                                                                                                                                                                                                                                                                                             Vascular endothelial growth factor-D; VEGF; human; re-endothelialisation; vascular endothelial growth factor receptor; VEGFR; vascular trauma; blood vessel; cardiovascular surgery; anti-restenosis agent; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endothelial cells. The compound is useful for treating neoplastic disease such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas and sarcomas. Plt4 receptor tyrosine kinase binding compounds can be used for manufacturing medicament useful for diagnostic screening, imaging and treatment of malignancies characterised by Flt4-expressing blood cells. The Flt4 gene maps to chromosomal region 5q35 and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in their 3' sequences and are differentially expressed in HEL and DAMI cell lines. Flt4 belongs to a subfamily of class III receptor tyrosine kinases (RTKs). It is used as a target for tumour imaging and anti-tumour therapy. The present sequence is a human prepro-vascular endothelial growth factor D (VEGF-D), a specific example of Flt4 binding compound. A recombinantly matured VEGF-D lacking residues 1-92 and 202-354
WO200024412-A2
                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                restenosis; stenosis;
                                                                                                                                                                                                                                                                                                                                                                                                            Human vascular
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                                                                          Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iirrsiqipeedrcshskklcpidmlwdsnkckcvlqeenplagtedhshlqepalcgph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                          endothelial growth factor (VEGF)-D protein
                                                                                                                        /note= "Cleavage results
VEGF-D protein"
93..201
                          /label= Carboxy_terminal_peptide
/note= "Cleavage results in partially-processed VEGF-D
protein"
                                                                                                                                                                                    /note= "Cleavage results in partially-processed VEGF-D protein" . 22..92
                                                                                                                                                  /label= Amino_terminal_peptide
/note= "Cleavage results in fully-processed mature
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                       /label= Recombinantly_matured_VEGF_D_protein
/note= "Processed vascular epithelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
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                                                                                                                                                                                                                                                                                                                                percutaneous transluminal coronary angioplasty.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present amino acid sequence is the complete human prepro-vascular endothelial growth factor (VEGF)-D. VEGF-D has the ability to stimulate re-endothelialisation of an injured blood vessel, without significant stimulation of smooth muscle cell proliferation. It can bind to and stimulate VEGFR-2 (vascular endothelial growth factor receptor) and/or VEGFR-3 phosphorylation in cells that express such receptors. An anti-restenosis agent comprising either a VEGF-D gene or protein is used in a method to reduce or prevent restenosis and stenosis of a blo vessel following vascular trauma e.g., cardiovascular surgery and percutaneous transluminal coronary angioplasty.
                                                                                                   Human; angiogenic protein; wound healing; vascular tissue repair; peripheral arterial disease; critical limb ischaemia; coronary disea angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis; rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy;
                        WO200075163-A1
                                                                                                                                                                                               05-APR-2001
                                                                                                                                                                                                                                                  AAY97573 standard;
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                                                Homo sapiens
                                                                                                                                                                                                                         AAY97573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                     infectious disease;
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DB; AAD00340.
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                                                                           endothelial
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l growth factor proteins
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                                                                                                                                                                    protein sequence
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                                                                          neurodegeneration;
l growth factor-D1;
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the nucleic acids
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RESULT 1
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                                                                                                                                                                                                                                                                                                                    Matches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                   lymph)angiogenesis. The proteins are also used to identify specific binding agents (potential therapeutic agents) and to raise antibodies. The antibodies are useful as therapeutic (ant)agonists; for detection, purification and targeting of proteins for in vivo or in vitro diagnosis (including imaging) or for therapy (including when linked to e.g. a label or cytotoxin); and for immunotyping of cells, e.g. for detecting minimal residual disease or haematopoietic progenitor/stem cells. It is also contemplated that the sequences might be useful for treating a very wide range of other disorders, e.g. autoimmune diseases; allergy; cancer; infectious diseases (viral, bacterial, fungal or parasitic); neurodegeneration, also as chemotactic agents or for stimulating
            Human VEGF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detecting mutations or the presence or amount of angiogenic protein expression. Particularly they are used to stimulate wound healing, growth of damaged bone and tissue, and for repair of vascular tissue, especially peripheral arterial disease, critical limb ischaemia or coronary disease. Antagonists of the sequences are used to inhibit angiogenesis in tumours and to treat inflammation (where associated with increased vascular respectively).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding angiogenic proteins, useful e.g. for promoting healing of wounds and treating peripheral arterial disease, critical limb ischaemia or coronary disease -
                                       27-FEB-2001
                                                                                        AAB37606 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    increased vascular permeability), diabetic retinopathy, rheumatoid arthritis or psoriasis. Agonists are also useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ameliorate disease and to detect diseases, or susceptibility, detecting mutations or the presence or amount of angiogenic p
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            regeneration of the nervous system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the DNA sequences encoding them, are used to prevent,
                                                                                                                                                                                                         sequence is vascular endothelial growth factor-D1 (VEGF-D1), h is an angiogenic protein of the invention. The angiogenic p
                                                                                                                                                       trpcasgktacakhcrfpkekraaqgphsrknp
                                                                                                                                                                                 TRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 153
                                                                                                                                                                                                                                                             iirrsiqipeedrcshskklcpidmlwdsnkckcvlqeenplagtedhshlqepalcgph
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                                                                                         Protein;
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Pred. No. 2.7e-70;
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The present invention relates to a method for screening a human subject CC for an increased risk of developing a lymphatic disorder e.g. hereditary CY lymphedoema. The method comprises assaying nucleic acid of a human Subject to determine a presence or an absence of a mutation altering the Sequence or expression of vascular endothelial growth factor receptor-3 CY (VEGFR-3)/fms-like tyrosine kinase 4 (Flt4) allele (see AAC68952 and CY AAB37604) and determining an increased risk of developing lymphatic CY disorder from presence or absence of the mutation. The presence of a mutation altering the encoded amino acid sequence or expression of at least 1 VEGFR-3 allele. In the nucleic acid sequence or expression of at 1.3 (1) vegence of the mutation altering the encoded amino acid sequence or expression of at cleast 1 VEGFR-3 allele. In the nucleic acid correlates with an increased risk of developing a lymphatic disorder. Treatment for hereditary 1.3 (1) vegence can be provided through the administration of vascular endothelial growth factor C (VEGF-C) and proteins. The present sequence is the protein sequence for VEGF-D.
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Best Local
AAB70685;
                                                      AAB70685 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening a human for an increased risk of developing lymphatic disorder comprises assaying nucleic acid for alterations in the sequences expressing vascular endothelial growth factor receptor-3
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16-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Pages 66-67; 99pp; English.
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16-MAY-2001

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method for inducing angiogenesis in a tissue, or area, in need of angiogenesis, in a mammal. The method comprises administering recombinant vascular endothelial growth factor [VEGF-D] or its angiogenically active fragment or mutant (I). The present sequence represents the human VEGF-D protein, which can be used in the method of the invention. (I) has cardiant and vasotropic activities, and is an angiogenesis inducer. The method can be used for inducing angiogenesis in a tissue in need of angiogenesis, or in an area in need of angiogenesis in a tissue in need of angiogenesis in a tissue in need of angiogenesis in a tissue in sectual for treating various ischaemic conditions manifested by vascular insufficiency such as peripheral vascular disease, coronary artery disease or myocardial
05-JUL-1997
                                            AAW14994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                                                       AAW14994 standard;
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                                                                                                                                                                                                                                                                                                                                                             3 Polypeptide sequences (AAW14993-95) are the respective translated sequences of reading frames 1, 2 and 3 of clone HF175 (AAT62961), th human homologue of murine clone F0401 (AAT62960), which codes for a novel c-Fos induced growth factor (FIGF) (see also AAW14992). Examination of the 3 polypeptides indicates that reading frame 2 has the longest region free of nonsense codons. FIGF is a C-fos-dependent autocrine growth factor able to induce cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide molecule encoding c-Fos induced growth factor protein useful in therapy, in manufacture of compositions for treatment developmental disorders and in generation of transgenic animal
                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Fig 2; 64pp; English.
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29-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT62961
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                                                                                                                                                                     Local Similarity
                                                                                                  trpcasgktacakhcrfpkekraaqgphsrknp
             TRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 153
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                                                                                                                                                                                                                        . 620
                                                                                                                                                          Conservative
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95GB-0019928.
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    stop codon in reading frame 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
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98.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *residue 605 corresponds to an stop codon in reading frame 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "residue 597
stop codon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stop
                                                                                                                                                                    Score 872; DB 18;
Pred. No. 6.9e-68;
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Murine c-Fos

induced growth factor

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RESULT 1
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Best Local
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                                                                                                                                                                                                                                                                                                                    This invention describes the novel preparation of biologically active dimers of recombinant human growth factors of the cysteine knot family starting from cellular inclusion bodies. Such dimers are are useful in pharmaceutical compositions and the method provides yields of 31-39.7%, in examples, compared with about 10% for the conventional method (see Biochemistry, 28 (1989) 2956). AAX08278-708301 are human growth factor protein fragments used in the method of the invention.
                             05-JUL-1997
                                                                      AAW14992 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                           yield
                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Page 9; 14pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                    Preparing active growth factor dimers from inclusion bodies in high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erdmann
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                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                          MMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFH 120
                                                                                                                     TRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 153
                                                                                                                                                              \verb|mtfdedrcecvckapcpgdliqhpencscfeckeslesccqkhkifhpdtcscedrcpfh|
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                                                                                                                                                                                                                                                                                                   337 AA;
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                             (first entry)
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                                                                                                                                                                                                                                                          82.4%;
82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mueller C,
                                                                      358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fragment FIGF (VEGF-D)
                                                                                                                                                                                                                                                         Score 739.5; DB 2
Pred. No. 1.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cysteine knot;
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Best Local S
Matches 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       c-Fos induced frowth factor; FIGF; Fos regulated gene;
proto-oncogene; lung disorder; cancer; tumour; therapy;
antibody; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide molecule encoding c-Fos induced growth factor protein - useful in therapy, in manufacture of compositions for treatment of developmental disorders and in generation of transgenic animal
                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 1; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-226216/20.
N-PSDB; AAT62960.
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29-SEP-1995;
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121 TRPCASGKTACAKHCREPKEKRAAQGPHSRKNP 153
|| || || || || || || || || || || :|::||
327 trtcasrkpacgkhwrfpketr-agglysgenp 358
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                                                                                                           cal Similarity
126; Conserv
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                                                                                                                                                                         Conservative
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95GB-0019928.
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                                                                                                                                                                                    82.4%; Score 739.5; DB 18; Length 358; 82.4%; Pred. No. 1.2e-56;
                                                                                                                                                                        Mismatches
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Search completed: October 17, 2001, 14:46:03 Job time: 129 sec

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Result
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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RESULT 1 US-08-915-795-3 Sequence 3, Application US/08915795 Sequence 3, Application US/08915795 PATENT NO. 6235713 GENERAL INFORMATION: APPLICANT: MATC G. ACHEN APPLICANT: MATC W. ACHEN APPLICANT: MATC W. ACHEN APPLICANT: Steven A. STACKER APPLICANT: Steven A. STACKER APPLICANT: Steven A. STACKER APPLICANT: MATC W. ACHEN APPLICANT: Steven A. STACKER APPLICANT: Steven A. STACKER APPLICANT: Steven A. STACKER APPLICANT: Washington STAIE: COMPUTER: INFORMATION STAIE: DC CITY: Washington STAIE: CCOMPUTER READALLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READALLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READALLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READALLE FORM: MEDIUM TYPE: PLOPS/MS-DOS SOFTWAREE: PATCHING SYSTEM: PC-DOS/MS-DOS SOFTWAREE: PATCHING SYSTEM: DOS SOFTWAREE: PATCHING SYSTEM: PC-DOS/MS-DOS SOFTWAREE: PATCHING SYSTEM: PC-DOS/MS-DOS SOFTWAREE: GLOST DATA: COMPUTER: LONG MAME: EVANS, JOSEPH D. REGISTRATION UNMBER: US/08/915,795 FILING DATE: CLASSIFICATION: 536 ATTORNET/ACHIN INFORMATION: TELEFRAN: (202) 628-8800 TELEFRAN: (202) 628-880 TELEFRAN: (202) 628-880 TELEFRANICONEC CHARACTERISTICS: LENGTH: 325 anino acids TYPE: anino acids TYPE: anino acids TYPE: maino acids THERMATION: NO ORIGINAL SOURCE: HUMAN Breast US-08-915-795-3	ALIGNMENTS	28 93.5 10.4 833 1 US-08-264-534-6 29 93.5 10.4 833 1 US-08-083-590A-2 30 93.5 10.4 833 1 US-08-465-500-6 31 93.5 10.4 833 2 US-08-346-126-6 32 93.5 10.4 833 2 US-08-346-126-6 33 93.5 10.4 833 2 US-08-346-126-6 34 93.5 10.4 833 3 US-08-346-128-6 35 93.5 10.4 833 3 US-08-89-3828-6 36 91.5 10.2 713 3 US-08-89-3828-6 37 91.5 10.2 713 3 US-08-89-385-9 38 91.5 10.2 717 3 US-08-872-855-9 39 90.5 10.1 1810 5 PCT-US95-11684-4 39 90.5 10.1 1810 5 PCT-US95-11684-4 39 90.5 10.0 799 2 US-08-525-940-23 40 89.5 10.0 881 2 US-08-976-838-21 41 89.5 10.0 881 2 US-08-976-838-21 42 89.5 10.0 881 2 US-08-976-838-21 43 89.5 10.0 915 2 US-08-525-940-18 45 89.5 10.0 915 2 US-08-976-838-18 46 89.5 10.0 915 2 US-08-976-838-18 47 89.5 10.0 915 2 US-08-976-838-18 48 89.5 10.0 915 2 US-08-976-838-18 49 Sequence 21, Appli 40 89.5 10.0 915 2 US-08-976-838-18
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Query Match Best Local Similarity

100.0%;

Score 897; DB 4 Pred. No. 1e-76;

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Length 325;

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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Hum
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                                                                                                     Matches 153;
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Best Local Similarity
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NAME: EVANS, JOSEPh D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
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                                                                                                                                                                                                                                                                               TYPE: amino acid
                61 MMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFH 120
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                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                        1 IIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPH 60
                                                                                                                                                                                                                                                     TOPOLOGY:
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                                           IIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPH 261
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1200 G Street, NW, Suite 700
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linear
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                                                                                                     Conservative
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Pred. No. 1.1e-76;
Mismatches 0;
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RESULT 3
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Best Local
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Patent No. 6235713
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Andrew F.
APPLICANT: Steven A.
APPLICANT: Kari ALII
                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
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NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,
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COMPUTER READABLE FORM:
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TELECOMMUNICATION INFORMATION:
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327 TRTCASRKPACGKHWRFPKETR-AQGLYSQENP 358
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                                                                                        61 MMPDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFH 120
                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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CLASSIFICATION:
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                                  TRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP 153
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Steven A. STACKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kari ALITALO
                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                 Mouse Lung
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                                                                                                                                                                                                                                                                                                                                                                                                     single
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                                                                                                                                                                                                                   Score 739.5; DB 4
Pred. No. 5.9e-62;
9; Mismatches 17
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Best Local Similarity
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APPLICANT: Marc G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                                                                                                                         APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                            APPLICANT: HU, JING-SHAN APPLICANT: ROSEN, CRAIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: GROV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 MTFDEDRCECVCKAPCPGDLIQHPENCSCFECKESLESCCQKHKIFHPDTC 312
STREET: 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 MMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTC 111
                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPH 60
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                                                      1100 NEW YORK AVENUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202) 628-8844
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Steven A. STACKER
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                                                                                       STERNE, KESSLER,
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85.6%;
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                                                                                       GOLDSTEIN & FOX
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; Sequence 2, Application US/08824996B
; Patent No. 5935820
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 350
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Best Local
                                               FILE REFERENCE: PF112D1
CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: 08/207,550
EARLIER FILING DATE: 1994-03-08
NUMBER OF SEQ ID NOS: 9
                                                                                                                                            APPLICANT: Cao, Liang
TITLE OF INVENTION: Polynucelotides Encoding Vascular Endothelial Growth
TITLE OF INVENTION: Factor 2
                                                                                                                                                                                                  APPLICANT: Hu, Jing-Shan APPLICANT: Rosen, Craig
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 06-JUN-1995
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (202)371-2600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 IIRRSLPATLPQ----CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDIC 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 --HSHLQE-----
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COMPUTER: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 CVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKT 129
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                      Craig A.
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; ORGANISM: Homo sapiens
US-08-824-996-2
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Best Local Similarity
Matches 57; Conserv
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 TELEFAX: (202)3
                                              REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: .TO B
FILING DATE: 24-DEC-1997
                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
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                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US FILING DATE: 8-MAR-1994
                                 TELEPHONE:
                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1100 NEW CITY: WASHINGTON
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(202)371-2540
OR SEQ ID NO: 4:
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ROSEN, CRAIG A.
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                                   (202)371-2600
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29.8%;
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US-08-510-133A-33
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Best Local Simi
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GENERAL INFORMATION:
                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
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             TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 28113/32863
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Joukov, Vladomir
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                                                                          TYPE: amino acid
                                                                                                                                                                                                                                            REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/510,133A FILING DATE: 01-Aug-1995 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Marshall, O'Toole, STREET: 6300 Sears Tower, 233 CITY: Chicago
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                                                                                         LENGTH: 350 amino acids
                                                                                                                                                                    TELEFAX: 312/474-0448
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South Wacker Drive
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Query Match
Best Local Similarity

27.3%; 29.8%;

Score 244.5; DB Pred. No. 1e-15;

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Length 350

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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NAME: Gass, David A.
REGISTRATION
REGISTRA
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212 GPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQ 271
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                         --HSHLQE-----PALCGPH-----69
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6300 Sears Tower, 233
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Pred. No. le-15;
6; Mismatches 47;
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; MOLECULE TYPE:
US-08-999-811-2
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; Sequence 2, Application US/08999811
; Patent No. 5932540
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS LENGTH: 419 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/999,81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20005
COMPUTER READABLE FORM:
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NAME: MARKOWICZ, KAREN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 8-MAR-1:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 06-JUN-
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APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2 NUMBER OF SEQUENCES: 15
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341 CVCKRTCPRNQPLNPGKCAC-ECTESPQKCLLKGKKFHHQTCSC-----YRRPCTNRQK 393
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                               70 CVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKT 129
                                                                                                               48 --HSHLQE-----
                                                                                                                                                                                                                          Local Similarity es 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
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394 ACEPGFSYSEE 130 ACAKHCRFPKE 140

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; MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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NAME: ERIC K. STEFFE
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                                               281 GPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQ 340
                                                                                                               224
                                                                                                                                                                          Local Similarity hes 57; Conserv
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CTTY: WASHINGTON
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                70 CVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKT 129
                                                                                48 --HSHLQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
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                                                                                                                                           1 IIRRSI--QIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQE-----ENPLAGTED-- 47
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                                                                                                            IIRRSLPATLPQ----CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDIC 280
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                                                                                                                                                                                                                                                                                                                                                                  (202)371-2540
                                                                                                                                                                          Conservative
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                                                                                                                                                                                         Score 244.5;
Pred. No. 1.:
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                                                                                                                                                                          Mismatches
                                                                                                                                                                                       1.2e-15;
                                                                                                                                                                                                       DB 3;
                                                                                                                                                                          47;
                                                                                                                                                                                                      Length 419;
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                                                                              -MMFDEDRCE 69
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US-09-042-105-18
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                                                                                                                                     Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202)371-254 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
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NAME: ERIC K. STEFFE
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSITUCATION DATA:
PRIOR APPLICATION NIMBER: TO BE ASSIGNED
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                                                               224 IIRRSLPATLPQ----CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDIC 280
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281 GPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQ 340
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                                 48 --HSHLQE-----
                                                                                                                                                                                                                                                                     STRANDEDNESS
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STREET: 1100 NEW YORK AVENUE
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                                                                                                   1 IIRRSI--QIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQE-----ENPLAGTED-- 47
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                                 ----PALCGPH-----
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                                                                                                                                 Score 244.5; DB Pred. No. 1.2e-15; Mismatches 4
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                                                                                                                                                                 DB 3;
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                               -----MMFDEDRCE 69
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US-08-795-430-8
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Query Match
Best Local Similarity
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                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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PRIOR APPLICATION NUMBER: 08/510,133
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PRIOR APPLICATION NIMBER: 08/585,895
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APPLICATION NUMBER: PCT/I
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses T
                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                          TELEPHONE: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/340,011 FILING DATE: 14-NOV-1994
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STATE: Illino
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                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                   NAME: Gass, David A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                             amino acid
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27.3%;
29.8%;
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Score 244.5; DB 4; Pred. No. 1.2e-15;
                   Length 419;
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; Sequence 35, Applicati
; Patent No. 6221839
; GENERAL INFORMATION:
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                                                                                                                                    Query Match
Best Local Similarity 29.8
Matches 57; Conservative
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INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
281 GPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQ 340
                                                                        224 IIRRSLPATLPQ---CQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDSTDGFHDIC 280
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                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
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APPLICANT: Annkov, Vladomir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Receptor Ligand
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                                     --HSHLQE----
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                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Gass, David A. REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/510,133A FILING DATE: 01-Aug-1995 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                       LENGTH: 419 amino acids
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                                                                                                                                                                   Score 244.5; DB 4;
Pred. No. 1.2e-15;
                                                                                                                                                 Mismatches
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South Wacker Drive
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                                   --- MMFDEDRCE 69
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                                                                                                                                                                                                                                                                                            Query Match 27.3%; Score 244.5; DB 5; Best Local Similarity 29.8%; Pred. No. 1.2e-15; Matches 57; Conservative 26; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9609001 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/465,96
FILING DATE: 6 JUN 95
APPLICATION NUMBER: 08/207,55
FILING DATE: 8 MAR 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 3258
                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: LI
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 419 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HU, ET AL.
TITLE OF INVENTION: Human Vascular EndothelialGrowth Factor 2
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
130 ACAKHCRFPKE 140
                                       341 CVCKRTCPRNQPLNPGKCAC-ECTESPQKCLLKGKKFHHQTCSC-----YRRPCTNRQK 393
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                                                                                                                         281 GPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQ 340
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CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                     48 --HSHLQE-----
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ZIP: 07068
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Db 394 ACEPGFSYSEE 404

Search completed: October 17, 2001, 14:47:13 Job time: 199 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
GenCore version 4.5
(c) 1993 - 2000 Comp
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tenascin-like prot
hypothetical prote
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30 93 10.4 2201 2 A32160 tenascin-C - human 31 92.5 10.3 577 2 A60501 thrombomodulin pre 32 92.5 10.3 846 2 A30889 integrin beta chai 33 92.5 10.3 1077 2 T41146 probable cysteine- 34 92 5 10 3 1680 2 A43434 furin kFC 3 4 21 7
92 10.3 1113 2 JE0315 92 10.3 1188 2 D86236 92 10.3 1188 2 D86236 91.5 10.2 527 2 A42032
91.5 10.2 572 2 T29880 91.5 10.2 722 2 T29820 91.5 10.2 1223 1 TVCHLV
91.5 10.2 1299 2 T43251 91 10.1 197 2 T10081
91 10.1 680 2 PNOS10 90.5 10.1 379 2 A59180 90.5 10.1 1620 2 T27283
3NMENTS
RESULT 1 \$69207 vascular endothelial growth factor C precursor - human
C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Datte: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 08-Oct-1999 C;Accession: S69207; S61795; S71443; S69208; G02659 R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel
EMBO J. 15, 1751, 1996 A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand A;Reference number: S69207; MUID:96203994
A:Accession: S69207 A:Status: nucleic acid sequence not shown A:Molecule type: mRNA
A;Residues: 1-419 <jou> A;Cross-references: EMBL:X94216; NID:gl177488; PIDN:CAA63907.1; PID:e221096; PID:gl18 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995</jou>
A; Note: this is a revision to the sequence from reference S61795 R; Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel
A;Reference number: S61795; MUID:96178224 A:Accession: S61795
A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 70-419 <joui></joui>
A;Note: this sequence has been revised in reference S69207 A;Accession: S71443 A;Molecule type: protein
W.I.
A;Residues: 1-419. <lee> A;Residues: 1-419.<lee> A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989</lee></lee>
submitted to the EMBL Data Library, May 1996 A;Reference number: H01557
A;Accession: GU2659 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molonila troe: mBNA
A;Residues: 1-419 <mor> A;Residues: 1-419 <mor> A;Cross-references: EMBL:U58111; NID:g1373426; PIDN:AAB02909.1; PID:g1373427</mor></mor>
C;GenetLos: A;Gene: GDB:VEGFC; VRP A:Cross-references: GDB:3890883: OMTM-601528
F;1-12/Domain: signal sequence #status predicted <sig></sig>

F;13-102/Domain: propeptide #status predicted <PRO>

9;

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R;Dignam, S.S.; Case, S.T. Gene 88, 133-140, 1990
A;Title: Balbiani ring 3 in A;Reference number: JQ0542;
                                                                                      185k secretory protein - midge (Chironomus N;Alternate names: balbiani ring 3 protein C;Species: Chironomus tentans C;Date: 31-Dec-1991 #sequence_revision 31-D
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$08167

$08167

Balbiani ring 3 protein - midge (Chironomus tentans)

C;Species: Chironomus tentans

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #:
                                                    C; Accession: JQ0542
R; Dignam, S.S.; Case
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A; Residues: 1-1700
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A;Title: The balbiani ring 3 gene in Chironomus tentans has A;Reference number: S08167; MUID:90172404
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;Superfamily: unassigned Balbiani ring proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 GPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQ
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                                                                                                                                                                                                                                                                                                                                           50 HLQEPALCGPHMMFDEDRCECVCKTP-----CPKDLIQHPKNCSCFECKESLETCCQKHK 104
                                                                                                                                                                                                                                                                                                                                                                                                                        13 RCSHSKKLCPIDM------LWDSNKCKCVLQEENPLAG---
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                                                                                                                                                                                                                                       TWNSQTCQCS--CP-ATGKCTGAQVWCSKACKCVCPAQKK 1394
                                                                                                                                                                                                                                                                                                               DKAKPASCGDKKSWNDDSCSCQCKSKMPCGGCPPNQQWNEKDC--
                                                                                                                                                                                                                                                                         LFHPDTCSCEDRCPFHTRPCASGKTACAKHCR--FPKEKR 142
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42; Conserv
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57; Conser
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29.8%;
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MUID:90269600
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Pred. No: 9.3e
22; Mismatches
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                  tentans
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                  which
                                                                                  disintegrin (EC 3.4.24.-) precursor - 1 (Species: Bos primigenius taurus (catt C;Date: 19-Jul-1996 #sequence_revision C;Accession: $66129; $32205 R;Glynn, P.; Howard, L.
                submitted to the EMBL Data Library, A;Description: identification of a: A;Reference number: S66129
A;Accession: S66129
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R;Deng, G.; McIntoSh, M.A.
J. Bacteriol. 176, 5929-5937, 1994
A;Title: An amplifiable DNA region from the Mycoplasma
A;Reference number: Z18888; MUID:95014025
                                                                                                                                                                                                                                                        Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1187 <DEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein P3 - Mycoplasma hyorhinis
C;Species: Mycoplasma hyorhinis
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
A; Molecule type: mRNA
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A;Experimental source: salivary gland
C;Superfamily: unassigned Balbiani ring
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A; Residues: 1-160 < DIG>
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Best Local S
Matches 36
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                                                                                                                                                                                                                                                                                                                              CEACK - - CQ - - - - ECEENCSCSELTCGCQEATCSCAQEHCGCQEESCACPNTTCACTEEH
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                                                                                                                                                                                                                                                                                                                                                                 C-VCKTPCPKDLIQHPKNCSCFE----CKESLETCCQKHKLFHPDTCSC-
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26.8%;
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                                                                                                                      (cattle)
ision 26-Jul-1996
                                                    mammalian
                                                                     October 1995
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A;Gene: FlyBase:Ten-m
A;Cross-references: FlyBase:FBgn0004449
C:Superfamily: unassigned EGF-related pu
F;514-540/Domain: EGF homology <EGF>
F;610-637/Domain: EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: disintegrin homology
C;Keywords: hydrolase; metalloproteinase; zinc
F;1-13/Domain: signal sequence #status predicted <SIG>
F;14-748/Product: metalloproteinase #status predicted <MAT>
F;456-546/Domain: disintegrin homology <OIS>
F;383,387,393/Binding site: zinc, catalytic (His) #status predicted
F;384/Active site: Glu #status predicted
Ş
                                           В
                                                                               Qy
                                                                                                                                 В
                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A54148; A; Accession: A54148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Levine, A.; Bashan-Ahrend, A.; Budai-Hadrian, O.; Cell 77, 587-598, 1994
A;Title: odd Oz: a novel Drosophila pair rule gene.
A;Reference number: A54148; MUID:94243925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Drosophila sp.
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 11-Jan-2000
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A54148
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                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-2406 <LEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Levine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: A54148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   odz protein - fruit fly (Drosophila sp.)
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A; Residues: 1-113,'LAM',117,'LLLMEDLKDSFRLMVAR',135-171,'R',173-652,'L'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, March 1993 A; Description: Identification of a mammalian \mathfrak{m}_{\mathsf{M}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z21961; NID:g1044810; PIDN:CAA79973.1; PID:g1044811 A;Note: this is a revision to the sequence from reference S32205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: this sequence has been revised in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: 221961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: $32205
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                                           CTCEAKWSGD-----DCS----KELCDLDCGQHGRCEGDACACDPEWGGEYCNTRLCDV 713
                                                                                   CVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCED----
                                                                                                                                                                       EEDRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDCGYSDQCKDECCYDANQ-PEGKKCKLKPGKQCSPSQGPCCTAHCAFKSKTEKCRDDSD 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEC----VCKTPCPKDLIQHPKNCSC-----FECKESLETCCQKHKLFHPDTCSCED--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKLNNNKFSLCSIRNISQVLEKKRNNCFVESGQP-----ICGNGMVEQGEE 470
  RCPFHTRPCASGKTAC----AKHC 135
                                                                                                                              EEVDCPHPN--CSGHGFCADGTCICKKGWKGPDCATMDQDALQCLPDCSGHGTFDLDTQT 663
                                                                                                                                                                                                                                         Similarity
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26.2%;
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22.3%;
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Pred. No. 0.13;
l8; Mismatches
                                                                                                                                                                                                                                    Score 105; DB 2;
Pred. No. 0.54;
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                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gartenberg, D.;
                                                                                                                                                                                                                                                           Length 2406;
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hypothetical protein C54G7.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #tc;Accession: T15840
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A; Residues: 1-2515 <BAU>
A: Cross-references: EMBL:X73154;
                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid A;Reference number: Z18416
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  В
                                    QΥ
                                                                                                                                                                      A;Gene: CESP:C54G7.3
A;Introns: 16/1; 53/2; 92/1; 160/3; 295/1; 346/1; 392/1; 440/1; 475/3; 579/1; 615/3; 46/1; 2561/2; 2603/2; 2626/2; 2665/2; 2716/3; 2804/3; 2884/3
                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-2946 < DUZ>
                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDB.
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A;Cross-references: FlyBase:FBgn0004449
C;Superfamily: unassigned EGF-related p;
F;298-324/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Ten(m), a Drosophila gene related to A; Reference number: S47008; MUID:94349920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Baumgartner, S.; Martin, D.; Hagios, C.; Chiquet-Ehrismann, EMBO J. 13, 3728-3740, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S47008
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C; Species: Drosophila melanogaster
C; Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_ch
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RPSTSILAGHQCTHNSE-CPSFSFCFSNSCNC-----
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                                    RRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
                                                                          Similarity 26.4 38; Conservative
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26.2%;
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                                                                                            Score 103; 1
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                                                                    Pred. No. 0.9.
5; Mismatches
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Pred. No. 0.
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                                                                                            DB .91;
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.56;
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  -MAGFRATSGICEPAIAVGEPC 1119
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                                                                                                            2; Length 2946;
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F; 23-1746/Product: tenasoin #status predicted 
F; 34-1746/Product: tenasoin #status predicted 
F; 346-372/Domain: EGF homology <EGF2>
F; 377-403/Domain: EGF homology <EGF2>
F; 377-403/Domain: fibronectin type III repeat homology <FN3A>
F; 711-793/Domain: fibronectin type III repeat homology <FN3B>
F; 802-884/Domain: fibronectin type III repeat homology <FN3C>
F; 892-976/Domain: fibronectin type III repeat homology <FN3E>
F; 984-1064/Domain: fibronectin type III repeat homology <FN3E>
F; 1073-1155/Domain: fibronectin type III repeat homology <FN3B>
F; 1164-1246/Domain: fibronectin type III repeat homology <FN3B>
F; 1254-1335/Domain: fibronectin type III repeat homology <FN3B>
F; 1343-4423/Domain: fibronectin type III repeat homology <FN3H>
F; 1431-1511/Domain: fibronectin type III repeat homology <FN3J>
F; 1526-1734/Domain: fibronectin type III repeat homology <FN3J>
F; 1536-1734/Domain: fibronectin type III repeat homology <FN3D>
F; 1536-1734/Domain: fibronectin type III repeat ho
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Eur. J. Biochem. 202, 643-648, 1991
A;Title: Complete primary structure of porcine
A:Paference number: S19694; MUID:92104189
                               R;Bierkamp, C.; Campos-Ortega, J.A. Mech. Dev. 43, 87-100, 1993
A;Title: A zebrafish homologue of the Drosophila A;Reference number: $42612; MUID:94128602
A;Accession: $42612
                                                                                                                                                                                                    C;Species: Brachydanio rerio (zebra fish)
C;Date: 20-Feb-1995 #sequence_revision 20
C;Accession: S42612
                                                                                                                                                                                                                                                                                                                                         RESULT
S42612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                  transmembrane protein precursor - zebra fish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-1746 <NIS>
A; Cross-references: EMBL:X61599; NID:g2124; PIDN:CAA43796.1; PID:g2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: S19694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N; Alternate names: contactin; hexabrachion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tenascin
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQCVCDEGFAGADCSERRCPSDCHNRGRCLDGRCEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRETCPVPCSEEHGRCVDGRCVCQE--GFAG-ED---CNEP-LC-LHNCHGRGRCVENEC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKKLCPIDMLWDSNKC----KCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRC---EC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VCDEGFTGEDCGELICPKDCFDRGRCINGTCY-CDEGFEGEDCGRLACPHGCRGRGRCEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCEDRCPFHTRPCASGKTACAKHC 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --KTPCPKDLIQHPK--NCSCFECKESLE-----TC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----RCP--FHTR-PCASGKTAC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.1%; 28.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 100; DB Pred. No. 1.1; 4; Mismatches
                                                                                                                                                                                                                                       20-Feb-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394
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                                                                                              neurogenic
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                                                                                                                                                                                                                                   #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SLKTVCSYNSYCSLMSS 1173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection
                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -CQKHKLFHP 108
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                                                                                                  Notch and
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QΥ
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C;Superfamily: unassigned EGF-related p:
F;295-328/Domain: EGF homology <EGX1>
F;422-450/Domain: EGF homology <EGF1>
F;457-488/Jomain: EGF homology <EGF>
F;533-564/Domain: EGF homology <EGF3>
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A; Residues: 1-2437 <ENIE>
A; Cross-references: EMBL:X69088; NID:g433866; PIDN:CAA48831.1;
C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repe
F;755-786/Domain: EGF homology <EGF1>
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-832 < KOP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Delta, a Drosophila neurogenic gene, A; Reference number: A31246; MUID:89196890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Kopczynski, C.C.; Alton, A. Genes Dev. 2, 1723-1735, 1988
A; Title: Delta, a Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Drosophil C; Date: 31-Mar-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurogenic protein Delta precursor - fruit fly (Drosophila melanogaster)
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F;1185-1216/Domain: EGF homology <EGF>
F;1185-1270omain: EGF homology <EGF>
F;1915-194/T/Domain: ankyrin repeat homology <AN1>
F;1948-1980/Domain: ankyrin repeat homology <AN2>
F;1948-2014/Domain: ankyrin repeat homology <AN3>
F;2015-204/T/Domain: ankyrin repeat homology <AN4>
F;2048-2080/Domain: ankyrin repeat homology <AN5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A31246
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                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 40; Conserv
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Best Local
                                        112
309
                                                                                 249
                                                                                                                                                                199 PRDDSFGHSTCSETGEIICLTG--WQGDYCHIPKCA-----KGCE-HGHCDKPNQCVC 248
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                                                                                                                     60 HMMFDEDRC-ECVCKTPCPKDLIQHPKNCSCFE-----CKESLETCCQKHKLFHPDTC- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 KCKCVLQEENPLAGTE-DHSHLQEPALCG---PHMMFDEDRCEC------VCK--TPCP 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
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NTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCHCR
                                                                                                                                                                                                        PEEDRCSHS-----KKLCPIDMLWDSNKC---KCVLQEENPLAGTEDHSHLQEPALCGP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYLCRCPPE---YTGPHCQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---CRFPKEKRAAQGPHSRK
                                                                                 QLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRPCKNGGTCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNPCANGGQCSAFE-SHYICTCPPN---FHGQTCRQDVNECAVSPSPCRNGGT-CINEVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCE-DRCPFHTRPCASGKTACAKH-- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KCDCVLGFSDRLCLTPVNHACMNSPCRNGGTCSLLTLDTFTCRCQPGWSGKTCQLADPCA 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #sequence_revision 31-Mar-1990 #text_change 11-Jan-2000
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27.9%;
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                                    -SCEDR---CPFHTRPCASG-----KTACAKHCR 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
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                                                                                                                                                                                                                                              Score 98.5; D
Pred. No. 0.81
L2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 99.5; D
Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                 57;
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RESULT

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R;Gao, Z.; Garbers, J.;
J. Biol. Chem. 273, 3415-342
A;Title: Species diversity i
                                                                                                                                                                                                                                                                                                                                                                                           zonagnesin - mouse
N;Alternate names: sperm-specific membrane protein
C;Species: Mus musculus (house mouson)
A; Description: functions in multiple cell adhesion processes A; Note: found exclusively on the apical region of the sperm C; Keywords: cell adhesion
                                                                   A; Map position: 5
C; Function:
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C;Superfamily: unassigned EGF-related p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 422-436,'ET',439-458,'A',460-489,'T',491-621 <KNU>
A;Cross-references: GB:X05140; NID:g7851; PIDN:CAA28786.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X06289; NID:g7852; PID:g7853 R;Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; EMBO J. 6, 761-766, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: gene Dl protein
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jul-2000
C;Accession: S00670; A26637
                                                                                                            A;Gene:
                                                                                                                                   C; Genetics:
                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-5376 <GAO>
                                                                                                                                                                                                A; Molecule
                                                                                                                                                                                                                                        A; Reference number: A; Accession: T42215
                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revisio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;1-18/Domain: signal sequence #status
F;19-88/Product: neurogenic repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and A; Reference number: A91081; MUID: 87218537 A; Accession: A26637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Vaessin, H.; Bremer, K.A.; Knust, E.; EMBO J. 6, 3431-3440, 1987
                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                     C; Accession: T42215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: Delta; Dl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-880 < VAE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: The neurogenic gene Delta
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                                                                 Function:
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Chem. 273, 3415-3421,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HMMFDEDRC-ECVCKTPCPKDLIQHPKNCSCFE-----CKESLETCCQKHKLFHPDTC- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRDDSFGHSTCSETGEIICLTG--WQGDYCHIPKCA-----KGCE-HGHCDKPNQCVC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEEDRCSHS ----- KKLCPIDMLWDSNKC --- KCVLQEENPLAGTEDHSHLQEPALCGP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
40; Conserv
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EGF homology <EGF2>
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                                                                                                                                                EMBL: U97068; NID: g3327420; PID: g3327421; PIDN: AAC26680.1
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22.9%;
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; MUID:98123114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 98.5; DB:
Pred. No. 0.85;
12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted <MAT>
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R;Pauley, A.; Stellyes, L.
R;Pauley, A.; Stellyes, L.
submitted to the EMBL Data Library, June 1995
submitted to the EMBL Data Library, June 1995
committed to the EMBL Data Library, June 1995
submitted to the EMBL Data Library, June 1995
                                                                          hypothetical protein F30H5.3 - Caenorha C;Species: Caenorhabditis elegans C;Date: 20-Sep_1999 #sequence_revision C;Accession: T16210
                                                                                                                                                                                                                                                                      QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Characterization of a thrombomodulin A;Reference number: A25918; MUID:87067408 A;Accession: A25918
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C;Superfamily: thrombomodulin; C-type lectin homology; EGF homology
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A; Residues: 1-356 < JAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Jackman, R.W.; Beeler, D.L.; VanDeWater, L.; Ro. Proc. Natl. Acad. Sci. U.S.A. 83, 8834-8838, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 30-Jun-1988 #sequence_revision C;Accession: A25918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
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nes 43; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERGGCQHECKGSAGASNCLCPADAALQADGRSCGLPAEHPCHQLCEHFCHLHGLGNYTCI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEDRCSHSKK-----LCPIDMLWDSNKCKCVLQEENPLAGTEDH-SHL----QEPAL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --FECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCR 136
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: EGF homology <EG4>
: EGF homology <EG5>
: EGF homology <EG6>
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22.1%;
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25.4%;
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Pred. No. 0.47;
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Pred. No. 3.3;
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A;Introns: 12/1; 59/2; 85/3; 124/3; 217/2; 534/3; 560/1; 1549/1
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A;Accession: T16210
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1599 <PAU>
A;Residues: 1-1599 <PAU>
A;Cross-references: EMBL:UZ9096; NID:g861390; PID:g861393; PIDN:AAA68408.1; CESP:F30H5.3
A;Experimental source: strain Bristol N2
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EMBL; U43142; AAA853
EMBL; U58111; AAB020
HSSP; P15692; 1VPF.
Kukk E., Lymboussaki A., Taira S., Kaipainen A., Jel
Joukov V., Alitalo K.;
"VEGF-C receptor binding and pattern of expression w
suggests a role in lymphatic vascular development.";
Development 122:3829-3837(1996).
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MEDLINE=97164697; PubMed=9012504;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                       SEQUENCE FROM N.A. STRAIN-BALB/C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                            -PALCGPH---
                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 (PARTIAL).

N-LINKED (GLCNAC. . . ) (PO'
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 244.5; DB 1;
Pred. No. 1.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VASCULAR ENDOTHELIAL GROWTH 4 X 24 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                            Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                 PRECURSOR
                                                                                                                                                                                                                     415
                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal;
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                                                                                                                                                                  (VEGF-C)
                                                  Jeltsch
                                                                                                                                                                                                                                                                                                                                                                                                                  ----ENPLAGTED--
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                               with
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(POTENTIAL).
(POTENTIAL).
                                                                                                                         Euteleostomi;
                                                                                                              Murinae; Mus
                                                                                                                                                                                                                                                                                                                -YRRPCTNRQK
                                                                                                                                                                                                                                                                                                                                                                           -MMFDEDRCE 69
                                                                                                                                                                  (FLT4 LIGAND)
                                                 Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                           419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT 3
BAR3_CHITE STANDARD;
AC Q03376;
DT 01-OCT-1993 (Rel. 27, Created)
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Best Local
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CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U73620; AAC52984.1; -. EMBL; U58112; AAB46707.1; -. HSSP; P15692; 1VPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Turner K.J., Wood C.R.; "Characterization of murine Flt4 ligand/VEGF-C. Oncogene 15:613-618(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fitz L.J., Morris J.C., Towler P., Wang J., Gassaway R., Nickbarg E., Giannotti J., Finnerty H., Zollner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002400; -
Pfam; PF00341; PDGF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:109124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97388482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                             130
                                                                                                                                      337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: HOMODIMER, SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: GROWTH FACTOR ACTIVE
                                                                                                                                                                                                                                IIRRSLPATLPQ---CQAANKTCPTNYVWNNYMCRCLAQQDFIFYSNVEDDSTNGFHDVC
                                                                                                                                                                                                                                                          IIRRSI--QIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQ------
                                                                                      --LKHC
                                                                                                             ACAKHC
                                                                                                                                    CVCKRTCPRNQPLNPGKCAC-ECTENTQKCFLKGKKFHHQTCSC----YRRPCANR--
                                                                                                                                                           CVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKT
                                                                                                                                                                                   GPNKELDEDTCQCVCKGGLRPSSCGPHKELDRDSCQCVCKNKLFPNSCGANREFDENTCQ
                                                                                                                                                                                                            --HSHLQE-----PALCGPH----
                                                                                                                                                                                                                                                                                   56;
                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth
                                                                                                              135
                                                                                      391
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
                                                                                                                                                                                                                                                                                                                                              Ā,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor; Glycoprotein; Signal;
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361
294
318
342
361
171
201
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                                                                                                                                                                                                                                                                                             26.48;
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                                                                                                                                                                                                                                                                                                                                              MW.
                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                             Score 236.5; 1
Pred. No. 7.8e
24; Mismatches
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N-LINKED (GLCNAC...

N-LINKED (GLCNAC...

N-LINKED (GLCNAC...

N-LINKED (GLCNAC...

D9D3DD3CECC659D6 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                          VASCULAR ENDOTHELIAL GROWTH FACTOR C. 4 X 24 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDE-LINKED (BY SIMILARITY).
PDGF/VEGF FAMILY OF GROWTH
                                                                                                                                                                                                                                                                                             236.5; DB
No. 7.8e-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Long A., Burgess P., (
Kovacic S., Ciarletta
R., Beier D.R., Leak I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IN ANGIOGENESIS,
                           1700
                                                                                                                                                                                                                                                                                                                                             CRC64;
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                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
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                                                                                                                                                                                                                                                                                                          415;
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Best Local Similarity
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Q9NOLB;
01-OCT-2000
01-OCT-2000
01-OCT-2000
                                                                                                                       MACEU
                            WAP.
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                                                                                                                                                                                                                                                                                      1246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paulsson G., Lendahl U., Galli J., Ericsson C., Wieslander L.;
"The Balbiani ring 3 gene in Chironomus tentans has a diverged
repetitive structure split by many introns.";
J. Mol. Biol. 211:331-349(1990).
-!- FUNCTION: USED BY THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR
STRUCTURE, THE LARVAL TUBE. BALBIANI RING PROTEIN 3 COULD PLAY A
ROLE AS A TRANSPORT PROTEIN THAT BINDS TO OTHER PROTEINS
INTRACELLULARLY AND IN THE GLAND LUMEN IN ORDER TO PREVENT THESE
FROM FORMING WATER-INSOLUBLE FIBERS TOO EARLY.
 Eukaryota; Metazoa;
              Macropus eugenii (Tammar wallaby)
                                                                                                                                                                                                                                  1301
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S08167; S08167.
HSSP; P18055; 2MRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Salivary gland; MEDLINE=90172404; Pubm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Chironomoidea; Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chironomus tentans (Midge)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BALBIANI RING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993 (Rel. 01-OCT-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X52263; CAA36506.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat;
                                                                                                                                                                                                     105 LFHPDTCSCEDRCPFHTRPCASGKTACAKHCR--FPKEKR 142
                                                                                                                                                                                                                                                           50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: HAS 82 APPROXIMATE REPEATS OF CYS-X-CYS-X-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: SALIVARY GLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: SECRETED
                                         ACIDIC
                                                                                                                                                                                                                                DKAKPASCGDKKSWNDDSCSCQCKSKMPCGGCPPNQQWNEKDC---ECKCSATGNCPAGQ 1357
                                                                                                                                                                          TWNSQTCQCS--CP-ATGKCTGAQVWCSKACKCVCPAQKK 1394
                                                                                                                                                                                                                                                                                                             RCSHSKKLCPIDM------LWDSNKCKCVLQEENPLAG-----TEDHS 49
                                                                                                                                                                                                                                                         HLQEPALCGPHMMFDEDRCECVCKTP-----CPKDLIQHPKNCSCFECKESLETCCQKHK 104
                                                                                                                                                                                                                                                                                    RC----VCPKNMEKPADNCKTKWWNDEMCQCVCKPGCPEGGCKGVMKWNANTCSCECPA 1300
                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR00876; MINEMATODE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90172404; PubMed=1689777;
G., Lendahl U., Galli J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000853;
                                                                                                                                                                                                                                                                                                                                                                                                              1700
                                                    (Rel. 40,
(Rel. 40,
(Rel. 40,
                                                                                                                                                                                                                                                                                                                                           Conservative
                                       PROTEIN PRECURSOR (TWAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Swiss Institute of Bioinformatics
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Rel. 30,
PROTEIN
                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         1700
 Chordata;
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26.2%;
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                                                      Last sequence update)
Last annotation updat
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3 PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                      Score 150.5; DB 1
Pred. No. 6.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
BALBIANI RING PROTEIN
Craniata; Vertebrata;
                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                          191
                                                   update)
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                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                           55,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and the
                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                          Indels
 Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                     1700;
                                                                                                                                                                                                                                                                                                                                          41;
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                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT
TENA_PIG
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Best Local :
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DISULFID
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DISULFID
TENA_PIG STA
Q29116; P98142;
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            three four-disulfide core during lactation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND 3D-STRUCTURE MODELLING TISSUE=Lactating mammary gland; mEDLINE=20390063; PubMed=10801834;
                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Milk; Whey; Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
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                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ005356; CAB90357.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simpson K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9315;
{1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Metatheria; Diprotodontia; Macropodidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicholas K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The gene for a novel member of the whey acidic protein three four-disulfide core domains and is asynchronously
                                                                                 153
                                                                                                     114
                                                                                                                              105
                                                                                                                                                    65
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                                                                                                                                                                                                 10
                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE WAP-TYPE 'FOUR-DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: SECRETED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: COULD BE A PROTEASE INHIBITOR
                                                                                 DDQCKENKKCCSS---ACGRRCTNPFPEEYEASQ
                                                                                                     EDRCPFHTRPCASGKTACAKHCR--FPKEKRAAQ 145
                                                                                                                             LGCEGKAKC-CASSCGQ-
                                                                                                                                                                                               EEDRCSHSKKLCPIDMLWDSNKCKCVLQEEN---PLAGTEDHS--HLQEPALCGPHMMFD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWP;
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                                                                                                                                                    ---EDRCECVCKTPCPKDLIQHPKNCSCF-----ECKESLETCCQKHKLFHPDTCSC 113
                                                                                                                                                                         DDASCPQNMRCCQRGCSW----LCMNTTQEKDGLCPVATSHSSSSEEQQRKQLCDKTCKTD
                                                                                                                                                                                                                        l Similarity 38; Conser
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                        STANDARD;
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2; Mismatches
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                        PRT;
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38, Created)

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Glycoprotein;
Extracellular
SIGNAL
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01-OCT-2000 (Rel. 40
TENASCIN PRECURSOR (GMEM) (JI) (MIOTENI
MATRIX ANTIGEN) (GP
                                                                                       PRINTS; F
PRINTS; F
PROSITE;
PROSITE;
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between
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Pfam; PF00008; EGF; 14.
Pfam; PF00147; fibrinogen_C;
Pfam; PF00041; fn3; 10.
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or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     astrocytes.";
J. Biochem. 122:1146-1152(1997)
-!- FUNCTION: SAM (SUBSTRATE-AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98158323; pubMed=9498558; Wakatsuki S., Ho S.H., Arioka M., Yamasaki M., Kitamoto K.; Wakatsuki S., Ho S.H., Arioka M., Yamasaki M., Kitamoto K.; "Isolation and characterization of a 230 kDa protein (p230) specifically expressed in fetal brains: its involvement in neurite outgrowth from rat cerebral cortex neurons grown on monolayer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
TISSUE-Submaxillary gland;
TISSUE-aprically pubmed=1722152;
Gillespie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X61599; CAA43796.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishi T., Weinstein J., Gillespie W.M., Paulson J.C.; "Complete primary structure of porcine tenascin: detection tenascin transcript in adult submaxillary glands."; Eur. J. Biochem. 202:643-648(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Fetal brain;
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ALTERNATIVE PRODUCTS: 3 ISOFORMS; MAJOR, MINOR-1 AND MINOR-2 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ARE PRODUCED IN A TISSUE-AND TIME-SPECIFIC MANNER DURING DEVELOPMENT.

TISSUE SPECIFICITY: SUBMAXILLARY GLANDS AND BRAIN.

DEVELOPMENTAL STAGE: PREDOMINANTLY EXPRESSED IN THE EMBRYONIC AND EARLY POSYNATAL STAGES. LITTLE OR NO DETECTION IN ADULT BRAIN.

EARLY POSYNATAL STAGES. LITTLE OR NO DETECTION IN ADULT BRAIN.

INDUCTION: BY TGF-BETA.

SIMILARITY: CONTAINS 15 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 FIBRINGGEN-LIKE DOMAIN.

SIMILARITY: CONTAINS 1 FIBRINGGEN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: SAM (SUBSTRATE-ADHESION MOLECULE) THAT APPEARS TO INHIBIT CELL MIGRATION. MAY PLAY A ROLE IN SUPPORTING THE GROWTH OF EPITHELIAL TUMORS.

FUNCTION: PLAYS A ROLE DURING EARLY BRAIN DEVELOPMENT PARTICULARLY IN GROWTH CONE GUIDANCE. INVOLVED IN NEURITE OUTGROWTH FROM CORTICAL NEURONS GROWN ON THE MONOLAYER OF ASTROCYTES.

SUBUNIT: HEXAMERIC. A HOMOTRIMER MAY BE FORMED IN THE TRIPLE COILED-COIL REGION AND MAY BE STABILIZED BY DISULFIDE RINGS AT BOTH ENDS. TWO OF SUCH HALF-HEXABERACHIONS MAY BE DISULFIDE LINKED GUIDANCE. INTEREST OF SUCH HALF-HEXABERACHIONS MAY BE DISULFIDE LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EM
                                                                                    FRO0011; EGFLAMININ.
FRO0014; FNTYPEIII.
E; PS00022; EGF_1; 15.
E; PS01186; EGF_2; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long and this statement is not removed requires a license agreement (See I
                                                                                                                                                                                                                                                                                                                               IPR000561; -. IPR001777; -.
                                                                                                                                                                                                                                                                                                       IPR002049;
                                                                                                                                                                                                                                                                                                                                                                                                                                       equires a license agreement (S
email to license@isb-sib.ch).
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(Rel. 40, Last annotation update)
ECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN)
(MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR
GEN) (GP 150-225) (TENASCIN-C) (TN-C) (P230).
          matrix;
                                                   Cell adhesion; Repeat; EGF-like domain; Coiled coil;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A ROLE DURING EARLY BRAIN DEVELOPMENT PARTICULARLY
          Alternative splicing; Signal.
2 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rmatics and the EMBL outs
There are no restrictions
ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1597-1608 AND
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FIBRONECTIN TYPE-III 7
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FIBRONECTIN TYPE-III 7
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FIBRONECTIN TYPE-III 9
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FIBRONECTIN TYPE-III 1
BY SIMILARITY
BY
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        (GLCNAC.
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Best Local S
Matches 44
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P46530;
O1-NOV-1995 (Rel. 32, Created)
O1-NOV-1995 (Rel. 32, Last sequence update)
15-UTL-1998 (Rel. 36, Last annotation updat
NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN PREC
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CARBOHYD
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Eukaryota; Metazoa; Chordata; Craniata; Verte
Actinopteryqii, Meopteryqii; Teleostei; Eutel
Cypriniformes; Cyprinidae; Rasborinae; Danio.
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CARBOHYD
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MEDLINE=94128602; PubMed=8297791;
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              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                             BRAIN AND HEAD REGIONS.
SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE E
SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                           EMBRYO DEVELOPMENT. MAY BE INVOLVED IN THE FORMATION OF THE BUDGET OF THE AUTOMOTE AND BRAIN VESICLES.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

DEVELOPMENTAL STAGE: EXPRESSED IN ALL CELLS IN PREGASTRULATION STAGES. DURING GASTRULATION IS DIFFERENTIALLY EXPRESSED, ACCUMULATING PREDOMINANTLY IN THE PRECHORDAL MESODERM AND NOTOCHORD. AT THE END OF GASTRULATION EXPRESSED ALONG THE ANTERIOR POSTERIOR AXIS INCLUDING THE DEVELOPING NEURAL PLATE AND DIFFERENTIATING MESODERM. ALSO PRESENT IN THE DEVELOPING
                                                                                                                                                                                                                                                          pattern of transcription during h. Dev. 43:87-100(1993).
                                                                                                                                                                                                                               FUNCTION: IMPLICATED IN CELL FATE SPECIFICATIONS EMBRYO DEVELOPMENT. MAY BE INVOLVED IN THE FORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _BRARE
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N PRECURSOR.
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Euteleostei; Ostariophysi;
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  Pfam; PF00008; EGF; 36.

Pfam; PF00063; ank; 6.

Pfam; PF00065; notch; 3.

Pfam; PF00066; notch; 3.

PRINTS; PR00009; EGFTGF.

PRXITS; PR00010; EGFBLOOD.

PROSITE; PS50088; ANK_REP_REGION; 1

PROSITE; PS500297; ANK_REP_REGION; 1

PROSITE; PS00010; ASX_HYDROXYL; 23.

PROSITE; PS001187; EGF_2; 28.

PROSITE; PS01187; EGF_CA; 22.
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P00740; 1IXA.
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RY MEDILINE-87067408; pubmed=3024152;

RA Jackman R.W., Beeler D.L., Vandewater L., Rosenberg R.D.;

RA Jackman R.W., Beeler D.L., Vandewater L., Rosenberg R.D.;

RT Similarity to the low density lipoprotein receptor.";

RT Similarity to the low density lipoprotein receptor.";

RT Proc. Natl Acad. Sci. U.S.A. 83:8834-8838(1986).

C -!- FUNCTION: THROMBOMODULIN IS A SPECIFIC ENDOTHELIAL CELL RECEPTOR THAT FORMS A 1:1 STOICHIOMETRIC COMPLEX WITH THROMBIN. THIS COMPLEX WITH THROMBIN. THIS COMPLEX WITH THROMBIN. THIS COMPLEX IS RESPONSIBLE FOR THE CONVERSION OP PROTEIN C OT THE ACTIVATED PROTEIN CA). ONCE EVOLVED, PROTEIN CA ACTIVATED PROTEIN C (PROTEIN CA). ONCE EVOLVED, PROTEIN CA SCISSIONS THE ACTIVATED COFACTORS OF THE COAGULATION MECHANISM, FACTOR VIIIA, AND THEREBY REDUCES THE AMOUNT OF THROMBIN GENERATED.

C --- TISSUE SPECIFICITY: ENDOTHELIAL CELLS ARE UNIQUE IN SYNTHESIZING THROMBOMODULIN.

C --- TISSUE SPECIFICITY: ENDOTHELIAL CELLS ARE UNIQUE IN SYNTHESIZING THROMBOMODULIN.
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      This SWISS-PROT entry is copyright. It is petween the Swiss Institute of Bioinformat the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                  copyright. It is produced through a collaboration tute of Bioinformatics and the EMBL outstation sizes Institute. There are no restrictions on its stitutions as long as its content is in no way nent is not removed. Usage by and for commercial
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Pfam; PF00008; EGF; 5.
PROSITE; PS00010; ASZ_HYI
PROSITE; PS00022; EGF_1;
PROSITE; PS01186; EGF_2;
_BRACL STANDARD; PRT; 1696 AA PCK5_BRACL STANDARD; PRT; 1696 AA Q9NNI5; Q9NJ16; Q9NNI4; 01-OCT-2000 (Rel. 40, Created) 01-OCT-2000 (Rel. 40, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A25918; A25918.
                                                                                                      YPTICRCPEG
                                                                                                                             FPKEKRAAQG
                                                                                                                                                                                                                           C--GPHMMFDEDRCECV----CKTPCPKDLIQHPKNCSCF------
                                                                                                                                                                            CQKHKLFHPDTCSCEDRC----PFHTRPCASG-----
                                                                                                                                                                                                                                                   ERGGCQHECKGSAGASNCLCPADAALQADGRSCGLPAEHPCHQLCEHFCHLHGLGNYTCI
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS01187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell;
                                                                                                                                                                                                                                                                                                                                                                                       148
164
182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                               ΑA;
                                                                                                      204
                                                                                                                              146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ASX_HYDROXYL; 2.
; EGF_1; FALSE_NEG.
; EGF_2; 3.
; EGF_CA; 2.
                                                                                                                                                    NCEYQCQPVGRSEHKCICAEGFAPVPGAPHKCQMFCNQTSCPADCDPH 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor;
                                                                                                                                                                                                                                                                                                                                                               37795
                                                                                                                                                                                                                                                                                                             10.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain.
                                                                                                                                                                                                                                                                                                                                                               WW;
                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blood coagulation;
                                                                                                                                                                                                                                                                                                             Score 98;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF-LIKE, CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF-LIKE, CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                               29B41F097ABE1093 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                              0.068;
                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                               67;
                                                                                                                                                                                                                                                                                                                         Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                            KTACAKHC -- R 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                            ECKESLETC
                                                                                                                                                                                                                                                                                                                                                                                     (BY
                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                  10;
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homologue of PC6 in the protocohordate amphioxus.";

12 Biochim. Biophys. Acta 1477:338-348 (2000).

23 Biochim. Biophys. Acta 1477:338-348 (2000).

24 CIVITY ORERESENT A WIDESPREAD ENDOPROTEASE ACTIVITY WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE OF CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR PROPROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-1-ZAA BONDS, WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.

25 C-1- CATALYTIC AND ACID AND YAA IS ARG OR LYS.

26 C-1- SUBCELLULAR LOCATION: ISOFORM A NAD ISOFORM C ARE SECRETED.

27 ISOFORM B IS A TYPE I MEMBRANE PROTEIN.

28 PRODUCED BY ALTERNATIVE SPLICING.

29 PRODUCED BY ALTERNATIVE SPLICING.

30 OMAIN: THE PROPEDFIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
                   VARSPLIC
VARSPLIC
                                                                                                                                                                                                         DOMAIN
TRANSMEM
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ACT_SITE
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ACT_SITE
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CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF184615; AAF26300.1; -. EMBL; AF184616; AAF26301.1; -. EMBL; AF184617; AAF26302.1; -.
                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00136; PROSITE; PS00137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oliva A.A. Jr., Chan S.J., Steiner D.F.; "Evolution of the prohormone convertases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM A; ISOFORM B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Me
Branchiostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (Rel. 40, Last annotation update) PROPROTEIN CONVERTASE SUBTILISIN/KEXIN TYPE 5
                                                                                                                            VARSPLIC
                                                                                                                                                CARBOHYL
                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20175281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PROPROTEIN CONVERTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RETICULUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00138; SUBTILASE_SER; 1.
e; Serine protease; Glycoprotein; Zymogen; Signal;
on pair of basic residues; Repeat; Alternative splicing;
                   1324
1288
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111
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tazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBTILASE_ASP;
SUBTILASE_HIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=10708868;
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1343
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                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
DTILLNKED (GLCNAC. . .) (POTENTIAL).
DDTILLNGECTISCGPGEYMDRREKKCKACHPTCKECSDEY
DDTCTACNDGFLLTDASSCEAGCP -> AENQNQASFCPFA
                                                                                                                                                                                                         CYS-RICH MOTIF (CRM) REGION.
CLEAVAGE (AUTO-) (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARI
CHARGE RELAY SYSTEM (BY SIMILARI
CHARGE RELAY SYSTEM (BY SIMILARI
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE
                   \begin{tabular}{ll} {\bf MISSING} & ({\tt IN} & {\tt ISOFORM} & {\tt C}). \\ {\tt CHPTCKECSDEYDDTCTACNDGFLLTDASSCEAGCPPGQFL} \\ \end{tabular}
                                                             PREVSVLAELALGHLRYSLTDVPPQSNSPPDTVLGADRARL TTATSAAGRCA (IN ISOFORM C).
                                                                                                                                                                                                                                                                                                                 HOMO
                                                                                                                                                                                                                                                                                                                                          CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PROPROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions on it ng as its content is in no ved. Hearn
                                                                                                                                                                                                                                                                                                                                                                                                                                              CONVERTASE SUBTILISIN/KEXIN
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                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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                                                                                                                                                                                                      M (BY SIMILARITY).
M (BY SIMILARITY).
M (BY SIMILARITY).
IARCVDRRDRSWCDLVLRFNFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q04592; Q62040:
Q1-FEB-1995 (Rel. 31, Created)
Q1-FCB-1995 (Rel. 40, Last sequence update)
Q1-OCT-2000 (Rel. 40, Last sequence update)
Q1-OCT-2000 (Rel. 40, Last annotation update)
Q1-OCT-2000 (Rel. 40, Last annotation update)
PROPROTEIN CONVERTASE SUBTILISIN/KEXIN TYPE 5 PRECURSOR (EC 3.4.21.-)
(PROPROTEIN CONVERTASE PC5) (SUBTILISIN/KEXIN-LIKE PROTEASE PC5)
(CONVERTASE PC5) (PC6) (SUBTILISIN-LIKE PROPROTEIN CONVERTASE 6)
                       Bendayan M., Seidah N.G.;
                                                                                                                                                                                                 candidate proprotein convertase expressed
nonendocrine cells.";
                                                                                                                                                                                                                                                                                                                                                                                               "Identification and functional expression of a new member of the mammalian Kex2-like processing endoprotease family: its striking structural similarity to PACE4.";
J. Biochem. 113:132-135(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1096
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain, and Intestine; MEDLINE=93224489; PubMed=8468318;
                                                                        De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama
                                                                                               PARTIAL SEQUENCE, MEDLINE=97103178;
                                                                                                                                                                                                                                               Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seida "cDNA structure of the mouse and rat subtilisin/kexin-like
                                                                                                                                                                                                                                                                                                                            TISSUE=Adrenal
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93327934; PubMed=8335106;
                                                                                                                                                                                                                                                                                                  MEDLINE=93342056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakayama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCK5_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakagawa T., Murakami K., Nakayama K.;
"Identification of an isoform with an extremely large Cys-rich region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 330-1877 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDEDYYLTEDTCVRRTNCPSFTYPDDQDRECRPCHDNCEACDGPNNQNCNSCKEGFYKTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a Kex2-like processing endoprotease.";
tt. 327:165-171(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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1696
ns of proprotein
compartments.";
                                                                                                                                                                         Acad.
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                                                                                                                                                                                                                                                                                                                            cortex;
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                                                                                               AND SUBCELLULAR LOCATION PubMed=8947550;
                                                                                                                                                                       Sci.
                                                                                                                                                                                                                                                                                                  PubMed=8341687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1696
A; 188410
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                         90:6691-6695(1993)
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No. 0
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Murinae; Mus
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PIR; PIR;

JX0248; JX0248 A48225; A48225

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1MPT

EMBL; D17583; BAA04507 EMBL; D12619; BAA02143 EMBL; L14932; AAA74636

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AND ECSA/SHOT; ARE PRODUCED BY ALTERNATIVE SPLICING.

-i- TISSUE SPECIFICITY: PC5A IS EXPRESSED IN MOST TISSUES BUT IS MOST ABUNDANT IN THE INTESTINE AND ADDRENALS. PC5B IS EXPRESSED IN THE INTESTINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.

-i- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO, EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE RIBS AND THE LIVER, BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENCIATED DECIDUA. AT E7.5, INTENSE EXPRESSION OBSERVED IN DIFFERENCIATED DECIDUA. AT E8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK SAC FOLLOWED BY A CONFINATION TO DERMANYOTOME COMPARTMENT. BETWEEN E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL CELLS OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS STAGE, STRONG EXPRESSION AND IN THE MUSCLE OF THE TONGUE. AT E16.5, ABUNDANT EXPRESSION THE CREEDED AT EACIAL CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5, ABUNDANT EXPRESSION AND STRONG EXPRESSION AND STRONG THE CARTILAGE AT E16.5, ABUNDANT EXPRESSION AND FACIAL CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5, ABUNDANT EXPRESSION AND STRONG EXPRESSION AND STRONG THE CARTILAGE AT E16.5, ABUNDANT EXPRESSION AND STRONG EXPRESSION AND STRONG EXPRESSION AND STRONG THE CARTILAGE AT E16.5, ABUNDANT EXPRESSION AND STRONG EXPRESSION EXP
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Rancourt S.L., Rancourt D.E.;
Runcine subtilisin-like proteinase SPC6 is expressed implantation, somitogenesis, and skeletal formation."
Implantation, 50mitogenesis, and skeletal formation."
Dev. Genet. 21:75-81(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Cell Biol. [5]
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                                              RETICULUM.

DOMAIN: AC 1 AND AC 2 (CLUSTERS OF SORTING INFORMATION. AC 1 DIRECTS T WITH THE TGN SORTING PROTEIN PACS-1 SIMILARITY: BELONGS TO PEPTIDASE EF SUBTILASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPROTEASE ACTIVITY WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
                                                                                                                                                                                                                                                                                                                                             ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF ISOFORM B OCCUR AT E12.5.

DOMAIN: THE PROPERTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; PC5B/LONG (SHOWN HERE)
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SUBCELLULAR LOCATION: PC5A IS SECRETED THROUGH THE REGULATED SECRETORY PATHWAY. PC5B IS A TYPE I MEMBRANE PROTEIN LOCALIZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE AC OF GROWTH FACTORS.

CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR PROPROTEINS BY CLEAVAGE OF ARG-YAA-YAA-ARG-|-ZAA BONDS, WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT EARLY ENDOSOMES.
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                                                                                                 G PROTEIN PACS-1.
TO PEPTIDASE FAMILY
                                                                                                                                                                                                  USTERS OF ACIDIC AMINO ACIDS)
DIRECTS TGN LOCALIZATION AND
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                                                                                                      ALSO KNOWN AS
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Pfam; PF00082; Peptiidase_S8; 1.
PRINTS; PR00723; SUBTILASE_ASP;
PROSITE; PS00136; SUBTILASE_HIS;
PROSITE; PS00137; SUBTILASE_HIS;
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InterPro;
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PROSITE; PS00137; SUBFILASE_HIS; 1.
PROSITE; PS00138; SUBFILASE_SER; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
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                                                                -ACAK----H--CRFPKEKRAA----QGPH
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                                                                                                                       HVAVEGVCKHCPERCQDCIHEKTCKECMPDFFLYNDMCHRSCPKSFYPDMRQCVPCHKNC
                                                                                                                                       HLQEPALCG--PHMMFD---EDRC-EC-----VCKTPCPKDLIQHPKNC----SC
                                                                                                                                                          EGRCYHS----CPEGFYAKDGVCEHCSSPCKTCEGNATSCNSCEGDFVLDHGVCWKTCPEK 1342
                                                                                                                                                                            EDRCSHSKKLCPIDMLWDSNKCK-----CVLQEENPLAGTE-----DH-----S
                                               LACREGFTVVHDVCTAPKECAAVEYWDEGSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CLEAVAGE (AUTO-)
CELL ATTACHMENT :
                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYS-RICH MOTIF (CRM) REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                (IN ISOFORM PC5A)
 PRT;
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                                                                                                                                                                                               Mismatches
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EC850E2DF20EA1C3
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No. 0.
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M (BY SIMILARITY).
M (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                          (POTENTIAL
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                                                                                                                       1402
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hastin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syland S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Dong F.N., Zhong W., Zhong S., Zhao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu S., Zhu X., Smith H.O.,
RA Albers S.M., Woodsge T., Worley K.C., Wu D., Yang S., Zhou X., Smith H.O.,
RA Shows Sequence of Drosophila melanogaster.";
RT. Science 287.1385.7000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RA Adams D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Berandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borksva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borksva D., Botchan M.R., Bouck J., Brokstein P., Canter A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleisschmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N. I. Harnand T. J. Hernandez J. P. Harris M.,
Harris N. I. Harnand T. J. Harnandez J. P.
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STRAIN-OREGON-R; TISSUE-Embryo;

MEDLINE-89196890; PubMed-3149249;

Kopczynski C.C., Alton A.K., Fechtel K., Kooh.P.J., Muskavitch M.A.T.;

"Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes a protein related to blood coagulation factors and epidermal growth factor of vertebrates.";

Genes Dev. 2:1723-1735(1988).
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01-MAR-1989 (Rel. 10, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
NEUROGENIC LOCUS DELTA PROTEIN PRECURSOR.
SEQUENCE OF 422-621 FROM N.A. TISSUE=Embryo;
                                                                           Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with
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with EGF-like repeats.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=BERKELEY;
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"The neurogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. 6:3431-3440(1987).
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enic gene Delta
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ta of Drosophila melanogaster is
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PRESENTABLE PROPERTIES AND PROPERTIE
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InterPro: IPRO00561; -.
InterPro: IPRO01861; -.
InterPro: IPRO01881; -.
InterPro: IPRO01881; -.
Pfam; PPO01414; DSL; 1.
Pfam; PPO00008; EGF: 9
PROSITE: PS00010; ASX_HYI
    DOMAIN
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TRANSMEM
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CHAIN
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                                                                                                                                                                                                                                                                           Differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S00670; S00670.
PIR; A26637; A26637.
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Development 110:905-914(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0000463; Dl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91209246; PubMed=2128477;
Hannlin M., Kramatschot ה
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Knust E., Dietrich U., Tepass U.,
Campos-Ortega J.A.;
"EGF homologous sequences encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IS REQUIRED FOR THE COR
CELL LINEAGES.
- SUBCELLULAR LOCATION: T
- TISSUE SPECIFICITY: DET
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TISSUE SPECIFICITY: DETECTED IN ALL AREAS WITH NEUROGENIC
ABILITIES, FOR EXAMPLE THE NEUROGENIC ECTODERM AND THE PRIMORDIA
OF THE SENSE ORGANS. LATER EXPRESSION IS RESTRICTED TO THOSE CELLS
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IN REQUIRED FOR THE CORRECT SEPARATION OF NEURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P00740;
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Y00222; CAA68369.1; -.
AE003725; AAF55657.1; -.
X05140; CAA28786.1; -.
                                                                                                                                                                                                                                                                                                 PS00010; ASX_HYDROXYL;
PS00022; EGF_1; 9.
PS01186; EGF_2; 9.
PS01187; EGF_CA; 2.
                                                                                                                                                                                                                                                           domain;
Neurogenesis; Repeat; T
Glycoprotein; Signal.
18 POTENTIAL.
18 NEUROGENIC
653 EXTRACELLUL
654 POTENTIAL.
18 R33 CYTOPLASMIC
258 EGF-LIKE 1.
289 EGF-LIKE 2.
289 EGF-LIKE 2.
372 EGF-LIKE 3.
372 EGF-LIKE 3.
416 EGF-LIKE 5.
POTENTIAL.
CYTOPLASMIC
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
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NEUROGENIC LOCUS DELTA PROTEIN
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                       (POTENTIAL).
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AND EPIDERMAL
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RESULT 11
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                                                                  NTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCHC
                                                                                                                                         QLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRPCKNGGTCF
                                                                                                                                                                          HMMFDEDRC-ECVCKTPCPKDLIQHPKNCSCFE-----CKESLETCCQKHKLFHPDTC-
                                                                                                                                                                                                                                                PEEDRCSHS-----KKLCPIDMLWDSNKC---KCVLQEENPLAGTEDHSHLQEPALCGP
                                                                                                                                                                                                             PRDDSFGHSTCSETGEIICLTG--WQGDYCHIPKCA-----KGCE-HGHCDKPNQCVC
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                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                88840
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                                                                                                       SCEDR - - - CPFHTRPCASG - - -
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                                                                                                                                                                                                                                                                                     12;
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EGF-LIKE 8, CALCIUM-E
EGF-LIKE 9, CALCIUM-E
EGF-LIKE 1, CALCIUM-E

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Pred. No. 0.33
L2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         M -> YVTPKİRKGSWEIRRNPHGGADSTYTKKRLGWVQNV
RETPKMLLLIEAV (IN REF. 1).
; EDBA107A0003D9A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  (IN REF. 1).
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-!- SIMILARITY: CONTAINS 1 FIBRINGEN-LIKE DOMAIN

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SEQUENCE FROM N.A.

MEDLINE-95155442; PubMed-7531707;

MEDLINE-95155442; PubMed-7531707;

Gherzi R., Carnemolla B., Siri A., Ponassi M., Balza E., Zardi L.;

"Human tenasoin gene. Structure of the 5'-region, identification,

Characterization of the transcription regulatory sequences.";

J. Biol. Chem. 270:3429-3434(1995).
                                                                                                                                                                 Leahy D.J., Hendrickson W.A., Aukhil I., Erickson H.P.;
"Structure of a fibronectin type III domain from tenascin
MAD analysis of the selenomethionyl protein.";
Science 258:987-991(1992).
-i- FUNCTION: SAM (SUBSTRATE-ADHESION MOLECULE) THAT APPER-
INHIBIT CELL MIGRATION. MAY PLAY A ROLE IN SUPPORTING
OF EPITHELIAL TUMORS.
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P24821; Q15567; Q14583;
Q1-MAR-1992 (Rel. 21, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN)
(GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR
MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C).
                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF FIBRONECTIN MEDLINE-93068293; PubMed=1279805;
                                                                                                                                                                                                                                                                                                                                 Gulcher J.R., Nies D.E., Marton L.S., Stefansson K.;
"An alternatively spliced region of the human hexabrachion repeat of potential N-glycosylation sites.";
Proc. Natl. Acad. Sci. U.S.A. 86:1588-1592(1989).
                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Glioblastoma;
TISSUE=Glioblastoma;
TISSUE=Glioblastoma;
TND=R9160821; PubMed=2466295;
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MEDLINE-91131572; PubMed-1704365;
Nies D.E., Hemesath T.J., Kim J.H.,
"The complete cDNA sequence of humar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human tenascin: primary structure, pre-mRNA splicing patterns localization of the epitopes recognized by two monoclonal antibodies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92052108; PubMed=1719530; Gulcher J.R., Nies D.E., Alexakos M.J.,
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marton L.S., Stefansson K.;
"Structure of the human hexabrachion
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OF EPITHELIAL TUMORS.

SUBGNIT: HEXAMERIC. A HOMOTRIMER MAY BE FORM COILED-COIL REGION AND MAY BE STABILIZED BY BOTH ENDS. TWO OF SUCH HALF-HEXABRACHIONS MA WITHIN THE CENTRAL GLOBULE.

SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.

ALTERNATIVE PRODUCTS: FOUR VARIANTS ARE PRODUCTS. FOUR VARIANTS ARE PRODUCTS. ALTERNATIVE PRODUCTS. FOUR VARIANTS ARE INDUCTION: BY TGF-BETA.

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SIMILARITY: CONTAINS 15 FIBRONECTIN TYPE III
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T.J., Kim J.H., Gulcher J.R., Stefansson K.; sequence of human hexabrachion (Tenascin). A containing unique epidermal growth factor
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Pfam; PF00008; EGF; 4.
Pfam; PF00059; lectin_c; 1
PRINTS; PR00907; THRMBOWOD
PROSITE; PS00010; ASX_HYDR
PROSITE; PS00022; EGF_1; PF
PROSITE; PS01186; EGF_2; 3
PROSITE; PS01187; EGF_CA;
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TRANSMEM
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DOMAIN
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P15306;
01-APR-1990
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InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dittman W.A., Kumada T., Sadier J.E., Majerus P.W.;

"The structure and function of mouse thrombomodulin. Phorbol
myristate acetate stimulates degradation and synthesis of
thrombomodulin without affecting mrna levels in hemangioma cells.";
J. Biol. Chem. 263:15815-15922(1988)
-I- FUNCTION: THROMBOMODULIN IS A SPECIFIC ENDOTHELIAL CELL RECEPTOR
THAT FORMS A 1:1 STOICHIOMETRIC COMPLEX WITH THROMBIN. THIS
COMPLEX IS RESPONSIBLE FOR THE CONVERSION OF PROTEIN C TO THE
ACTIVATED PROTEIN C (PROTEIN CA). ONCE EVOLVED, PROTEIN CA
SCISSIONS THE ACTIVATED COFACTORS OF THE COACULATION MECHANISM,
FACTOR VA AND FACTOR VIIIA, AND THEREBY REDUCES THE AMOUNT OF
                                                                                                                         Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dittman W.A., Majerus P.W.:
Dittman W.A., Majerus P.W.:
"Sequence of a cDNA for mouse thrombomodulin and predicted mouse and human amino acid sequences.";
Nucleic Acids Res. 17:802-802(1989).
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01-APR-1990 (Rel. 14, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
THROMBOMODULIN PRECURSOR (FFTOMORE)
                                                                                                                                                                             Endothelial
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Mammalia; Eutheria;
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SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A32001; A32001.
S08488; S08488.
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                                                                                                                                                                       PS01186;
PS01187;
PS50041;
Lial cell;
                                                                                                                                                                                                                                                                                                                                                                                              ; IPRO00152; -.; IPRO00561; -.; IPRO01304; -.; IPRO01491; -.; IPRO01881; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s (Mouse).
Metazoa; Chordata; C
Metazoa; Rodentia; S
  518
542
240
                                                                                               Signal;
                                                                                                                                              7; THRMBOMODULN.
10; ASX_HYDROXYL; 2.
22; EGE_1; FALSE_NEG.
86; EGF_2; 3.
87; EGF_CA; 2.
41; C_TYPE_LECTIN_2; 1.
41; Receptor; Blood coagu
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PRECURSOR (FETOMODULIN) (TM).
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nal; EGF-like
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
EGF-LIKE 1.
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Matches 43
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Mackrell A.J., Blumberg B., Haynes S.R., Fessler J.
Mackrell myospheroid gene of Drosophila encodes
homologous to vertebrate integrin beta subunits.",
Proc. Natl. Acad. Sci. U.S.A. 85:2633-2637(1988).
CHARACTERIZATION.
MEDLINE=94163982;
                                                                                                                                                                        SEQUENCE FROM N.A.
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(Rel. 12, Last sequence update)
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TA-SUBUNIT MYOSPHEROID PRECURSOR
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                                                                                                         membrane
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RESULT 14
FUR2_DROME
ID FUR2_DROME
AC P30432;
DT 01-APR-1993
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Matches 39
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grinblat Y., Zusman S., Yee G., Hynes R.O., Kafatos F.C.; "Functions of the cytoplasmic domain of the beta PS integring Drosophila development."; Development 120:91-102(1994).

-i- FUNCTION: NOT KNOWN. PROBABLY PLAYS A ROLE IN CELL ADH-
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00022; EGF_1; PROSITE; PS01186; EGF_2; Integrin; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rtam; rruus62; integrin_B; 1.
PROSITE; PS00243; INTEGRIN_BETA;
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PIR; A30889; A30889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
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                                                                                          CEDRCPFHTRPCASGKTACAKHCR
                                                                                                                                                                         EEDRCS-HSKKLCPI----DMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDE
                                                                                                              DCSGRGHCVCGACECHKRPNPIEIIS-GKHCECDNFSCERNRNQLCS-----GPDHGTCE
                                                                                                                                                                                             Similarity 27.3
39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                email to license@isb-sib.ch).
  (Rel.
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  25, Created)
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27.1%;
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UNKNOWN_1.
Transmembrane;
                                                                                                                                                                                                                                                ₹,
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IV.

N-LINKED (GLCNAC...
                                                                                                                                                                                            Score 92.5; D
Pred. No. 0.41
l3; Mismatches
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SER-RICH.
CYSTEINE-RICH
                     PRT;
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                                                                       641
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                     1680
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                                                                                                                                                                                                                Length
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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integrin
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RX MEDIINE=92381036; PubMed=1512259;
RA Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
RA Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., kurzik-Dumke U.,
RA Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.;
RT Gloring and functional expression of Drurin2, a subtilisin-like
RT Proprotein processing enzyme of Drosophila melanogaster with multiple
RT proprotein processing enzyme of Drosophila melanogaster with multiple
RT repeats of a cysteine motif.";
RL J. Biol. Chem. 267:17208-17215(1992).
CC -i- FUNCTION: FURIN IS LIKELY TO REPRESENT THE UBIQUITOUS ENDOPROTEASE
ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF
CC -I- FUNCTION STATE RELEASE OF AGTIVITY PATHWAYS AND CAPABLE OF
CC CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF (BY SIMILARITY).
CC -I- CATALYTIC ACTIVITY: RELEASE OF AMPURE PROTEINS FROM THEIR
CC PROPROTEINS BY CLEAVAGE OF ARG-NA-YAA-ARG-I-ZAA BONDS, WHERE XAA
CC CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS. RELEASES ALBUMIN,
CC PROPROTEINED DECLINE DECLINE CONTINUED TO MILLEBRAND FACTOR FROM THEIR
                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                        PROPEP
CHAIN
ACT_SITE
ACT_SITE
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PROSITE; pS00136; SUBTILASE_ASP; 1.
PROSITE; pS00137; SUBTILASE_HIS; 1.
PROSITE; pS00138; SUBTILASE_SER; 1.
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000209; -.
InterPro; IPR002174; -
InterPro; IPR002884; -
InterPro; F00757; Furin-like;
Pfam; PF01483; P; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0004598; Fur2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M94375; AAA28551.1;
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NCBI_TaxID=7227;
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15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESPECTIVE PRECURSORS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS SUBTILASE FAMILY. HIGH SIMILARITY WITH OTHER FURIN-LIKE E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A43434; A43434.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              melanogaster (Fruit fly).
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Zymogen.
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Last annotation update)
PRECURSOR (EC 3.4.21.75) (FURIN
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FURIN-LIKE PROTEASE 2

CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
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CHARGE RELAY SYSTEM (
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usage
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(BY SIMILA
(BY SIMILA
(BY SIMILA
, CYS-RICH.
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RESULT 15
SELP_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                       FUJII M., Saljoh K., Kobayashi T., Fujii S., Lee M.J., Sumino K.;

"Analysis of bovine selenoprotein P-like protein gene and availability of metal responsive element (MRE) located in its gromoter.";

Gene 199:211-217(1997)

-i- FUNCTION: IT CONSTITUTES A MAJOR SELENIUM POOL IN THE BRAIN AND MAY PLAY AN IMPORTANT ROLE IN DEVELOPING AND/OR MODULATING THE MORPHOLOGY OF NEURONS AND/OR GLIAL CELLS.

-i- SUBCELLULAR LOCATION: EXTRACELULAR (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: EXTRACELULAR (BY SIMILARITY)

IN THE CEREBELLAR CORTEX, HIPPOCAMPUS AND OLFACTORY BULB.

-i- MISCELLANEOUS: THE SELENOCYSTEINES ARE ALL ENCODED BY THE OPAL
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P49907; 019003;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence upd
01-0CT-2000 (Rel. 40, Last annotation u
SELENOPROTEIN P-LIKE PROTEIN PRECURSOR.
SEPP1 OR SELP.
                                                                                                                                                                                                                                    MEDLINE-9534621; PubMed=7637580; Saijoh K., Saito N., Lee M.J., Fujii M., Kobayashi T., Saijoh K., Saito N., Lee M.J., Fujii M., Kobayashi T., "Molecular cloning of cDNA encoling a bovine selenopro protein containing 12 selenocysteines and a (His-Pro) insertion, and its regional expression."; Brain Res. Mol. Brain Res. 30:301-311(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
SEQUENCE
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CARBOHYD
                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=98019090;
                                                                                                                                                                                                                                                                                                                                                    Bovidae; Bovinae;
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota, Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1016
                                                                                                                                                                                                                                                                                                                   TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N
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European Bioinformatics Institute.

SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -

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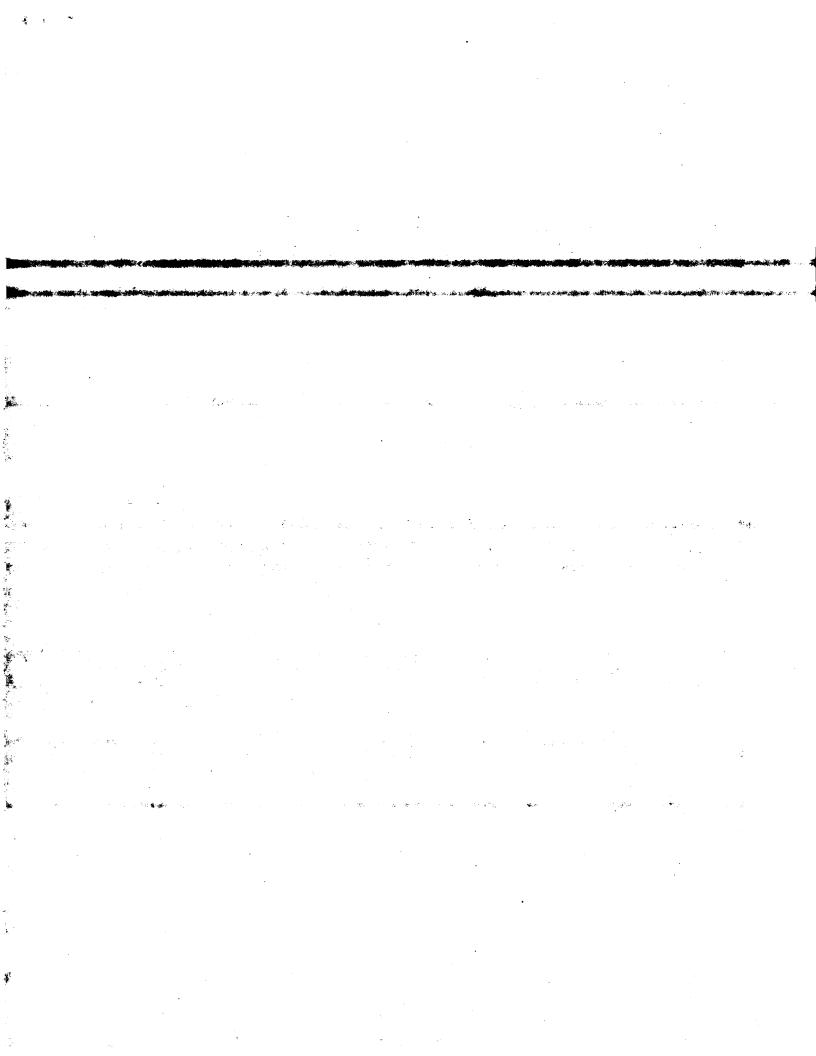
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EMBL; D88031; BAA23414.1; JOINED.
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                    118 PFHTRPC-----ASGKTAC---AKHCRFP 138
366 RLPPAACQAAGQQLNPTEASTKCSCKNKAKMCKCP 400
                                                        308 QFPKYSESALSSCCCHCRHLVFEKTGSAITCQCTEKL--PSLCSCQGLLAEENVIESCQC 365
                                                                                                             252 ENPPTSGLHHHHHRHK-----GPQRQGHSDNCDTPLGSESLQPSLPQKKLCRKRCINQLLC 307
                                                                                 82 QHPK-----NCSC-----FECKESLETCCQKHKLFHPDTCSCED------RC 117
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402 AA;
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11; Mismatches 4
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Search completed: October 17, 2001, 14:51:51 Job time: 477 sec

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Result
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4: sp_human:
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6: sp_mamm;
7: sp_mhc.
8: sp_ph
10: sp_h
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3 - 2000
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Q94446 chironomus
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043915;
01-JUN-1998
01-JUN-1998
01-MAR-2001
"Vascular endothelial growth factor D (VEGF-D) is a ligand for the tyrosine kinases VEGF receptor 2 (Fik1) and VEGF receptor 3 (Fit4)."; Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).

EMBL; Y12864; CAA73371.1; -...
EMBL; Y12865; CAA73371.1; JOINED.
EMBL; Y12865; CAA73371.1; JOINED.
EMBL; Y12867; CAA73371.1; JOINED.
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MEDLINE-98118549; PubMed-9435229;

Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F.,

Alitalo K., Stacker S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLING=98140120; PubMed=9479493;

MEDLING=98140120; PubMed=9479493;

ROCChigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,

Rossi E., Ballabio A., Zuffardi O., Oliviero S.;

"Human FIGE: cloning, gene structure, and mapping to chromosome Xp22.1

between the PIGA and the GRPR genes.";

Genomics 47:207-216(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97349118; PubMed=9205122;
Yamada Y., Nezu J., Shimane M., Hirata
"Molecular cloning of a novel vascular
VEGF-D.";
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[3]
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PR InterPro; IPR000072;

PR Pfam; PF00341; PDGF; 1.

PROSITE; PS00249; PDGF; 1.

PROSITE; PS00249; PDGF; 1.

SMARR; SM00141; PDGF; 1.

SMARR; SM00141; PDGF; 1.

SEQUENCE 358 AA; '^^.
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Best Local Similarity
Matches 153; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR D (C-FOS INDUCED
VEGF-D OR FIGF.
                                                                                                                                                                                                                                                                                                                                                                                 P97946;
01-MAY-1997 (TrEMBLrel.
01-MAY-1997 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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ProDom; PD001529; -; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
                                                                                                            Genomics 42:483-488(1997).
EMBL; X99572; CAA67892.1;
EMBL; D89628; BAA14002.1;
                                                                                                                                                                                                                                            Ordandini M., Marconcini L., Ferruzzi R., "Identification of a c-fos-induced gene tiplatelet-derived growth factor/vascular e
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=057BL/6J;
MEDLINE=97030254; PubMed=8876195;
                                                                                                                                                                                                                                   platelet-derived
family.";
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                              VEGF-D.
                                                                                                                                                      MEDLINE=97349118; PubMed=9205122;
Yamada Y., Nezu J., Shimane M., Hirata
"Molecular cloning of a novel vascular
                                                                                                                                                                                           FISSUE=LUNG;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
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                                                                                                                                                                                                                         Natl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
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Pred.
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Sciurognathi;
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               6636B17FBF07037C CRC64;
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No. 1.2e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                358
                                                                                                                                                       endothelial growth factor
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                                                                                                                                                                                                                                              that is related to endothelial growth
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DT 01-MAR-2001 (TrEMBLrel. 16, Las
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Best Local
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ProDom; PD001629; -; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
SEQUENCE 326 AA; 37112 MW;
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O35251;
O1-JAN-1998
O1-JAN-1998
O1-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-SPRAGUE DAWLEY;
MEDLINE-97349118; PubMed-9205122;
Yamada Y., Nezu J., Shimane M., Hirata
"Molecular cloning of a novel vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF014827;
HSSP; P15692; 1
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EMBL; AF014827; AAB66557.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VASCULAR ENDOTHELIAL VEGF-D.
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                                                                                                                                                                                                                                                                                                                                                                                                                          98;
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3 (TrEMBLrel. 05,
1 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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AA; 37112 MW;
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                                         Last sequence update)
Last annotation update)
FACTOR-D (FRAGMENT).
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Pred. No. 4.1e
9; Mismatches
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Pred No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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endothelial
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.7e-55;
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Matches 53
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Best Local S
Matches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu X., Yonekura H., Yamaqishi S., Yamamoto Y., Yamamoto "Structure and expression of bovine VEGF family."; submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases. EMBL, ABO04275; BAA77687.1; -.
                                                                                                                                                                                                                                                                                                        SMART; SM00141; PDGF; Signal.
                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00249; PDGF_1; PROSITE; PS50278; PDGF_2; SMART; SM00141; PDGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (Tremblrel. 12, 01-NOV-1999 (Tremblrel. 12, 01-MAR-2001 (Tremblrel. 16, VASCULAR ENDOTHELIAL GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mandriota S.J., Pepper M.S.;
Submitted (OCT-1998) to the I
EMBL; AF099135; AAG29747.1;
NON_TER 1
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000072;
Pfam; PF00341; PDGF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
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                                                                               Local Similarity
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GPNKELDEETCQCVCKGGLQASSCGPHKELDRDSCQCVCKNKLFPSSCGANREFDENTCQ
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21
420 AA;
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122 AA;
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                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                               20 PO
420 V
46681 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122
13820 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                    26.0%;
28.5%;
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90.9%;
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Pred.
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Last annotation update)
FACTOR C PRECURSOR.
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Pred.
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                                                                                                                                                                                                                                                                    POTENTIAL.
VASCULAR ENDOTHELIAL GROW
58BA84317A3C8E2D CRC64;
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                                        HSHLQE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC504B00E29D54EB
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                                                                                                                                                                                    233.5;
No. 6.5
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No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420
                                                                                                                                                                                  5; DB 6;
i.5e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
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                                        -PALCGPHMMFDEDRCE 69
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                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                         GROWTH
                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                         FACTOR
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Best Local
Q94438;
Q94438;
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057352;
01-JUN-1998
01-JUN-1998
01-MAR-2001
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Eichmann A., Corbel C., Jaffredo T., Breant V., Joukov V., Kumar V.,
Alitalo K., Le Douarin N.M.;
"Avian VEGF-C: cloning, embryonic expression pattern and stimulation
of the differentiation of VEGFR2-expressing endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00249; PDGF_1; PROSITE; PS50278; PDGF_2; SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Archosauria; Aves; Neognathae; Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00438; GFCYSKNOT. ProDom; PD001629; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y15837; CAA75799.1; HSSP; P15692; IVPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGF-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00341; PDGF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        precursors."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coturnix
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                                                                                                                                                         AEEVCR
                                                                                                                                                                                                         CAKHCR 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIRRSLP-ATQTQCHVANKTCPKNHVWNNQICRCLAQHDFGFSSHLGDSDTSEGFHICGP
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                                                                                                                                                                                                                                                         CKKTCPKHHPLNPAKCIC-ECTESPNKCFLKGKRFHHQTCSCYRPPCTVRTKRCDAGFLL
                                                                                                                                                                                                                                                                                                             CKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPDTCSC-EDRCPFHTRPCASGKTA 130
                                                                                                                                                                                                                                                                                                                                                          NKELDEETCQCVCKGGVRPISCGPHKELDRASCQCMCKNKLLPSSCGPNKEFDEEKCQCV
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(Tremblrel. 06, 1
(Tremblrel. 16, 1
(DOTHELIAL GROWTH 1
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                          PRELIMINARY;
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29.0%;
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Last annotation updat
FACTOR C PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 231; DB 13; Pred. No. 1.2e-16;
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VASCULAR ENDOTHELIAL GROWTH FACTOR
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                          1698
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nes; Phasianidae; Phasiani
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01-FEB-1997
01-OCT-2000
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01-FEB-1997
01-OCT-2000
                                                                         InterPro; IPR000561; -.
InterPro; IPR000853; -.
PRINTS; PR00876; MTNEMATODE.
PROSITE; PS00022; EGF_1; UNKNOWN_2.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
SEQUENCE 1704 AA; 185745 MW; 3A
                                                                                                                                                                                                                      TISSUE-SALIVARY GLAND;
Case S.T., Cox C., Bell W.C.,
Submitted (APR-1996) to the EI
EMBL; U54641; AAA99804.1; -.
                                                                                                                                                                                                                                                                                                                                                                                          Chironomus thummi thummi (Midge).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Mentezoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Chironomoidea; Chironomidae; Chironominae; Chironomus.
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TISSUS-SALIVARY GLAND;
TISSUS-ST., COX C., Bell W.C., Hoffman R.T., Martin J., I
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
EMBL; U54640; AAA99803.1; -.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Chironomoidea; Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220
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Interpro; IPRO00853; -.
PRINTS; PRO00876; WINEMATODE.
PROSITE; PS00022; ECF_1; UNKNOWN_1.
SEQUENCE 1698 AA; 186164 MW; 82
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Chironomus
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745 MW; 3A3F20247C8F1E28
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Last sequence
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     Score
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Q9NKD7 PRELIMINARY; PRT; 648 AA.

Q9NKD7;
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C1-2000 (TrEMBLrel. 15, Last sequence update)
C1-2000 (TrEMBLrel. 16, Last annotation update)
C1-2000 (TrEMBLrel. 16, Last annotation update)
C1-2000 (TrEMBLrel. 16, Last annotation update)
C1-2000 (TrEMBLrel. 15, Last sequence update)
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Matches 46; Conserv
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REPEAT REGIONS IN POTENTIAL M
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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Last annotation update)
METAL BINDING PROTEIN G
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Pred. No. 0.00
20; Mismatches
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7; Mismatches 37;
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                                                                                Hexapoda; Insecta;
                                                                                                                                                                                                                   update)
                                        Brachycera;
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NCBI_TaxID=7227;

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RESULT 11
Q9VJU4
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                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
02-MAR-2001 (TrEMBLrel. 16, Last annotation update)
03-MAR-2001 (TrEMBLrel. 16, Last annotation update)
03-MAR-2001 (TrEMBLrel. 16, Last annotation update)
03-MAR-2001 (TrEMBLrel. 16, Last annotation update)
03-MAY-2000 (TrEMBLrel. 13, Created)
03-MAY-2000 (TrEMBLrel. 13, Last sequence update)
03-MAY-2000 (TrEMBLrel. 16, Last annotation update)
03-MAY-2000 (TrE
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003408; AAF44845.1; -
FlyBase; FBgn0028939; BG:DS00180.14.
InterPro; IPR000561; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ashburner M., Misra S., Roote J., Lewis S.E., Line, Misra S., Roote J., Lewis S.E., Line, Misra S., Roote J., Lewis S.E., Line, Misra S., Boyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.
MEDLINE=20196006;
                                                                                                                                                                                                                                                                                                                                                                                           Q9VJU4;
                                                       SEQUENCE FROM N.A.
                                                                                                            NCBI_TaxID=7227;
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STRAIN=Y, CN BW SP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01186; EGF_2; UNKNOWN_6
SMART; SM00181; EGF; 1.
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"An exploration of the sequence of a 2.9-Mb region of the genome of
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MEDLINE=99403001; PubMed=10471707;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        648 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
PubMed=10731132;
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RESULT
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RA Harris N.L. Harvey D. Heiman T.J. Wei M.-H. Ibegwam C.

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA McIntov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,

RA McIntov G., Milshina N.Y., Mobarry C., Morris J., McPherson D.L.,

RA McIntov G., Milshina N.Y., Mobarry C., Morris J., McPherson D.L.,

RA McIntov G., Milshina N.Y., Mobarry C., Morris J., McPherson D.L.,

RA McIntov G., Milshina N.Y., Mobarry C., Morris J., McPherson D.L.,

RA Rimert K., Remington K., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,

RA Zheng R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

Event. Annoracy.
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Best Local
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O74567 PRELIMINARY;
O74567;
01-NOV-1998 (TrEMBLrel. 08,
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PROSITE; PS01186; EGF_2; UNKNOWN_6.
SMART; SM00181; EGF; 1.
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HSSP; P02876; 9WGA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amanatides P.G. Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Levis S.E., Richards S., Ashburner, Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Neison C.R., Miklos G.L.G., Man K.H., Man K.
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nes 51; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                 CSSPGVCTCLEGFQALLSFYCIPVCSKTCIHGSCVAPNECRCFTG--YRPNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \tt HEGFEKTSPHRCSPTCRPGCGQNSRCAAPDTCACDVGYVFVNGSTTECEPFCPRNCRNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PYCNPPCTNGTCISPGHCACSEGHVFAEGSRHECVPSCRSGCENGYCSSPGRCEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNECRCHPGHEQRLGVPWICDPICSSGCANGYCQGAEVCACKMGYAHKDNTLASGCE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEEDRC--SHSKKL-----CPIDMLWDSNKCKCVL---QEENPLA-GTEDHS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FE-----CKESLET-CCQKHKLFHPDTCSCE-----DRC-PFHTRPCASG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF53366.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75366 MW; 95159C04C9C09BD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 112.5; DB Pred. No. 0.0005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---HMMFDEDRCECV--CKTPCPKDLIQHPKNCSC
                                                                                                                                                                                                                                                                                                                                                                                             KTACAKHCRFPKEKRAAQGPHSRKNP 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367
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ALD DE CONTROL OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bhandari D., Bolshakov S.,
A Bortkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
A Bortkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
A Bortkova D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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Best Local :
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01-MAY-2000 (Trem
01-MAR-2001 (Trem
01-MAR-2001 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; i
Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    filamentous fungi and BR3 salivary protein of the Proc. Natl. Acad. Sci. U.S.A. 95:6212-6216(1998). EMBL; X95671; CAA64974.1; -. InterPro; IPR000561; -. PROSITE; PS01186; EGF_2; 1. SEQUENCE 704 AA; 77925 MW; 63414BDDEC365EBC CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG15011
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Rey M., Ohno S.A., Pintor-Toro J.A., Jose A., Llobell A.,
"Unexpected homology between inducible cell wall protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9VZF2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9VZF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QI74 PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KHKLFHPD---TCSCED-----RCPFHTRPCASGKTACAKHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNKGEVFDQKTKTCSCPDGQYWNGKQCVCPYGKIFDGKQCVEDCGKDAHFDNNQKKCVCN 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CS-----CPDGQYWNGKQCACPYGQIFNGKQCVPD------CGKDATYDYNQKKCVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSHSKKLCPIDMLWDSNKCKCVL-QEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNGEIYDSKSKTCSCPDSQYWDGSKC----ACPYGTVWDGKHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PCPKDLIQHPKNCSC----FECKESLETC--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.3%;
23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endopterygota; Diptera; Brachycera; Muscomorpha; ilidae; Drosophila.
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13,
16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitosporic Ascomycota; Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fly)
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annotation update)
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protein QID74 of,
le insect Chironomus.";
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McCeod M.P., McPherson D.,
RA McIson S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA McIson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syliskas R., Tector C., Turner R., Venter E., Mang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Zhon Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster.";
BML; AE003480, AAF47871.1; -.
DR Flybase; FBgn0035518; CG15011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                      Q10741;
Q10741;
01-NOV-1996;
01-NOV-1996;
                                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pe
                                                                                                                                                                                                                                                                 01-NOV-1996 (TrembLrel. 01, 01-NOV-1996 (TrembLrel. 01, 01-MAR-2001 (TrembLrel. 16, DISINTEGRIN-METALLOPROTEASE
                Howard L., Lu X., Mitchell S., Griffths S., Glynn I "Molecular cloning of MADM: a catalytically active disintegrin-metalloprotease expressed in various of Biochem. J. 317:45-50(1996).
              Biochem.
                                                                                                                                                                                                                                                       METALLOPROTEINASE)
                                                                                         MEDLINE=96276398;
                                                                                                                            SEQUENCE FROM
                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                               Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01422; zf-NF-X1; 7.
PROSITE; PS0062; EGF_L; UNKNOWN_1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
SMART; SM00438; ZnF_NFX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCEDRCPFHTRPCASGKTACAKHCRFPKEKRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---CEKVCHAGPCGDGECPLQVRSCPCGKNCCGDQCPPCEKİCGKQLSCNKHK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KCNQVCHQPGKCPPCTSKSLQPCEC--QRESKMVNCSDRKWKCQNVCGAPFACGLHI--- 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCS---HSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQE----PALCGPHMMFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDRCECVCKT-----PCPKDLIQHP--KNCSCFECKESLETC----CQKHKLFHPDTC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                          N.A.,
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                                                                                         PubMed=8694785;
                                                                                                                                                                                                                                                     (MADM).
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84556 MW;
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25.7%;
                                                                                                                            PARTIAL
INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                    PRECURSOR (EC 3.4.24.-)
                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                         Created)
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                            SEQUENCE
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                                     cell
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                                                      mammalian
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                                                                                                                                                                                                 Bovoidea;
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Best Local Similarity
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CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                             Q9NL50;
01-OCT-2000
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ACT_SITE
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CHAIN
                                                                           Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Oesttroidea; Sarcophagidae; Sarcophaga.
                                                                                                                                                                                    Q9NL50
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METAL
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SIGNAL
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InterPro;
Kobayashi A., Hori S.,
"Sarcophaga prepupal h
Submitted (AUG-1999) t
                                                                                                                                       01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
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PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                           01-OCT-2000 (TrembLrel. 15
01-OCT-2000 (TrembLrel. 15
01-MAR-2001 (TrembLrel. 16
120-KDA PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                  TISSUE-HEMOCYTE;
                                            SEQUENCE FROM N.A.
                                                                    NCBI_TaxID=7386;
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STMTLARITY: HIGH, IN THE MIDDLE REGION,
                                                                                                                                                                                                                                            CAKEGICNGITALCPASDPKPNFTDCNRHTQVCINGQCAGSICEKH 575
                                                                                                                                                                                                                                                                                         CDCGYSDQCKDECCYDANQ-PEGKKCKLKPGKQCSPSQGPCCTAHCAFKSKTEKCRDDSD
                                                                                                                                                                                                                                                                                                                                     DKLNNNKFSLCSIRNISQVLEKKRNNCFVESGQP-----ICGNGMVEQGEE 470
                                                                                                                                                                                                                                                                                                                                                            DRCSHSK-KLCP---IDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDR 67
                                                                                                                                                                                                                                                                                                             CEC----VCKTPCPKDLIQHPKNCSC-----FECKESLETCCQKHKLFHPDTCSCED---
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                                                                                                                                                                                                                                                                                                                                                                                                                                           748
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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213
455
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748
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383
387
393
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551
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22.3%;
., Natori S.;
hemocyte-specific 120-kDa
to the EMBL/GenBank/DDBJ c
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. 15, Last sequ
. 16, Last anno
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ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

VINC (CATALYTIC) (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                            Score 108; DB 6;
Pred. No. 0.0016;
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                                                                                         Muscomorpha;
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Best Local S
Matches 33
                                                                                                                                                                                                       SMART; SM00181; EGF; Signal.
                                                                                                                                                                                                                                    EMBL; AB031297; BAA92143.1; -.
Interpro; IPR000561; -.
PROSITE; PS01186; EGF_2; UNKNOWN_7.
                                                                                                                                                                                             SEQUENCE
                     116
390
                                             330
                                                                                        295
                                                                 71
                                                                                                               11
                 ----RC-PFHTRPCASGKTACAKHCR 136
                                           ICKEPCVNGYCAAPDTCKCNEGYTYADTKEKVCEPYCPKGCKNGNCTAPGVCTCNPGYQS
                                                                  VCKTPCPKDLIQHPKNCSCFE-----
                                                                                        EPTC---KNGCENGFCSEPGKCEC------HEGYEKTEPHLCSP--
                                                                                                               EDRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCEC 70
LLFYHCIPICTKPCLQGTCTAPDTCR
                                                                                                                                   Similarity 22.0
33; Conservative
                                                                                                                                                                                             765 AA;
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83909
                                                                                                                                              12.0%;
22.6%;
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                                                                                                                                   Score 107.5; DB
Pred. No. 0.0018;
B; Mismatches (
                                                                                                                                                                                          POTENTIAL.
; FF258BF1288FF007 CRC64;
                                                                 -CKESLETCCQKHKLFHPDTCSCED----
                                                                                                                                      60;
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                                                                                                                                                         Length
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                                                                  115
                                                                                        329
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Search completed: Job time: 425 sec October 17, 2001, 14:50:59

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
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1: /SIDSB/gcgdata,

2: /SIDSB/gcgdata,

3: /SIDSB/gcgdata,

4: /SIDSB/gcgdata,

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Gapop 10.0 , Gapext 0.5
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598
1 FYDIETLKVIDEEWQRTQCS......KVANHTGCKCLPTAPRHPYS 109
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/SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*

/SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (without alignments)
57.000 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412676
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		عين			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	598	100.0	109	20	AAY23889	Human vascular end
2	598	100.0	109	21	AAB11931	Human truncated VE
ω	598	100.0	325	19	AAW53240	Homo sapiens vascu
4	598	100.0	325	22	AAY97572	Human VEGF-D prote
σ	598	100.0	354	19	AAW49036	Human zvegf2 growt
σ	598	100.0	354	19	AAW53241	Homo sapiens vascu
7	598	100.0	354	19	AAW44293	Human vascular end
œ	598	100.0	354	21	AAB10649	Human VEGD protein
9	598	100.0	354	21	AAB29049	
10	598	100.0	354	21	AAY70750	Human prepro-vascu
11	598	100.0	354	21	AAY70983	

13 598 100.0 354 22 AAY97573 Human VEGF-DI prot 14 582 97.3 354 22 AAB97606 Human VEGF-DI Hom 14 582 97.3 354 22 AAB97685 Human VEGF-D. Hom 15 582 97.3 3620 18 AAW14994 Human C-Fos induce 16 579 96.2 321 19 AAW32246 Rat vascular endot 17 575 96.2 358 19 AAW34296 Mus musculus vasculus vasculus 575 96.2 358 19 AAW34295 Musine C-Fos induce 20 575 96.2 358 19 AAW34295 Musine C-Fos induce 21 575 96.2 358 19 AAW32242 Musine C-Fos induce 22 532 89.0 178 20 AAY08285 Human growth facto 23 377 63.0 318 20 AAY08285 Human growth facto 24 377 63.0 318 20 AAY08286 Human growth facto 25 377 63.0 318 20 AAY08287 Human growth facto 26 377 63.0 350 20 AAY30519 A truncated vascular 37 63.0 350 20 AAY30519 A truncated vascular 37 63.0 377 63.0 350 22 AAY97577 Human VEGF-C full 37 377 63.0 419 18 AAW30932 Human VEGF-C full 37 63.0 419 18 AAW30932 Human VEGF-C full 37 63.0 419 18 AAW30932 Human VEGF-C full 37 63.0 419 20 AAY30518 Human vascular end 38 377 63.0 419 20 AAY30518 Human vascular end 39 377 63.0 419 20 AAY30518 Human vascular end 39 377 63.0 419 20 AAY30518 Human vascular end 40 377 63.0 419 20 AAY30518 Human vascular end 41 377 63.0 419 21 AAB3048 Human vascular end 42 377 63.0 419 21 AAB3048 Human vascular end 43 377 63.0 419 21 AAB3048 Human vascular end 44 377 63.0 419 21 AAY30518 Human vascular end 44 377 63.0 419 21 AAY30548 Human vascular end 44 377 63.0 419 21 AAY30548 Human vascular end 44 377 63.0 419 22 AAY30518 Human vascular end 44 377 63.0 419 21 AAY30548 Human vascular end 44 377 63.0 419 22 AAY30548 Human vascular end 44 377 63.0 419 21 AAY3054 Human vascular end 44 377 63.0 419 22 AAY3054 Human vascular end 44 377 63.0 419 21 AAY3054 Human vascular end 44 377 63.0 419 22 AAY3054 Human vascular end 44 377 63.0 419 22 AAY3054 Human vascular end 45 575 675 675 675 675 675 675 675 675 67																																		
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00.0 354 22 AA897573 Human VEGF-DJ 97.3 354 22 AAB97685 Human VEGF-DJ 97.3 354 22 AAB97685 Human vascular 96.8 326 19 AAW14996 B 326 19 AAW14296 B 326 19 AAW14296 B 327 20 AAY08284 B 328 19 AAW3242 B 337 20 AAY08287 Human growth B 36.2 358 19 AAW3242 B 37 20 AAY08285 B 19 AAW44296 B 20 AAY08285 B 20 AAY08287 Human growth B 30 113 20 AAY08284 B 30 113 20 AAY08284 B 30 113 20 AAY08284 B 30 113 20 AAY08284 B 30 113 20 AAY08284 B 30 113 20 AAY08284 B 30 113 20 AAY08284 B 30 113 20 AAY08284 B 30 113 20 AAY08284 B 30 113 20 AAY08284 B 40 113 20 AAY08284 B 40 113 20 AAY08284 B 40 113 20 AAY08284 B 41 113 20 AAY08284 B 41 113 20 AAY097145 B 41 113 20 AAW86237 B 41 113 20 AAW305118 B	377	377	377	377	377	377	377	377	377	377	377	377	377	377	377	377	377	377	377	377	377	377	377	532	575	575	575	575	575	579	582	582	598	598
22 AAY97573 22 AAB70665 32 AAB37606 33 AAW14996 34 AAW14996 35 AAW14996 36 AAW14996 36 AAW14996 37 AAY08286 39 AAW14992 30 AAY08287 31 AAW14992 31 AAW14295 32 AAY08287 32 AAY08287 33 AAW14295 34 AAW182885 35 AAW182885 36 AAW182885 37 AAW86222 38 AAW182886 38 AAW182886 39 AAW182886 40 AAY08284 40 AAW108284 40 AAW108284 41 AAW108284 42 AAW108287 43 AAW178777 41 AAW178777 41 AAW17877 41 AAW178774 41 AAW178774 41 AAW11478 41 AAW114 AAW1149 42 AAW1449 43 CULlar endclar e	ω ·	ω.	ω.	ω.	ω	ω.	·	w	ω.	ω.	ω.	ω.	ω.	w	ω.	ω.	ω	ω.	w	ω ·	ω.	Ψ	ω	9.	σ.	რ	σ,		σ,	σ.	7.	7.	00.	0
AAY97573 AAB37606 AAB37606 AAB37606 AAB37606 AAB40685 AAW14994 AAW44296 AAW53243 AAW708286 AAW44295 AAW44295 AAW4295 AAW44295 AAW44295 AAW6222 AAW6222 AAW86222 AAW86222 AAY30519 AAY23211 AAY97577 AAW86237 AAW86237 AAW7975740 AAW72320 AAW72320 AAW72320 AAW72320 AAW72320 AAW72320 AAW72320 AAW86203 AAW72320 AAW72320 AAW72320 AAW72320 AAW72320 AAW86203 AAW72320 AAW724	419	419	419	419	419	419	419	419	419	419	419	419	419	419	399	350	350	350	350	350	318	307	113	178	358	358	358	337	321	326	620	354	354	354
Human VEGF-DJ Human VEGF-DJ Human VASCULar Rat VASCULar Mus musculus Human growth Murine C-Fos Mus musculus Human growth Human growth Human Gef-C Human Gerout Human Get-d Human VEGF-C Human VEGF-C Human VEGF-C Human VEGF-C Human VEGF-C Human VEGF-C Human VEGF-C Human VEGF-C Human VEGF-C Human VEGF-C Vascular endc Human VEGF-C Vascular endc Human VEGF-C Vascular endc Human VEGF-C	22	22	21	21	21	21	21	20	20	20	19	18	18	18	20	22	21	20	20	16	20	20	20	20	19	19	18	20	19	19	18	22	22	22
Human VEGF-DJ Human VEGF-DJ Human C-FOS J Rat Vasculus Human growth Murine c-FOS Mus musculus Musmusculus Musman growth Human vascular Human VEGF-C	- 60	57	98	AAY70749	AAY97144	AAB29048	AAB10648	AAW86203	AAY22320	AAY30518	AAW75740	AAW11478	AAW00932	ω	w	7	4	AAY22321	AAY30519	AAR82686	AAY08284	AAW86222	AAY08285	AAY08287	AAW44295	AAW53242	AAW14992	AAY08286	AAW53243	9	9	AAB70685	AAB37606	AAY97573
an VEGF-DJ an vascular an c-Fos j vascular musculus an growth ine c-Fos musculus an growth an growth an growth an growth an vascula an roated hun ncated cula an veggr-C an veggr-C cular endc																					٠.	-												
os us					Vascul	Human '		Human 1	Full l	Vascul	Human '					Human '	Trunca	Trunca	A trun	Vascul	Human				Mouse .	Mus mu	Murine	Human '		Rat va	Human •			
	•		vascular end	prepro-vascu	ar endotheli	VEGF-C prote	VEGC protein	vascular end	ength human	ar endotheli	vascular end	ular				F-2	ted vascular	ted human VE	cated vascul	ar endotheli					vascular end							vascular end		

ALIGNMENTS

RESULT AAY23889 ID AAY2

AAY23889 standard; Protein; 109

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WPI; 1999-405368/34.
                                                                                                                                           29-MAY-1998;
24-DEC-1997;
                                                                                                                                                                                                                                                                                                            WO9933485-A1.
                                                                                                                                                                                                                                                                                                                                                                                                     Vascular endothelial growth factor; VEGF; VEGF-D; malignant melanoma; tumour; psoriasis; angiogenesis; lymphangiogenesis; skin graft; wound healing; lymphedema; scleroderma; anhydrotic ectodermal dysplas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human vascular endothelial growth factor (VEGF)-D.
                                                 Achen MG,
                                                                                           (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                23-DEC-1998;
                                                                                                                                                                                                                                                             08-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY23889;
                                            Alitalo K,
                                                                                                                                           98US-0087392.
97AU-0001131.
                                                                                                                                                                                                                98WO-US27373.
                                                 Stacker SA;
                                                                                                                                                                                                                                                                                                                                                                                                        nesis; lymphangiogenesis; skin graft;
scleroderma; anhydrotic ectodermal dysplasia.
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A human cell line stably expressing vascular endothelial factor $\mathsf{D},$ useful for treating melanomas or tumours expres

expressing VEGF-D

Claim

6; Page

72;

English.

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AAB11931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Sim
Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Truncated VEGF-D; vascular endothelial growth factor; human; monoclonal antibody; VEGF receptor; VEGFR-2; VEGFR-3; vascular permeability disorder; endothelial cell proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanomas, tumours or psoriasis. Angiogenesis and lymphangiogenesis stimulating amounts of VEGF-D can be administered to enhance the acceptance and/or healing of skin grafts or to stimulate the healing of a surgical or traumatic wound to the skin. Lymphangiogenesis stimulating amounts of VEGF-D can be used to treat lymphedema. Endothelial proliferation stimulating amounts of VEGF-D are used to treat scleroderma. Vascularisation stimulating amounts of VEGF-D can be used to treat anhydrotic ectodermal dysplasia. VEGF-D antibodies are useful for detecting tumours expressing VEGF-D. Fully-processed VEGF-D can be used to stimulate at least one VEGF-D bloactivity chosen from endothelial cell proliferation, migration, survival and differentiation
Novel compositions comprising antibodies reactive to vascular
                                                           WPI; 2000-442498/38
                                                                                                               Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; diabetic retinopathy; psoriasis; arthropathy;
detection; diagnosis; imaging; lymphatic vasculature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biological activity. VEGF-D antagonists, e.g. antisense nucleic acids or triplex DNA, VEGF-D variants or antibodies (especially chimeric antibodies), are useful for the treatment or alleviation of malignant
                                                                                                                                                                                                                         21-DEC-1998;
17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human truncated VEGF-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents human vascular endothelial grofactor (VEGF)-D. The specification describes a human cell line which stably expresses VEGF-D, or fragments/analogues having V
                                                                                                                                                                     (LUDW-) LUDWIG
                                                                                                                                                                                                                                                                                                              21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenic disorder; lymphangiogenic disorder;
neovascularisation disorder; endothelial cell differentiation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB11931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB11931 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lymphangiogenesis without inducing vascular permeability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                               Stacker SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                     INST CANCER
                                                                                                                                                                                                                         98US-0113254
99US-0134556
                                                                                                                                                                                                                                                                                                           99WO-US31332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 598; DB 20;
Pred. No. 3.5e-58;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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97WO-US14696

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RESULT
AAW53240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cterminal regions. The invention relates to a monoclonal antibody, or fragments thereof, which is specifically reactive with the truncated human VEGF-D, and methods of preparing the antibody. The antibody of the invention interferes with the binding of VEGF-D to the VEGF receptors VEGFR-2 and VEGFR-3, but does not interfere with the binding of VEGF to these receptors and additionally is not reactive with VEGF-C. The antibody may be used to treat disorders associated with vascular permeability, endothelial cell proliferation, anglogenesis, lymphangiogenesis, neovascularisation and endothelial cell ground arthropathies. The antibody may also be used to treat fluid accumulation in the heart and/or lung via modulation of vascular permeability. It may additionally be used to detect VEGF-D and may be used to image lymphatic
                                                                                                                                                                                                                                                                                                                                                                  wascular endothelial growth factor; VEGF-D; angiogenesis;
modification; acceleration; wound healing; tissue; organ;
transplants; collateral circulation; infarction; arterial stenosis;
coronary artery disease; inhibition; cancer; treatment;
21-AUG-1997;
                                     26-FEB-1998.
                                                                         WO9807832-A1
                                                                                                                           Region
                                                                                                                                                               Region
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                               gaseous exchange; chronic obstructive airway disease.
                                                                                                                                                                                                                                                                                                                                                diabetic retinopathy; lung disorders;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW53240 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endothelial growth factor-D, useful for treating, e.g. angiogenesis, lymphangiogenesis and neovascularization disorders -  \\
                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens vascular endothelial growth factor D (VEGF-D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                ntestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vascular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FYDIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CMNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fydietlkvideewqrtqcspretcvevaselgkstntffkppcvnvfrcggccneesli 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents a 109 amino acid truncated human VEGF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cmntstsyiskqlfeisvpltsvpelvpvkvanhtgckclptaprhpys 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 1; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endothelial
                                                                                                                                                                                                                                                                                           malabsorptive syndrome; biopsy; metastatic risk;
diagnosis; congestive heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                             258..
                                                                                                            /note=
                                                                                                                                                                   156..158
                                                                                                                                                                                  /note=
                                                                                                                                                                                                     126..128
                                                                                                                                              /note= "potential N-linked
                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein; 325
                                                                                                                               . 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth factor D), lacking both the N- and
                                                                                                                                                                              "potential N-linked glycosylation site"
                                                                                                          "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 598; DB 21;
Pred. No. 3.5e-58;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                 blood circulation;
                                                                                                                                            glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 109;
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                                                                                                                                            site"
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                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collateral circulation in tissue infarction or arterial stenosis.

C such as coronary artery disease, and inhibition of angiogenesis in the treatment of cancer or of diabetic retinopathy. It can also be used in the treatment of lung disorders to improve blood circulation in the lung and/or gaseous exchange between the lungs and the blood stream or to improve blood circulation to the heart and O2 gas gas remeability in cases of cardiac insufficiency, to improve blood forward gaseous exchange in chronic obstructive airway disease, or to treat malabsorptive syndromes in the intestinal tract.

Quantitation of VEGF.D in cancer biopsy specimens may be useful as an indicator of future metastatic risk. Antagonists can be used for treating e.g. conditions such as congestive heart failure, involving accumulations of fluid in the lung resulting from for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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23-AUG-1996;
23-AUG-1996;
11-NOV-1996;
14-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-FEB-1997;
10-FEB-1997;
19-JUN-1997;
              Human; angiogenic protein; wound healing; vascular tissue repair; peripheral arterial disease; critical limb ischaemia; coronary diseasej angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis; rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy;
                                                                                                                        05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated vascular endothelial growth factor-D - used to products for use in e.g. modifying angiogenesis or treating heart or intestinal disorders
                                                                                                                                                       AAY97572;
                                                                                                                                                                                      AAY97572 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of human breast vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Pages 57-58; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis in wound healing, tissue or organ transplantation, or to establish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for detection and diagnosis.
                                                                                                                                                                                                                                                                 124
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                                                                                                                                                                                                                                                            1998-179057/16.
                                                                                                                                                                                                                                                                                                                                                                                       109;
                                                                                          VEGF-D protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                        (first entry)
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96AU-0001825.
96AU-023751.
96AU-0003554.
96AU-0003554.
97AU-0031097.
97AU-0038814.
97AU-0007435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑĄ;
                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 598; DB 19; 100.0%; Pred. No. 1.3e-57; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stacker SA,
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                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                             coronary disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lung,
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RESULT
AAW49036
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                                                                                                                                                                                                                                                                                                                                                                                                                                            detecting mutations or the presence or amount of anglogenic protein CC expression. Particularly they are used to stimulate wound healing, CC especially peripheral arterial disease, critical limb ischaemia or cc coronary disease. Antagonists of the sequences are used to inhibit CC angiogenesis in tumours and to treat inflammation (where associated with CC arthritis or psoriasis. Agonists are also useful for stimulating CC (lymph)angiogenesis. The proteins are also useful for stimulating CC (lymph)angiogenesis. The proteins are also useful to raise antibodies. CC purification and targeting of proteins for in vivo or in vitro diagnosis (including imaging) or for therapputic (antiagonists; for detection, CC purification and targeting of proteins for in vivo or in vitro diagnosis CC (including imaging) or for therappy (including when linked to e.g. a label CC or cytotoxin); and for immunotyping of cells. e.g. for detection minimal CC residual disease or haematopoietic progenitor/stem cells. It is also CC contemplated that the sequences might be useful for treating a very wide crange of other disorders, e.g. autoimmune diseases; allergy; cancer; infectious diseases (viral, bacterial, fungal or parasitic); neurodegeneration of the nervous system etc.
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                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                         Matches
                                                                         AAW49036 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is vascular endothelial growth factor D (VEGF-D), which is an angiogenic protein of the invention. The angiogenic and the DNA sequences encoding them, are used to prevent, treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding angiogenic proteins, useful promoting healing of wounds and treating peripheral acritical limb ischaemia or coronary disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2000; 2000WO-US14925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 226-227; 244pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ameliorate disease and to detect diseases, or susceptibility, by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vascular endothelial growth factor-D; VEGF-D.
                                                                                                                                                                      124
                                                                                                                                                                                      61 CMNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYS 109
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                                                                                                                                                                                                                                                              1 FYDIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLI 60
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                                                                                                                                                                    cmntstsyiskqlfeisvpltsvpelvpvkvanhtgckclptaprhpys 172
                                                                                                                                                                                                                                                                                                                         109;
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                                                                         Protein;
                                                                                                                                                                                                                                                                                                                     100.0%; Score 598; DB 22; 100.0%; Pred. No. 1.3e-57; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hu J, Cao L;
                                                                         354 AA
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                           Length 325;
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                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                     Gaps
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26-OCT-1998 AAW49036;

(first entry)

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Query Match
Best Local S
Matches 109
                                                                                                                                                                    by the zvegf2 cDNA which was isolated from a human heart cDNA library. zvegf2 protein in a dimeric form acts as a mitogen for fibroblasts or smooth muscle cells. zvegf2 is claimed to be useful for stimulating the revascularisation of tissue or the re-endothelialisation of vascular tissue. zvefg2 is particularly claimed to be useful for the treatment of full-thickness skin wounds, including venous stasis ulcers and diabetic ulcers. The zvegf2 protein is also claimed to be useful as an additive in tissue adhesives for promoting revascularisation of the healing tissue. Antagonists against zvegf2 can be used to block its mitogenic, chemotactic and angiogenic effects. The antagonists may therefore be useful for reducing growth of solid tumours by inhibiting neovascularisation of the developing tumour or by directly blocking tumour cell growth, in the treatment of diabetic retinopathy, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated vascular endothelial growth factor - used to develop products for treating e.g. wounds, burns, myocardial infarction, tumours, psoriasis, arthritis, restenosis or organ transplants
                                                                                                             Sequence
                                                                                                                                                           arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Pages 53-54; 77pp; English.
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N-PSDB; AAV32823.
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06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      angiogenic effect; tumour; diabetic retinopathy;
scleroderma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence represents a human zvegf2 growth factor encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               zvegf2 growth factor; mitogen; fibroblast;
s stasis ulcer; diabetic ulcer; skin wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zvegf2
                      Similarity
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                                                                                                                354
    Conservative
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                                                                                                                AA;
                                                                                                                                                           scleroderma.
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96US-0759657
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275..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
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                         .0%;
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  0;
                      Score 598; DB 19; Pred. No. 1.4e-57;
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    Mismatches
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                                           Length
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Gaps
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RESULT
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in the lung and/or gaseous exchange between the lungs and the blood stream or to improve blood circulation to the heart and 02 gas permeability in cases of cardiac insufficiency, to improve blood flow and gaseous exchange in chronic obstructive airway disease, or to treat malabsorptive syndromes in the intestinal tract. Quantitation of VEGF-D in cancer blopsy specimens may be useful as an indicator of future metastatic risk. Antagonists can be used for treating e.g. conditions such as congestive heart failure, involving accumulations of fluid in the lung resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-1996;
05-FEB-1997;
10-FEB-1997;
                                                                                                                                       The sequence is that of human lung vascular endothelial growth factor D (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis in wound healing, tissue or organ transplantation, or to establish collateral circulation in tissue infarction or arterial stemosis, such as coronary artery disease, and inhibition of angiogenesis in the treatment of cancer or of diabetic retinopathy. It can also be used in the treatment of lung disorders to improve blood circulation
                                                                                                                                                                                                                                                                      Claim 16;
                                                                                                                                                                                                                                                                                               New isolated vascular endothelial growth factor-D - used to products for use in e.g. modifying angiogenesis or treating heart or intestinal disorders {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transplants; collateral circulation; infarction; arterial stenosis; coronary artery disease; inhibition; cancer; treatment; diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive airway disease;
                                                                                                                                                                                                                                                                                                                                                                                                            Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-1996;
23-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intestinal malabsorptive syndrome; biopsy; metastatic risk; detection; diagnosis; congestive heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vascular endothelial growth factor;
modification; acceleration; wound h
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                                                                                                                                                                                                                                                                                                                                                              AAV20807
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LUDWIG
                                                                                                                                                                                                                                                                 Pages 60-61; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                          Alitalo K,
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96US-0031097.
97AU-0004954.
97US-0038814.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acceleration; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97AU-0007435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96AU-0001825
96US-0023751
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RESULT
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Best Local Similarity
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                                                                                                                                                                          The present sequence represents human vascular endothelial growth factor D (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind the protein, may be useful in, e.g. gene therapy and in treatment of inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGF-D
                                                                                                                                                                                                                                    Claim 1;
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N-PSDB; AAV15156.
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                                                                                                                              Sequence
                                                                                                                                                                                                                                                                     VEGF-D protein encoded by DNA - useful for,
                                                                                                                                                                                                                                                                                                                                                    (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE
                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; vascular endothelial growth factor D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human vascular endothelial growth factor
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 61
                        93
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                                                                                                                                                    sequences may be used for screening VEGF-D protein.
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 CMNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYS 109
                                  FYDIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fydietlkvideewqrtqcspretcvevaselgkstntffkppcvnvfrcggccneesli 152
                     fydietlkvideewqrtqcspretcvevaselgkstntffkppcvnvfrcggccneesli 152
                                                                       109;
                                                                    h 100.0%; Score 598; DB 19; Similarity 100.0%; Pred. No. 1.4e-57; 09; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                   Page 18-20; 52pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354
                                                                                                                              354 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oedema
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                                                                                                                                                                                                                                  Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354
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                                                                                                                                                               for the compounds which bind
                                                                                                                                                                                                                                                                                                                                                      INC
                                                                                                                                                                                                                                                                    e.g.
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                                                                                                            Matches 109;
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Best Local Similarity
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18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                              regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote the prospective of the product of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, and the promote the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the produc
                                                                                                                                                                                                                                                                                             skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity vascularization. This sequence represents the human VEGD protein used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antitheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antitheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth; VEGD.
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 11; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dhanaraj
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                                                                                                            Conservative
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99US-0124967.
99US-0164131.
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                                                                                                         Score 598; DB 21;
Pred. No. 1.4e-57;
0; Mismatches 0;
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                                                                                                                                                                                                                The present sequence is the protein sequence of the human vascular endothelial growth factor D (VEGF-D). It was used to demonstrate the methods of the invention, which involve the screening of individuals to determine which vascular endothelial growth factor receptor 3 (VEGFR-3, also known as Flt4 or fms-like tyrosine kinase 4) alleles they possess and thus their likelihood of developing hereditary lymphoedema. Conditions associated with lymphoedema include Milroy-Nonne syndrome,
                                                                                                                                                                                                                                                                                                                                              Screening a human subject for increased risk of developing disorder, comprises assaying a nucleic acid to determine a altering the sequence of a vascular endothelial growth fact receptor-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vascular endothelial growth factor receptor 3; VEGF-D; Milroy-Nonne syndrome; lymphoedema praecox; VEGF-D; vascular endothelial growth factor D.
                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                      Disclosure; Page 64-65; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human VEGF-D protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB29049 standard; Protein; 354
                                                                                                                                                                                                      which is early onset lymphoedema and lymphoedema praecox, which is late
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferrell RE,
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                                                                                                                Local Similarity
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CMNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYS
                                                FYDIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLI 60
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DB; AAC62407.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNIV PITTSBURGH.
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                                                                                                                Score 598; DB 21;
Pred. No. 1.4e-57;
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                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                       a lymphatic mutation
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CMNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYS 109

Query Match Best Local S

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Local Similarity

100.0%; Score 598; DB 21; ilarity 100.0%; Pred. No. 1.4e-57; Conservative 0; Mismatches 0;

Length 354;

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CC ligand to Fit4 thereby inhibiting Fit4 mediated proliferation of vascular cells cells. The compound is useful for treating neoplastic disease cuch as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas can disease cuch as compounds carcinomas, squamous cell carcinomas, lymphomas, melanomas cuch as arcomas. Fit4 receptor tyrosine kinase binding compounds can be used for manufacturing medicament useful for diagnostic screening, imaging and cuch reatment of malignancies characterised by Fit4 expressing blood cells. The Fit4 gene maps to chromosomal region 5q35 and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in their 3' sequences and are cuch fiferentially expressed in HEL and DAMI cell lines. Fit4 cuch substantly of class III receptor tyrosine kinases (RTKS). It is used as a target for tumour imaging and anti-tumour therapy. CC The present sequence is a human prepro-vascular endothelial growth factor D (VEGF-D), a specific example of Fit4 binding compound. A cc recombinantly matured VEGF-D lacking residues 1-92 and 202-354 cc retains the ability to activate VEGFR-2 and VEGFR-3 receptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
Sequence
                                        associate
                                                                                                                                                                                                                                                                                                                                                                  referred as vascular endothelial growth factor receptor-3, VEGFR-3) endothelial cells of blood vessels adjacent to malignant neoplasm. T method involves administering a compound that inhibits binding of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and sarcomas, involves admi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating neoplastic diseases such as lymphoma, carcinomas, melanomas and sarcomas, involves administering a compound capable of inhibiting binding of ligand proteins to fms-like tyrosine kinase-4 receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; tumour imaging; anti-tumour therapy; treatment; dia-
neoplastic disease; lymphoma; carcinoma; breast; squamous cell;
sarcoma; malignancy; VEGF-D; vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                               The patent discloses a method to treat neoplastic disease cl
by expression of fms-like tyrosine kinase 4 (Flt4) receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 15-17; Page 142-143; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200021560-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prepro-vascular endothelial growth factor D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY70750 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEGFR-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor tyrosine kinase; RTK; Flt4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vascular endothelial growth factor receptor-3;
                                      as non-covalently linked dimers.
  354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaipainen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0169079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US23525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valltola R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jussila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fms-like tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                  characterised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis;
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KW COSC

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KW WO
                                                                                                                                                              The present amino acid sequence is the complete human prepro-vascular endothelial growth factor (VEGF)-D. VEGF-D has the ability to stimulate re-endothelialisation of an injured blood vessel, without significant stimulation of smooth muscle cell proliferation. It can bind to and stimulate VEGFR-2 (vascular endothelial growth factor receptor) and/or VEGFR-3 phosphorylation in cells that express such receptors. An
                                                                                                                                                                                                                                                                                                                                                                                                                              Preventing stenosis and restenosis endothelial growth factor proteins
                                               anti-restenosis agent comprising either a VEGF-D gene or protein is used in a method to reduce or prevent restenosis and stenosis of a blood vessel following vascular trauma e.g., cardiovascular surgery and percutaneous transluminal coronary angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vascular endothelial growth factor-D; VEGF; human; re-endothelialisation; vascular endothelial growth factor receptor; VEGFR; vascular trauma; blood vessel; cardiovascular surgery; anti-restenosis agent; prevention; restenosis; stenosis; percutaneous transluminal coronary angioplasty.
  Sequence
                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yla-herttuala S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YLAH/) YLA-HERTTUALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES (UYHE-) UNIV HELSINKI LICENSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-350584/30.
  354
                                                                                                                                                                                                                                                                                                                                                                    Page 53-55; 61pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0105587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US24054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Cleavage results protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein"
22..92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Signal_peptide
/note= "Cleavage results in partially-processed VEGF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Processed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEGF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Amino_terminal_peptide
/note= "Cleavage results in fully-processed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Recombinantly_matured_VEGF_D_
/note= "Processed vascular epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alitalo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LICENSING
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MO
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                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acids encoding them
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lial growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
(lymph)angiogenesis. The proteins are also used to identify specific binding agents (potential therapeutic agents) and to raise antibodies. The antibodies are useful as therapeutic (ant)agonists; for detection, purification and targeting of proteins for in vivo or in vitro diagnosis (including imaging) or for therapy (including when linked to e.g. a label or cytotoxin); and for immunotyping of cells, e.g. for detecting minimal residual disease or haematopoietic progenitor/stem cells. It is also
                                                                                                                            increased vascular permeability), diabetic retinopathy, rheumatoid arthritis or psoriasis. Agonists are also useful for stimulating
                                                                                                                                                              coronary disease. Antagonists of the sequences are used to inhibit angiogenesis in tumours and to treat inflammation (where associated with
                                                                                                                                                                                                 growth of damaged bone and tissue, and for repair of vascular tissue, especially peripheral arterial disease, critical limb ischaemia or
                                                                                                                                                                                                                                                     ameliorate disease and to detect diseases, or susceptibility, by detecting mutations or the presence or amount of angiogenic protein
                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding angiogenic proteins, useful e.g. for promoting healing of wounds and treating peripheral arterial disease, critical limb ischaemia or coronary disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis; rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy; infectious disease; neurodegeneration;
                                                                                                                                                                                                                                 expression. Particularly they are used to stimulate wound healing,
                                                                                                                                                                                                                                                                                          and the DNA sequences encoding them, are used to prevent,
                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 228-229; 244pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2000; 2000WO-US14925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; angiogenic protein; wound healing; v
peripheral arterial disease; critical limb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human VEGF-D1 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY97573 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CMNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYS 109
                                                                                                                                                                                                                                                                                                                              sequence is vascular endothelial growth factor-D1 (VEGF-D1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fydietlkvideewqrtqcspretcvevaselgkstntffkppcvnvfrcggccneesli 152
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                                                                                                                                                                                                                                                                                                             an angiogenic protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
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                                                                                                                                                                                                                                                                                                               invention.
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b ischaemia; coronary
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                       The present invention relates to a method for screening a human subject for an increased risk of developing a lymphatic disorder e.g. hereditary lymphedoema. The method comprises assaying nucleic acid of a human subject to determine a presence or an absence of a mutation altering the sequence or expression of vascular endothelial growth factor receptor-3 (YEGFR-3)/fms-like tyrosine kinase 4 (Flt4) allele (see AAC68952 and AAB37604) and determining an increased risk of developing lymphatic disorder from presence or absence of the mutation. The presence of a mutation altering the encoded amino acid sequence or expression of at least 1 VEGFR-3 allele in the nucleic acid correlates with an increased risk of developing a lymphatic disorder from the nucleic acid correlates with an increased risk of developing lymphatic disorder from presence or absence of the mutation. The presence of a mutation altering the encoded amino acid sequence or expression of at least 1 VEGFR-3 allele in the nucleic acid correlates with an increased risk of developing lymphatic acid correlates with an increased risk of developing lymphatic acid correlates with an increased risk of developing lymphatic acid correlates with an increased risk of developing lymphatic acid correlates with an increased risk of developing lymphatic acid correlates with an increased risk of developing lymphatic acid correlates with an increased risk of developing lymphatic acid correlates with an increased risk of developing lymphatic acid correlates with an increased risk of developing lymphatic acid correlates with an increased risk of developing lymphatic acid correlates with an increased risk of developing lymphatic acid correlates with an increased risk of developing lymphatic acid correlates with an increased risk of developing lymphatic acid correlates with a lymphatic acid correlates with a lymphatic acid correlates with a lymphatic acid correlates with a lymphatic acid correlates with a lymphatic acid correlates with a lymphatic acid correlates with a lymp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening a human for an increased risk of developing lymphatic disorder comprises assaying nucleic acid for alterations in the sequences expressing vascular endothelial growth factor receptor-3
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                                   The present invention describes a method for inducing angiogenesis in a tissue, or area, in need of angiogenesis, in a mammal. The method comprises administering recombinant vascular endothelial growth factor D (VEGF-D) or its angiogenically active fragment or mutant (I). The present sequence represents the human VEGF-D protein, which can be used in the method of the invention. (I) has cardiant and vasotropic activities, and is an angiogenesis inducer. The method can be used for inducing angiogenesis in a tissue in need of angiogenesis, or in an area in need of angiogenesis in a mammal. (I) is useful for treating various ischaemic conditions manifested by vascular insufficiency such as
                                                                                                                                                                                                                                         Use of recombinant vascular endothelial growth factor or its angiogenically active fragment or mutant, for inducing angiogenesis vivo or in vitro and for treating myocardial infarction, coronary
                                                                                                                                                                                                     Claim
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    c-fos induced growth factor; Figf; cardiant;
    dition; ischaemia; vascular insufficiency;
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sequences of reading frames 1, 2 and 3 of clone HF175 (AAT62961), human homologue of murine clone F0401 (AAT62960), which codes for novel c-Fos induced growth factor (F1GF) (see also AAM14922). Examination of the 3 polypeptides indicates that reading frame 2 has the longest region free of nonsense codons. FIGF is a c-fos-dependent autocrine growth factor able to induce cell division entry and, when over-expressed, a transformed phenotype in fibroblasts. It could be implicated in tumours and development. Recombinant FIGF can be produced in transformed host (e.g. CHO) cells. It can be used to identify its receptors and in an assay for the identification of agonists and antagonists. Antibodies
                                                                                                                                                                                    Nucleotide molecule encoding c-Fos induced growth factor protein useful in therapy, in manufacture of compositions for treatment developmental disorders and in generation of transgenic animal
                                                                                                                        3 Polypeptide sequences (AAW14993-95) are the respective translated sequences of reading frames 1, 2 and 3 of clone HF175 (AAT62961), t)
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29-SEP-1995;
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Query Match
Best Local Similarity
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ALIGNMENTS

3, Application US/08915795 5. 6235713

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; ORIGINAL SOURCE: ; TISSUE TYPE: US-08-915-795-3
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:

NAME: EVANS, JOSEPH D.

REGISTRATION NUMBER: 26,269

REFERENCE/DOCKET NUMBER: 1066

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Marc G. APPLICANT: Andrew F
APPLICANT: Steven A
APPLICANT: Kari ALI
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/915,795
                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
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LENGTH: 325 amino acid
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ZIP: 20
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CITY: Washington
STATE: DC
                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
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                                                                                             TOPOLOGY:
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Steven A. STACKER
Kari ALITALO
                                                                                                                                                                                                                         (202) 628-8844
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                          TOPOLOGY: linea MOLECULE TYPE: p1 HYPOTHETICAL: NO
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NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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1200 G Street, NW, Su
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Steven A. STACKER
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                                                                                                                                                        Score 598; DB 4;
Pred. No. 1.4e-62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  m, Edwards
Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               & Lenahan
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                                                                                                                                                                                   Length 354;
                                                                                                                                                           Indels
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                                                                                                                                           Sequence 8, Application US/08915795 Patent No. 6235713
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                                                                                                                            GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                     APPLICANT: Marc G. A
APPLICANT: Andrew F
APPLICANT: Steven A
APPLICANT: Kari ALIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
TISSUE TYPE:
                         CORRESPONDENCE ADDRESS:
                                          TITLE OF INVENTION: GROWTH FACTOR NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: EVANS, JOSEPH D.
REGIZION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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STREET:
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               ADDRESSEE:
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                                                                  Andrew F. WILKS
Steven A. STACKER
Kari ALITALO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 amino acids
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Steven A. STACKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marc G.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 CMNTSTSYISKQLFEISVPLTSVPELVPVKIANHTGCKCLPTGPRHPYS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CMNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPRHPYS 109
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STREET: 1200 G Street, NW, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYDTETLKVIDEEWQRTQCSPRETCVEVASELGKTTNTFFKPPCVNVFRCGGCCNEEGVM 152
E: Evenson, McKeown, Edwards & Lenahan P.L.L.C. 1200 G Street, NW, Suite 700
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

United States of America

Washington

20005

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; ORIGINAL SOURCE: |
; TISSUE TYPE: |
US-08-915-795-8
                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-999-811-4
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08999811 Patent No: 5932540
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER,
                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                   APPLICANT: HU, JING-SHAN APPLICANT: ROSEN, CRAIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 CMNTSTSYISKQLFEISVPLTSVPELVPVKIANHTGCKCLPTGPRHPYS
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                 FILING DATE: | CLASSIFICATION
                                                APPLICATION NUMBER:
                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                 CITY: WASHINGTON
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RESULT 7 US-09-042-105-4

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; ORGANISM: Homo sapiens
US-08-824-996-2
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                                                                                                                                                      Query Match
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Best Local :
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                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: 08/207,550
                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Folynuc TITLE OF INVENTION: Factor FILE REFERENCE: PF112D1
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hu, Jing-Shan
APPLICANT: Rosen, Craig A.
                                                                                                                                                                                                                                                                                                                EARLIER FILING DATE: 1994-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cao, Liang
                                                                                                                                                                                                                                                  LENGTH: 350
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REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1995 ATTORNEY/AGENT INFORMATION:
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 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 MNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCM 143
              62 MNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCL 100
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                                                                                                                         Local Similarity
les 63; Conserv
                                                             45
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                                                                             MNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCM 143
                                                             YNTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63;
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                                                                                                                           Conservative
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                                                                                                                                    63.0%;
63.6%;
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                                                                                                                                      Score 377; DB 2;
Pred. No. 1.4e-36;
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Pred. No. 1.4e-36;
5; Mismatches 21;
                                                                                                                           Mismatches
                                                                                                                                                    Length 350;
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US-08-510-133A-33
, Sequence 33, Application US/08510133A
; Patent No. 6221839
; GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/207,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                        105 MNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCM 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 00
CLASSIFICATION:
                                                                                                                                                                        62 MNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCL 100
                                                                                                                                                                                                                     45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US FILING DATE: 8-MAR-1994 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: HEREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                                                                                  ADDRESSEE: STERNE, KESSLER, OSTREET: 1100 NEW YORK AVENUE
APPLICANT: Alitalo, Kari
Joukov, Vladomir
TITLE OF INVENTION: Receptor
                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      amino acids
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                                                                                                                                                                                                                                                                                                 63.0%;
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 Receptor Ligand
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                                                                                                                                                                                                                                                                               Score 377; DB 3; 1
Pred. No. 1.4e-36;
5; Mismatches 21;
                                                                                                                                                                                                                                                                                                            Length 350;
                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                               Gaps
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; TOPOLOGY: linear; MOLECULE TYPE: Protein; SEQUENCE DESCRIPTION: SEQ ID NO: 33: US-08-510-133A-33
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Patent No. 6245530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Joukov, Vladimir TITLE OF INVENTION: Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Alitalo, APPLICANT: Joukov, V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 MNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCM 143
                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America ZIP: 60606-6402
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 MNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCL 100
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                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
APVER COST OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                    Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Illinois
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STREET: 6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 350 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Marshall, O'Toole, 6300 Sears Tower, 233
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63.6%;
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                                                                              us/08/585,895
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Pred. No. 1.4e-36;
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ower, 233 South Wacker Drive
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South Wacker Drive
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US-08-585-895-33

MOLECULE TYPE:

protein

TOPOLOGY:

SEQUENCE CHARACTERISTICS:

33:

LENGTH: TYPE: a

amino acids

TELEFAX: 25-3856

REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPAX: 312/474-0448

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER:

38,153

28113/33072

Gass,

David A.

Matches

63;

Conservative

15;

Mismatches

Query Match Best Local Similarity

63.0%;

Score 377; Pred. No. 1

DB 4; 1.4e-36;

Length 350; Indels

Gaps

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Sequence 2, App...
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                     INFORMATION FOR SEQ ID NO:
                                                                                                               APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
REGISTRATION NUMBER: 36,351
                                                                                                                                                                                                           FILING DATE: 8-MAR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
SEQUENCE CHARACTERISTICS:
                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                     REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: HEREW
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                           CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: STERNE, KESSLER, IT: 1100 NEW YORK AVENUE WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20005
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                                     (202)371-2540
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ROSEN, CRAIG A.
                                                           (202)371-2600
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Query Match

63.0%;

Score 377;

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Length 419;

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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-09-042-105-2
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Best Local
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                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: ERIC K. STEFFE
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 MNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCM 212
                                                                                                                                                                                                                                                 APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997
                                                      TYPE:
                                                                                                                                                                                  NAME: ERIC K. STEFFE REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US
FILING DATE: 8-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: WASHINGTON STATE: DC
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les 63; Conserv
                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                   CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: STERNE, KESSLER, G
                                                                    LENGTH:
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                                                    amino acid
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                                                                                                                   (202)371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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63.6%;
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                                                                                                                                                                                  36,688
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                                                                                                                                                                     1488.1000003/EKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOLDSTEIN & FOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
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63.6%;

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US-09-042-105-18
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Rest Local Similarity 0...
63; Conservative
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Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION:
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APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                            STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2. CLASSIFICATION:
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                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                    TELEPHONE:
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MEDIUM TYPE:
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                                                                                                                                                               linear
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                                                                                                                                           protein
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                                             63.0%; Score 377; DB 3; L
63.6%; Pred. No. 1.8e-36;
1c. Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                             TO BE ASSIGNED
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                                                                                                                                                                                                                                         18:
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                                                                           Length 419
                                                Indels
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-795-430-8
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US-08-795-430-8
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                      Query Match
Best Local Similarity
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                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/601,132
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/50 FILING DATE: 12-JAN-1996
                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 38 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/
FILING DATE: 01-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/340,011
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER: 08/510,133
01-AUG-1995
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                    63.0%;
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Score 377; DB 4; Le
pred. No. 1.8e-36;
pred. no. 1.8e-31;
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                                    Length 419;
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Matches

Conservative

15;

Indels

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Gaps

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RESULT 15
PCT-US96-09001-2
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US-08-510-133A-35
                                                                                          Sequence 2, Application PC/TUS9609001
GENERAL INFORMATION:
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Patent No. 6221839
Patent INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Alitalo, Vladomir
                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local (
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INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                              APPLICANT: HU, ET AL.
TITLE OF INVENTION: Human Vascular EndothelialGrowth Factor
NUMBER OF SEQUENCES: 10
                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   174 MNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCM 212
                                                                                                                                                                                                                                                                                               114 YNTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQC 173
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                                                                                                                                                                                                                                     62 MNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCL 100
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                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 28113/32863
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
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APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 419 amino acids
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CARELLA, BYRNE, BAIN, GILFILLAN,
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63.6%; Pred. No. 1.8e-36;
Mismatches 21;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
FILING DATE: 6 JUN 9
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                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 8 MAR 1994 ATTORNEY/AGENT INFORMATION:
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174 MNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCM
                                                              114 YNTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGGCCNSEGLQC 173
                                                                                                                                                Local
                                62 MNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCL 100
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                                                                                                                                                                                                                                                                                                                                                                                                                NAME: FERRARO, GREGORY REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 6 JUN APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                                                                                                                 63;
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63.6%; Pred. No. 1.8e-36;
vative 15; Mismatches 21;
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Search completed: October 17, 2001, 14:47:12 Job time: 198 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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glycoprotein hormo	glycoprotein hormo	hypothetical prote	glycoprotein hormo	gonadotropin alpha	glycoprotein hormo	gonadotropin alpha	pituitary glycopro	glycoprotein hormo	follitropin alpha	glycoprotein hormo	glycoprotein hormo	glycoprotein hormo	vascular endotheli	platelet-derived g	platelet-derived g

ALIGNMENTS

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C;Species: Mus muscular endothelial growth factor-2; vascular perme C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change (C;Accession: A44881; C44881; A60932; S52136
R;Breier, G.; Albrecht, U.; Sterrer, S. Pirother, Abbrecht, U.; Sterrer, S. Pirother, S. 
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C;Date: 03-Feb-1994 #sequence_revision
C;Accession: B44881; A43351; A61029
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C;Keywords:
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J. Biol. Chem. 267, 16317-16322, 1992
A;Title: Vascular endothelial growth factor. Regulation
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A; Residues: 1-190 <BRE>
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63; Conser
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pred. No. 9.8e-31;
pred. No. 9.8e-31;
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Folkman, J.
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STSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTAPR 105

EVVKFMD-VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCAGCCNDEALECVPT

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A; Nolecule type: protein
A; Molecule type: protein
A; Rolecule type: protein
A; Residues: 27-46 <SUG>
C; Comment: Homodimers could be demonstrated for recombinant VEGF-2 but not VEGF-3.
C; Comment: Homodimers could be demonstrated for recombinant VEGF-2 but not VEGF-3.
C; Keywords: alternative splicing; angiogenesis; disulfide bond; glycoprotein; homoc; c; Reywords: alternative splicing; angiogenesis; disulfide bond; glycoprotein; homoc; l-26/Domain: signal sequence #status predicted <SIG>
F; 1-26/Domain: signal sequence #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen A; Reference number: A35987; MUID: 90207249
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R; Sugihara, T.; Kaul, S.C.; Mitsui, Y.
Biochim. Biophys. Acta 1224, 365-370,
A; Title: Enhanced expression of multip
A; Reference number: S52136; MUID:9510;
A; Accession: S52136
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A; Residues: 1-14(,209-214 <BR2>
A; Residues: 1-14(,209-214 <BR2>
A; Cross-references: GB:S38100; NID:g249860; PIDN:AAB22254.1;
A; Note: sequence extracted from NCBI backbone (NCBIN:107624,
A; Note: sequence extracted from NCBI backbone (NCBIN:107624,
R; Clauss, M.; Gerlach, M.; Gerlach, H.; Brett, J.; Wang, F.;
J. Exp. Med. 172, 1535-1545, 1990
J. Exp. Med. 172, 1535-1545, 1990
                                                                                                                                                                                                                                                                   A;Cross-references: GB:M32167; NID:g204287; PIDN:AAA41211.1; PID:g204288
                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-190 <CO
                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Conn,
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                                                                                 Matches
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                                                                                                                Score 171.5; DB 2
Pred. No. 3.1e-10;
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Pred. No. 2.2e-10;
6; Mismatches 44
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0, 1994
                                                                                 Mismatches
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NCBIP: 107625)
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C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999 C;Accession: A41551; C41551; B41551; A40454; B40454; C40454; A40000; R;Houck, K.A.; Ferrara, N.; Winer, J.; Cachianes, G.; Li, B.; Leung, D.W. Mol. Endocrinol. 5, 1806-1814, 1991
A;Title: The vascular endothelial growth factor family: identification of a f. A;Accession: A41551; MUID:92168017
A;Accession: A41551
A;Molecule type: mRNA
                                                                                                                R; Weindel, K.; Marme, D.; Weich, H.A.
Biochem. Biophys. Res. Commun. 183, 1167-1174,
A;Title: AIDS-associated Kaposi's sarcoma cell
A;Reference number: JQ1463; MUID:92231879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vascular endothelial growth factor 206 precursor - human
N;Alternate names: vascular permeability factor
N;Contains: vascular endothelial growth factor 121 (VEGF 121);
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change
C;Accession: A41551; C41551; B41551; A40454; B40454; C40454; A4
R;Houck, K.A.; Ferrara, N.; Winer, J.; Cachianes, G.; Li, B.: L
A; Residues: 1-140,'N',183-232 <WEI>
A; Cross-references: EMBL:X62568; NID:g37658;
A; Experimental source: AIDS-Kaposi's sarcoma
                                                                                                                                                                                                                                                                                                                                                                          A;Cross references: GB:M27281; NID:g340300; R;Leung, D.W.; Cachianes, G.; Kuang, W.J.; Cscience 246, 1306-1309, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A40079; MUID:90069609
A;Accession: A40079
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R;Keck, P.J.; Hauser, S.D.; Krivi, G.; Sanzo, K.; Warren,
Science 246, 1309-1312, 1989
A;Title: Vascular permeability factor, an endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-140,'N',183-232 
A; Cross-references: GB:M63971;
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R;Tischer, E; Mitchell, R; Hartman, T; Silva, J; Biol. Chem. 266, 11947-11954, 1991
A;Title: The human gene for vascular endothelial A;Reference number: A40454, MUID:91268072
A;Accession: A40454
A;Molecule type: DNA
                                                                                          A; Reference number: JQ1463; A; Accession: JQ1463
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A; Cross-references: GB:M32977; NID:9181970; PIDN:AAA35789.1; PID:9181971
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A; Residues: 1-165,183-232 < KEC>
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A:Residues: 1-165,183-232 <TII>
A:Cross-references: GB:M63971;
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A;Status: nucleic acid sequenc
A;Molecule type: mRNA
A;Residues: 1-140,'N',183-232
                                                                    A; Molecule type: mRNA
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A; Residues: 1-141,227-232 <TI3>
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Residues: 1-141,227-232 <HOU>
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Residues: 1-232 <HOU1>
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Goeddel, D.V.; Ferrara, N.
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A;Cross-references: GDB:132244; OMIM:192240
A;Cross-references: GDB:132244; OMIM:192240
A;Map position: 6p21-6p12
C;Function:
C;Function: promotes fluid and protein leakage from blood vessels
A;Description: promotes fluid and protein leakage from blood vessels
C;Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; ext
E;1-232/Product: vascular endothelial growth factor 189 precursor
E;1-165,183-232/Product: vascular endothelial growth factor 121 precursor
E;1-141,227-232/Product: vascular endothelial growth factor 121 precursor
E;1-26/Domain: signal sequence #status predicted 4SIG>
F;1-26/Domain: signal sequence #status predicted 4SIG>
C;Species: Bos primi
C;Date: 16-Mar-1990
C;Accession: A33787
                                                                                     RESULT
A33787
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                                                              vascular endothelial growth factor (version
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A; Residues: 27-36;43-49, 'R';72-76,'Q',
C; Comment: The most common of several
C; Genetics:
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A;Title: Human vascular permeability factor. Isolation A;Reference number: A34492; MUID:90062112
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A; Residues: 1-146 < RED>
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A; Experimental source: AIDS-Kaposi's sarcoma_cell
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Best Local Similarity
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                                        Bos primigenius taurus
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37; Conser
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                     #sequence_revision
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Pred. No. 6e
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                     16-Mar-1990 #text_change 05-Nov-1999
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Gospodarowicz, D.;

Mitchell,

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Silva, M.;

Schilling,

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K.; Cr

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A:Molecule type: protein
A:Residues: 27-31 <FER>
A:Residues: 27-31 <FER>
C:Keywords: alternative splicing; glycoprotein
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-199/Product: vascular endothelial growth factor #status predicted
F:27-199/Product: vascular endothelial growth factor #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Ferrara, N.; Henzel, W.J.
Biochem. Biophys. Res. Commun. 161, 851-858,
A; Title: Pituitary follicular cells secrete (
A; Reference number: A33255; MUID:89286596
A; Accession: A33255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Blochem. Biophys. Res. Commun. 165, 1198-1206, 1989
A;Title: Vascular endothelial growth factor: a new member ca; Reference number: A33787; MUID:90121225
A;Accession: B33787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vascular endothelial growth factor precursor (version 2) - bovine (;Species: Bos primigenius taurus (cattle) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Nov-1999 C;Accession: B40080; B33787; A33255 R;Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N. Science 246, 1306-1309, 1989 A;Title: Vascular endothelial growth factor is a secreted angiogenic mitoger A;Reference number: A40080; MUID:90069608
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A;Title: Vascular endothelial growth factor: a new member of the A;Reference number: A33787; MUID:90121225
A;Accession: A33787
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-120 <TIS>
A;Cross references: GB:M33750; NID:g163810; PIDN:AAA30805.1; PID:C;Keywords: alternative splicing
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A; Residues: 27-190 <TIS>
A; Cross-references: GB:M31836; NID:g163808; PIDN:AAA30804.1;
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A; Residues: 1-190 <LEU>
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37; Conserv
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Pred. No. 9.9
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A; Accession: 552130
A; Status: prolit.
R;Maglione, D.; Guerriero, V.; Viglietto, G.; Delli-Bovi, P.; Proc. Natl. Acad. Sci. U.S.A. 88, 9267-9271, 1991
A;Title: Isolation of a human placenta cDNA coding for a prote A;Reference number: A41236; MUID:92021031
A;Accession: A41236
A;Status: preliminary
                                                                                                                                                 placental growth factor precursor - human C;Species: Homo sapiens (man) C;Date: 19-Jun-1992 *sequence_revision 19-Jun-1992 *text_change 05-Nov-1999 C;Accession: A41236
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A; Residues: 1-190 < SHA>
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995
C;Accession: S52130
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-148 < CLYT>
A;Cross-references: GB:S67522; NID:g456900; PIDN:AAB29223.1; PID:g456902
A;Note: sequence extracted from NCBI backbone (NCBIN:141422, NCBIP:141426)
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A;Title: Homologs of vascular endothelial
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A;Contents: NZ7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISKQLFEISVPLTSV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EWORT ---- QCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSY 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DWMRTLDKSGCKPRDTVVYLGEEYPESTNLQYNPRCVTVKRCSGCCNGDGQICTAVETRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -VTVSVTGVSSSSGTNSGVSTNLQRISVTEHTKCDCIGRTTTTPTTTREP 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.4%;
32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e and expression of the MUID:95143284
                                                                                                                                                                                                                                                                                                                                                 -PHQGQHIGEMSFLQHNKCECRPKKDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PELVPVKVANHTGCKCL-----PTAPRHP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 163.5; DE Pred. No. 2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 164; DB 2;
Pred. No. 1.4e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Verdouw, P.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth factor are encoded by the poxvirus
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                                                                        protein related to
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                                                                                                                           Persico, M.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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A;Molecule type: mRNA
A;Residues: 1-149 <MAG>
A;Cross-references: GB:X'
C;Genetics:
A;Gene: GDB:PGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-188 <TOW>
A; Cross-references: GB:U43837; NID:g1314335; PIDN:AAC52553.1; PID:g1314336
C; Comment: This factor is a mitogen, that is selective for endothelial cell ar endothelial growth factors 167 and VEGF 186.
C; Genetics:
vascular endothelial growth factor-related factor 186 precursor N;Alternate names: VRF 186 protein, VEGF 186 C;Species: Mus musculus (house mouse) C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change C;Accession: JC4679 R;Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.; Norden Biochem. Biophys. Res. Commun. 220, 922-928, 1996 A;Title: Characterization of the murine VEGF-related factor gene A;Reference number: JC4679; MUID:96183052 A;Accession: JC4679
                                                                                                                                                                                                                         RESULT
JC4679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vascular endothelial growth factor-related factor
y,Alternate names: VRF 167 protein
C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996
C;Accession: JC4680
R;Townson, S.; Lagercrantz, J.; Grimmond, S.; Sili
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A:Introns: 137/2
F:11-21/Domain: signal sequence #status
F:22-188/Product: vascular endothelial
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A;Title: Characterization of the murine VEGF-related factor gene.
A;Reference number: JC4679; MUID:96183052
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A;Map position: 14q24-14q31
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JC4680
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Best Local
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                                                                                                                                                                                                                                                                                                      102 LMIQYPSSQLGEM---SLEEHSQCECRP
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                                                                                                                                                                                                                                                                                                                                           FEISVPLTSVPELVPVKVANHTGCKCLP 101
                                                                                                                                                                                                                                                                                                                                                                                YARATCQPREVVVPLSMELMGNVVKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQI 101
                                                                                                                                                                                                                                                                                                                                                                                                                     WQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEWORTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISK 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.; Lagercrantz, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Pred. No. 8.3e
15; Mismatches
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Pred. No. 3.5e-09;
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growth factor-related factor #status
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                                                                                                    Nordenskjoeld,
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <LYT>
A;Cross-references: GB:S67520; NID:g456897;
A;Note: sequence inconsistent with nucleotic
                                                                      A; Reference number: A49530;
A; Contents: NZ2
A; Accession: B49530
                                                                                                                R; Lyttle, D.J.; Fraser, K.M.;
J. Virol. 68, 84-92, 1994
A; Title: Homologs of vascular
                                                                                                                                                           C; Accession: B49530
                                                                                                                                                                       C; Species: Orf virus
C; Date: 07-Apr-1994 #sequence_revision
                                                                                                                                                                                                                                                                                                      ОÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         placental growth factor precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change C;Accession: A56125 R;DiSalvo, J.; Bayne, M.L.; Conn, G.; Kwok, P.W.; Trivedi, P.G.; J. Biol. Chem. 270, 7717-7723, 1995
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C;Keywords: growth factor
F:1-21/Domain: signal sequence #status
F:22-207/Product: vascular endothelial
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lar endothelial growth factors
                                                                                                                                                                                                     vascular endothelial growth
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Best Local S
Matches 29
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                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 33.0 hes 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                                                                                                    DEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYIS
                                                                                                                                                                                                                                                                                                       KQLFEISVPLTSVPELVPVKVANHTGCKCLP 101
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                                                                                                                                                                                                                                                                             MQILKIP-PNRDPHSYVEMTFSQDVLCECRP
                                                                                                                                                                                                                                                                                                                                  NEVWGRSYCRPMEKLVYIADEHPNEVSHIFSPSCVLLSRCSGCCGDEGLHCVALKTANIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
29; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                              K.M.; Fleming,
                                                                                                                                                                                                                                                                                                                                                                                                          24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.7%;
33.0%;
                                                                                                    ar endothelial
MUID:94076465
                                                                                                                                                                                                     factor homolog A2R, 14.7K -
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Pred. No. 9.1e
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Score 145.5; DB 2
Pred. No. 1.1e-07;
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No. 9.1e-08;
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growth factor
                                                                                                                                              S.B.; Mercer, A.A.;
                                                                                                                                                                          18-Nov-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000072;
InterPro; IPR002400;
Pfam; PF00341; PDGF;
                                                                                                                     SEQUENCE FROM N.A. STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
Mammalia; 1
                                                                                               MEDLINE=97388482; PubMed=9247316;
                                                                                                                                                                                                                                  Kukk E., L.
Joukov V.,
                                                                                                                                                                                                                                                                        MEDLINE=97164697; PubMed=9012504;
                                                                                                                                                                                                                                                                                              STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FLT4-L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 601528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 MNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCM 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X94216;
U43142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U43142; AAA85214.1;
U58111; AAB02909.1;
P15692; IVPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                  Lymboussaki A.,
                                                                                                                                                                                                                                                                                                                                                                   Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419
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(Rel.
(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36, Created)
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175
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.0%;
 murine Flt4 ligand/VEGF-C.";
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Pred. No. 8.7e-32;
Pred. --hes 21;
                                                                                                                                                                                          pattern of expression vascular development.
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N-LINKED (GLO
N-LINKED (GLO
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N-LINKED (GLCNAC. ..) ()
9F598719DB3E014F CRC64
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VASCULAR ENDOTHELIAL GROWTH
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                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                   Long A., Burgess P., (
Kovacic S., Ciarletta
R., Beier D.R., Leak I
                                                                                                                                                                                                                                                    Kaipainen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415
                                                                                                                                                                                                            expression with VEGFR-3
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                                                                                                                                                                                                                                                      Jeltsch
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) (POTENTIAL).
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; Murinae; Mus
                                                                           Greco
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RESULT 3
VEGF_MOUSE
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Best Local S
Matches 62
                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
angiogenesis and endothelial Development 114:521-532(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
DOMAIN
                           Breier G.,
                                             SEQUENCE FROM N.A.
                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
Mitogen; Growth factor; Glyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U73620; AAC52984.1; -. EMBL; U58112; AAB46707.1; -. HSSP; P15692; 1VPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                    MEDLINE=92274860; PubMed=1592003;
                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002400; -. Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncogene 15:613-618(1997).
-!- FUNCTION: GROWTH FACTOR
                  Breier G., Albrecht U., Sterrer S., Expression of vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
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- SUBUNIT: HOM
- SIMILARITY: |
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                                                                                                                                                                                                                              MNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCL
                                                                                                                                                                                                                                                                          YDIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLIC
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                                                                                  Metazoa;
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271
271
295
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236
                                                                           ROT entry is copyright. It is produced through a c
Swiss Institute of Bioinformatics and the EMBL
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415
361
294
318
342
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236
                                                                          Rodentia;
                                                                                                                                                                                                                                                                                                                                          46471
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                                                                                                                                                                                                                                                                                                     . 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFIDE-LINKED (BY SIMILARITY).
TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                          MW.
                                                                                                                                                                                                                                                                                             15;
         cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVE
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Pred.
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N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.

VASCULAR ENDOTHELIAL GROWTH

4 X 24 AA TANDEM REPEATS.
                                                                         Craniata; Vertebrata;
Sciurognathi; Muridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                          D9D3DD3CECC659D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              (PARTIAL).
                                                                                                                                                                                                                                                                                            Mismatches
        al growth factor differentiation.
                                                                                                                                                                                                                                                                                                    374;
No. 1.
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                           Risau W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no rest
                                                                                                                                                                                                                                                                                                    DB 1;
.8e-31;
                                                                          Muridae;
                                                                                                                       (VEGF)
                                                                                                                                                                                                                    208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat.
                                                                                                                                                                                                                                                                                                              Length 415;
          during
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                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
(POTENTIAL).
                                                                                  Euteleostomi;
                                                                                                                       (VASCULAR
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                                                                          Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions on
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                  embryonic
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EMBL; S38083;
EMBL; S38100;
EMBL; M95200;
EMBL; U41383;
                                                                                                           VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                       Mitogen;
SIGNAL
CHAIN
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                          VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
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MEDLINE=9235593; PubMed=1644816;
Claffey K.P., Wilkison W.O., Spiegelman B.M.;

"Vascular endothelial growth factor. Regulation by cell differentiation and activated second messenger pathways.";

J. Biol. Chem. 267:16317-16322(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:103178; Vegf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shima D.T., Kuroki M., Deutsch U., Ng Y., Adamis A.P., D'Amore I "The mouse gene for vascular endothelial growth factor. Genomic structure, definition of the transcriptional unit, and
                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A43351; A43351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
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Pfam; PF00341; PDGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                characterization of transcriptional and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96216498; PubMed=8632007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE CHOROID PLEXUS, PARAVENTRICULAR NEUROEPITHELIUM, PLACENTA AN KIDNEY GLOMERULI. ALSO FOUND IN BRONCHIAL ENTHELIUM, ADRENAL GLAND AND IN SEMINIFEROUS TUBBLIES OF TESTIS, HIGH EXPRESSION OF VEGE CONTINUES IN KIDNEY GLOMERULI AND CHOROID PLEXUS IN ADULTS. SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO CELL-ASSOCIATION/HEPARIN-BINDING.
TISSUE SPECIFICITY: IN DEVELOPING EMBRYOS, EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: THREE FORMS (VEGF-1, VEGF-2 AND VEGF-3) ARE PRODUCED AS A RESULT OF ALTERNATIVE SPLICING OF THE SAME GENE. THE LONGEST FORM (VEGF-3, SHOWN HERE) CONTAINS A BASIC INSERT LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: VEGF-1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL GROWTH. INDUCES PERMEABILITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEGF-3 REMAINS CELL-SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER, DISULFIDE-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
  l Similarity
38; Conser
                                                                                                                                                                                                                                                                                                                                                                                            Growth
                                                                                                                                                                                                                                                                                                                                                                                                           PS00249; PDGF_1; 1.
PS50278; PDGF_2; 1.
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-3 FROM N.A
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AAA40547.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB22253.1;
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HSSP; P15692; 2VGH.
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-i- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
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                                                                                                           Siegel N., Haymore B.L., Leimgruber R., Feder J "Human vascular permeability factor. Isolation J. Biol. Chem. 264:20017-20024(1989).
                                                                                                                                                                                                                                                                    "The human gene for vascular endothelial growth factor. Multiple protein forms are encoded through alternative exon splicing."; J. Biol. Chem. 266:11947-11954(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=90069608; PubMed=2479986;
Leung D.W., Cachianes G., Kuang W
"Vascular endothelial growth fact
                      Kochs G., Marme D., Hug H., Weich H.A.; "Synthesis and assembly of functionally endothelial growth factor homodimers in Eur. J. Biochem. 211:19-26(1993).
                                                               MEDLINE=93145946; PubMed=7678805; Fiebich B.L., Jaeger B., Schoellm
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=92231879; PubMed=1567395;
Weindel K., Marme D., Weich H.A.;
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Mammalia; Eutheria;
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01-APR-1990 (Rel. 14, Last sequence update)
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                                                                                         SEQUENCE OF
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                                                                                                                                                                                                   "AIDS-associated Kaposi's sarcoma cells in culture express endothelial growth factor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 246:1306-1309(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF_HUMAN
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 CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                      J.C.,
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                                                                                                                                                                                                                                                                                                               E., Mitchell
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                                                                                                                                                                                                                                                                                                                                                                                permeability factor,
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Primates;
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(2.5
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                                                    Schoellmann C.
H., Weich H.A.;
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ANGSTROMS)
                                                                                                                                             Heuvelman D.,
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7; Mismatches 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
Catarrhini; Hominidae;
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                                                                                                                                                                                                           modified and this statement is not removed.
                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                            "Solution structure of the heparin-binding endothelial growth factor."; Structure 6:637-648(1998).
-i- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "1H, 13C, and 15N backbone assignment and receptor-binding domain of vascular endoth protein Sci. 6:2250-2260(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fairbrother W.J., Champe M.A., Starovasnik M.A.; "1H, 13C, and 15N backbone ass:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [10]
STRUCTURE BY NMR OF 34-135.
MEDLINE=97477915; PubMed=9336848;
MEDLINE=97477915; PubMed=9336848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS)
MEDLLNE=98035455; pubMed=9351807;
Muller Y.A., Christinger H.W., Keyt B.A
"The crystal structure of vascular endo"
                                                                                                                                                                                                entities
                                                                                                                                                                                                                                                                                                                                                                                                                                           Fairbrother W.J., Starovasnik M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Crystal structure of the complex peptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wiesmann C., Christinger H.W., Coch: Fairbrother W.J., Keenan C.J., Meng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97352774; PubMed-9207067;
Muller Y.A.; Li B., Christinger H.W.,
de Vos A.M.;
"Vascular endothelial growth factor: «
                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98298440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY
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                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
                                                                                                                                                                                                                                                                                                  SIMILARITY).
ALTERNATIVE PRODUCTS:
ALTERNATIVE SPLICING (
                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMODIMER, DISULFIDE-LINKE SUBCELLULAR LOCATION: SECRETED BUT TO THE EXTRACELLULAR MATRIX UNLESS
                                  M32977;
M639781;
M63971;
M63971;
M63972;
M63973;
M63974;
M63975;
M63977;
M63977;
M63977;
M63977;
                                                                                                                                                                                                                                                                                          VEGF-189 AND VEGF-215)
                                                                                                                                                                                                                                                                                                                                                                       PERMEABILITY
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            A40079;
A40080;
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                                                                                                                                                                                    requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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A40079.
A40080.
A40454.
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AAA36804.1;
AAA36804.1;
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CAA44447.
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                                    A34492.
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AAA36804.
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AAA36807.1;
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Meng G., de V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between VEGF and
                                                                                                                                                                                                                                                                                                                                                                                   IN ANGIOGENESIS, AL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nt and secondary structure of
endothelial growth factor.";
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othelial growth factor (VEGF)
copy flexibility and receptor
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                                                                                                                                                                                                                                                                                                   GF ARE PRODUCED (VEGF-121, VEGF-
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L outstation -
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Matches 37
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                 Redmer D.A., Dai Y., Li J., Charnock-Jones D.S., Smith S. Reynolds L.P., Moor R.M.;
"Characterization and expression of vascular endothelial factor (VEGF) in the ovine corpus luteum.";
J. Reprod. Fertil. 108:157-165(1996)
-i- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ECELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VA
                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OV-1997 (Rel. 35, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR
PERMEABILITY FACTOR) (VPF).
                                                                                                                                                                                                                                     VEGF_SHEEP
P50412;
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                                                                                                                          Bovidae; Caprinae;
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM;
                                                                                     MEDLINE=97117958; PubMed=8958842;
                                                                                                TISSUE=Kidney;
                                                                                                                                                        Eukaryota;
                                                                                                                                                                   Ovis aries
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                               Mammalia; Eutheria;
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SUBUNIT: HOMODIMER, DISULFIDE-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; B40454; B40454.

; C40454; C40454.

; J01463; J01463.

; J01464; J01464.

; S17348; S17348.

; S17348; S17348.

; S17348; S17348.

; S1794; O8-APR-98.

; 1VPF; O8-APR-98.
          PERMEABILITY
                                                                                                                                                                                                                                                                                                                              EESNITMQIMRIK-----PHQGQHIGEMSFLQHNKCECRPKKDR 136
                                                                                                                                                                                                                                                                                                                 STSYISKOLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPR 105
                                                                                                                                                                                                                                                                                                                                                       ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00341; PDGF;
                                                                                                                                                                                                                                                                                                                                                                           . Similarity 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00249; PDGF_1; PS50278; PDGF_2;
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                                                                                                                                                      Metazoa;
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142
215
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209
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                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                    28.3%;
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MISSING (IN ISOFORM VEGF-121).
; 7B9759AD5871FF33 CRC64;
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Pred. No. 1.
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K -> N (IN ISOFORM VEGF-121 AND
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                                                                          S.K.,
                           ENDOTHELIAL
                                                       growth
                                                                                                                                              Bovoidea;
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*P15691;
*01-APR-1990 (Rel. 1:
*01-APR-1990 (Rel. 1:
*01-OCT-1996 (Rel. 3:
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CARBOHYD
Tischer E., Gospodarowicz D., Mitchell R., Lau K., Crisp T., Fiddes J.C., Boraham J.A. "Vascular endothelial growth factor: a new derived growth factor gene family.";
                                                                                                                                                                                                                                 01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR
                                          MEDLINE=90121225;
                                                                           Science 246:1306-1309(1989)
                                                                                        Leung D.W., Cachianes G., Kua
"Vascular endothelial growth
mitogen.":
                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE MEDLINE=90069608; PubMed=2479986;
                                                                                                                                    SEQUENCE FROM
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                      NCBI_TaxID=9913;
                                                                                                                                                                                                  Bos taurus (Bovine).
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-!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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a; Eutheria; Cei
; Bovinae; Bos.
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; PS50278; PDGF_2;
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                                                                                                 Kuang W.-J., wth factor is
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No. 1.4e-10;
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01-OCT-1996
15-JUL-1999
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SEQUENCE
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SIGNAL
                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
VASCULAR ENDOTHELIAL GROWTH FACTOR HON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR;
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MEDLINE=89286596; PubMed=2735925;
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      virus
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P; P15692; 2VGH.
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                                                                                                                                                                                                                                     EEFNITMQIMRIK-PHQS-QHIGEMSFLQHNKCECRP 131
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M33750;
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AAA30805.1;
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INTERCHAIN (BY SIMILARITY).
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W; EDBF903E46E24789 CRC64;
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No. 2.3e-10;
                                                                            update)
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01-FEB-1996 (Rel. 33, 1
01-OCT-1996 (Rel. 34, 1
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Mammalia; Eutheria;
           MEDLINE=95143284;
                          TISSUE-Heart;
                                   SEQUENCE FROM
                                                                                          Sus scrota (Pig).
                                                                                                       VEGF.
                                                                                                               PERMEABILITY FACTOR) (VPF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                       NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.
-:- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P15692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S67522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     poxvirus orf virus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lyttle D.J., Fraser K.M., Fleming "Homologs of vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94076465; PubMed=8254780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=73495;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parapoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA.viruses,
                                                                                                                                                                                                                                           96
                                                                                                                                                                                                                                                                 69
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                                                                                                                                                                                                                                                                                       36
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                                                                                                                                                                                                                                                                 ISKQLFEISVPLTSV-----PELVPVKVANHTGCKCL-----PTAPRHP
                                                                                                                                                                                                                                                                                       DWMRTLDKSGCKPRDTVVYLGEEYPESTNLQYNPRCVTVKRCSGCCNGDGQICTAVETRN
                                                                                                                                                                                                                                                                                                              EWQRT---
                                                                                                                                                                                                                                            TT ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00341; PDGF;
                                                                                                                                                                                                                                                                                                                                   l Similarity
38; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00249; PDGF_1; FALSE_---
PS50278; PDGF_2; 1.
PS50278; PDGF_2; 1.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000072; -.
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                                                                                                                                                                                                                                                                                                                                                                                          148
                                                                                                                                                                                                                                          VTVSVTGVSSSSGTNSGVSTNLQRISVTEHTKCDCIGRTTTTPTTTREP
                                                                                                                                                                                                                                                                                                                                   Conservative
 Tang
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77
81
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                                  N.A.
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                                                                                                                                                                                                                                                                                                             -QCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSY 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB29223.1;
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                                                                                                                                                                                  STANDARD;
PubMed=7841203;
Z.H., Gho B.C.H
                                                                                                                                                                                                                                                                                                                                                                                                       88
130
132
71
71
80
95
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                                                                  Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                          16078
                                                                                                                                                                                                                                                                                                                                             27.4%;
                                                                                                                          GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
                                                                                                                                      Last sequence update)
Last annotation updat
                                                                                                                                                              Created)
 Gho B.C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               no
                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                            Score 164;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VASCULAR ENDOTHELIAL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMOLOG
                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.B., N
 Verdouw P.D.;
                                                                                                                                                                                   190
                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal.
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h factor are
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.2e-10;
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                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 its content
                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                   Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
"Isolation of a human placenta cDNA coding the vascular permeability factor."; Proc. Natl. Acad. Sci. U.S.A. 88:9267-9271. [2]
                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1260:235-238(1995).

1. FUNCTION: GROWTH FACTOR ACTIVE IN ANGIGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY (BY SIMILARITY).

1. SUBURILITY HOWODIMER, DISULFIDE-LINKED (BY SIMILARITY).

1. SUBCELLULAR LOCATION. SECRETED BUT REMAINS ASSOCIATED TO CELLS TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
                                                                                                                                                                                                              01-OCT-1996
01-OCT-2000
                                                                                                                                                                                                                                          P49763;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                       MEDLINE=92021031; PubMed=1924389;
Maglione D., Guerriero G., Viglie
                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                    PLACENTA GROWTH FACTOR PRECURSOR PGF OR PLGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                   rissue=Placenta;
                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       PLGF_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence and expression of the porcine vascular
                                                                                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                                                                                                                       65
                                                                                                                                                                                                                                                                                                                                                                                                   38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Eleuropean Bioinformatics Institute. There are no rest
                                                                                                                                                                     sapiens (Human)
                                                                                                                                                                                                                                                                                                                                         EEFNITMQIMRIK-----PHQGQHIGEMSFLQHNKCECRPKKDR 135
                                                                                                                                                                                                                                                                                                                                                                     STSYISKOLFEISVPLTSVP----
                                                                                                                                                                                                                                                                                                                                                                                                   EVVKFMD-VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT
                                                                                                                                                                                                                                                                                                                                                                                                                    ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X81380;
P15692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00249; PDGF_1; PS50278; PDGF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000072;
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51
82
86
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100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAA57143.1; -. 2VGH.
                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26
190
93
127
129
76
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22368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          factor;
                                                                                                                                                                                                           34, Last sequence update)
40, Last annotation updat
                                                                                                (PLGF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor
                                                                                                                                           Primates;
                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           r; Glycoprotein; Signal.

6 POTENTIAL.

6 VASCULAR ENDOTHELIAL GROWTH F.

3 BY SIMILARITY.

9 BY SIMILARITY.

9 BY SIMILARITY.

1 INTERCHAIN (BY SIMILARITY).

5 INTERCHAIN (BY SIMILARITY).

1 INTERCHAIN (BY GIMILARITY).

1 INTERCHAIN (BY GIMILARITY).

2368 MW; 04D40B8D7913047F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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                                                      Viglietto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                     ELVPVKVANHTGCKCLPTAPR 105
                                                                                                                                        Craniata; Vo
Catarrhini;
              88:9267-9271(1991;
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDGF/VEGF FAMILY OF GROWTH FACTORS
                                                                                                                                                                                                (PLGF-1/PLGF-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163.5; DB 1;
No. 4.6e-10;
                                                                                                                                                                                                                                                                      170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                        Vertebrata; Euteleostomi;
                                                       Delli-Bovi P.,
                                                                                                                                                                                                                                                                      AA
                                                                                                                                         Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as its content
                                         for a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
                                         protein
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                                                       Persico
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL
                                           related
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
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MBL outstation -
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CARBOHYD
VARSPLIC
CONFLICT
SEQUENCE
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DISULFID
                                                                                       CARBOHYD
                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                       MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X54936; CAA38698.1;
EMBL; A18411; CAA01393.1;
EMBL; S72960; AAB30462.2;
HSSP; P15692; IVPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth fact
chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hauser S., Weich H.A.;

"A heparin binding form of placenta growth factor (Expressed in human umbilical vein endothelial cells placenta.";
                                                                                                                                                                                                                                            Heparin-binding
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-!- SUBCELLULAR LOCATION: BOTH FORMS ARE SECRETED BUT THE LONGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maglione D., Guerriero V., Viglietto G., Ferraro M.G., Aprelikova Alitalo K., del Vecchio S., Lei K.-J., Chou J.Y., Persico M.G.; "Two alternative mRNAs coding for the angiogenic factor, placenta growth factor (PIGF), are transcribed from a single gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maglione D., Guerriero V., Viglietto G., Alitalo K., del Vecchio S., Lei K.-J., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (PLGF-2).
MEDLINE=93205407; PubMed=7681160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (PLGF-2). TISSUE=Placenta;
                                                                                                                                                                                                                                                                                      Mitogen;
                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor bioactivity, in vitro and in vivo, to Flt-1 but not to Flk-1/KDR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Park J.E., Chen H.H., Winer J., Houck K.A., "Placenta growth factor. Potentiation of va-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95014370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncogene 8:925-931(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94198032; PubMed=8148155
                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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FUNCTION: GROWTH FACTOR OF UNKNOWN FUNCTION. BINDS TO FUNCTION: GROWTH FACTOR OF CHIKNOWN FUNCTION. BINDS TO FUNCTION OF LOW LEVELS OF VEGF.
IS ABLE TO POTENTIATE THE ACTION OF LOW LEVELS OF VEGF.
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SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
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some 14.";
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PS50278; PDGF_2; 1.
Growth factor; Glycoprotein; Signal;
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                                         (IN ISOFORM PLGF-1).
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vascular endothelia
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modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHE CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M84230; AAA37057.1; HSSP; P15692; 2VGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) (VASCULAR PERMEABILITY
                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
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EEVKEMD-VYKRSYCRPIEMLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDESLECVPT 70
                                             ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 64
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6; Mismatches 40
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P52584;
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01-OCT-1996 (Rel. 3
01-OCT-2000 (Rel. 4
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DISULFID
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Mitogen;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR HOMOLOG PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
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-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        poxvirus orf virus.";
J. Virol. 68:84-92(19)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, Parapoxvirus.
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                                               SVPLTSVPELVPVKVANHTGCKCLP---TAP
                                                                                                                                               TQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEI 76
SG--SGSNGMQRLSFVEHKKCDCRPRFTTTP 122
                                                                                             SECKPRPIVVPVSETHPELTSQRFNPPCVTLMRCGGCCNDESLECVPTEEVNVSMELLGA
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32; Conserv
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PS50278; PDGF_2; 1.
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35.2%;
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INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTE)
W; 917C0F6883030C39 CRC64;
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) CRC64;
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RESULT 13 VEGB_MOUSE

VEGB_MOUSE

STANDARD;

PRT;

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Best Local Similarity
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01-OCT-1996
01-OCT-1996
15-DEC-1998
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Mitogen;
                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                              EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of the murine VESF-related factor gene.";
Biochem. Biophys. Res. Commun. 220:922-928(1995).
-!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olofsson B., Pajusola K., Kaipainen A., von Euler G., Joukov Saksela O., Orpana A., Pettersson R.F., Alitalo K., Eriksson "Vascular endothelial growth factor B, a novel growth factor endothelial cells.";
                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VASCULAR
                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Townson S., Lagercrantz J., Grimmond S., Nordenskjoeld M., Weber G., Hayward N.K.;
                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96183052; PubMed=8607868;
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                                                                              14 WORTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTSTSYISKQL
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rPro; IPR000072; -.; PF00341; PDGF; 1.
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: U43837;
LMIQYPSSQLGEM --- SLEEHSQCECRP
                          FEISVPLTSVPELVPVKVANHTGCKCLP
                                                      YARATCOPREVVVPLSMELMGNVVKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQI 101
                                                                                                                                                                                                                                                                                                               P15692;
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                                                                                                                                                                                                            PS00249; PDGF_1; 1.
PS50278; PDGF_2; 1.
Growth factor; Signal; Heparin-binding.
1 21 POTENTIAL.
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                                                                                                             Conservative
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Pred.
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Sciurognathi;
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                            101
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No. 2.1e-08;
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D BY HEPARIN.
N HEART, BRAIN, KIDNE
                                                                                                                                     Length
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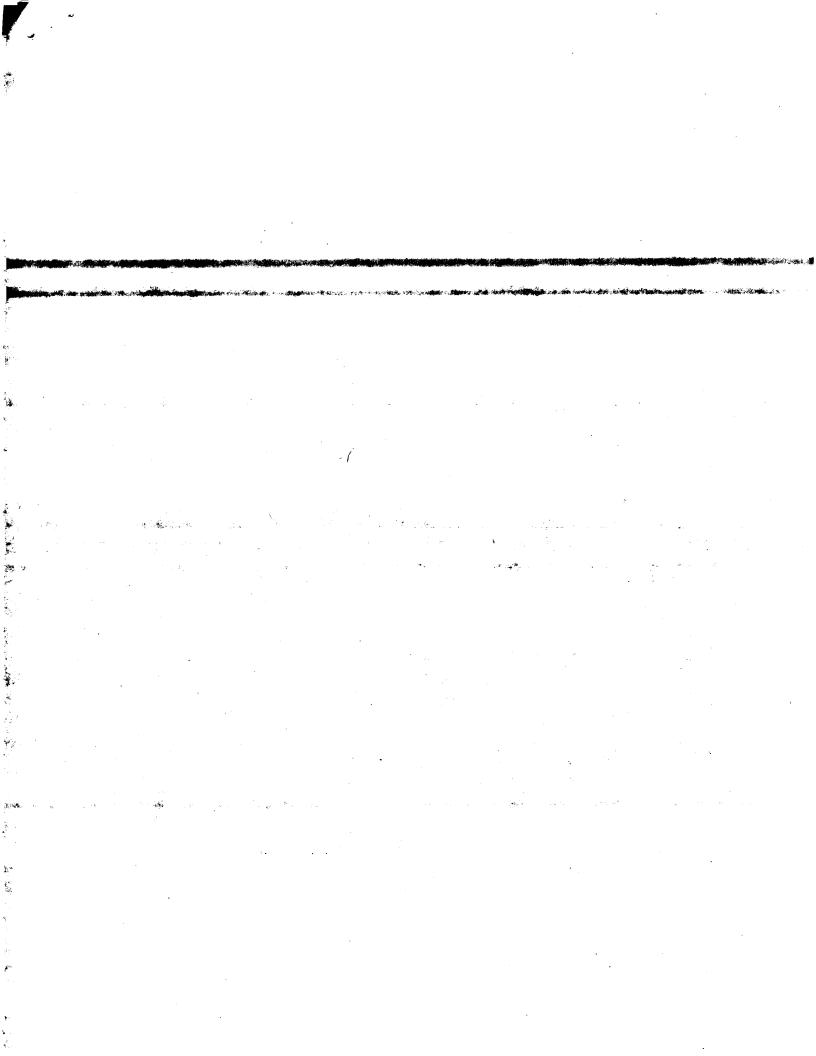
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Best Local
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EMBL; U43369;
HSSP; P15692;
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01-OCT-1996 (
01-OCT-1996 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vascular endothelial growth factor,";
Genome Res. 6:124-131(1996).
-!- FUNCTION: CERCENT.
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                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00341; PDGF; 1
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Hayward N., Weber G.,
"Cloning and characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=96197355; PubMed=8637916;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                       Mitogen; Growth
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                                    TSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLP
QHQVRMQILMIRYPSSQLGEM---SLEEHSQCECRP
                                                                          KVVSWIDVYTRATCQPREVVVPLTVELMGTVAKQLVPSCVTVQRCGGCCPDDGLECVPTG
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                                                                                                            EEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNTS
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Metazoa; Chordata; C

Metazoa; Primates; (
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(Rel. 34, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                    Conservative
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AAA91463.1; -.
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arson E., Rakar
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Pred.
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Alitalo K., E
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Nordenskjoeld
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FORM HETERODIMER
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PLGF_MOUSE
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Achen M.G., Gad J.M., Stacker S.A., Wilks A.F.;
"Placenta growth factor and vascular endothelial growth factor are co-expressed during early embryonic development.";
Growth Factors 15:69-80(1997).
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InterPro; IPR000072; -.
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MEDLINE=97059399; PubMed=8903720;
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                                                                                                                                                                                                                                                                                                                                Pfam; PF00341; PDGF;
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CELL GROWTH (BY SIMILARITY).
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                                                                     Local Similarity
40
             SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
NEVWGRSYCRPMEKLVYILDEYPDEVSHIFSPSCVLLSRCSGCCGDEGLHCVPIKTANIT 99
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BY SIMILARITY.
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SUMMARIES

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InterPro; IPR00072; -
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; -; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
SEQUENCE 326 AA; 37112 MW;
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EMBL: Y12863; CAA7370.1; --
HSSP: P15692; IVPP.
InterPro; IPR000072; --
Pfam; PF00341; PDGF; 1.
PrODOM; PD001629; -; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS00278; PDGF_2; 1.
SMART; SM0141; PDGF; 1.
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01-JAN-1998
01-MAR-2001
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035251;
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STRAIN-SPRAGUE DAWLEY;
MEDLINE-97349118; PubMed-9205122;
Yamada Y., Nezu J., Shimane M., Hirata
"Molecular cloning of a novel vascular
"Molecular cloning of a novel vascular
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EMBL;
EMBL;
EMBL;
EMBL;
HSSP;
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Mammalia; Eutheria;
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF014827; AAI
HSSP; P15692; 1VPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEGF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat)
      158
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                                                                                                                                                                                               Local Similarity
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FYDIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLI 60
                                                                                                         FYDIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLI
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Y12870; CAA73371.1;
D89630; BAA24264.1;
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Rodentia;
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Last annotation updat
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No. 1.7e-59;
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Best Local Similarity
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O57352;
O1-JUN-1998 (TrEMBLrel. 06, C
O1-JUN-1998 (TrEMBLrel. 16, L
O1-MAR-2001 (TrEMBLrel. 16, L
VASCULAR ENDOTHELIAL GROWTH F
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MGD; MGI:108037; Figf.
InterPro; IPR000072; -.
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; -; 1.
PROSITE; PS00249; PDGF_1; 1
PROSITE; PS50278; PDGF_2; 1
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P97946;
01-MAY-1997 (TrEMBLrel
01-MAY-1997 (TrEMBLrel
01-MAR-2001 (TrEMBLrel
VASCULAR ENDOTHELIAL G
SEQUENCE FROM N.A. MEDLINE=98167900;
                                                             Coturnix coturnix japonica (Japanese quail). Eukaryota; Metazoa; Chordata; Craniata; Vert
                                                    Archosauria;
                                                                                   VEGF-C
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EMBL; D89628; BAA14002.1;
HSSP; P15692; 1VPP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=93934;
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MEDLINE=97030254; PubMed=8876195;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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  PubMed=9435294;
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93.6%;
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FACTOR C PRECURSOR.
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FACTOR D (C-FOS INDUCED
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Sciurognathi; Muridae;
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                                                    Galliformes;
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No. 6.
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mes; Phasianidae; Phasiani
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                                                    Phasianinae;
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Matches 63
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SEQUENCE
                                                                                                                                                                                                                Signal.
SIGNAL
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR.
BOS TANTHE (POSTICE)
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alitalo K., Le Douarin N.M.;
"Avian VEGF-C: cloning, embryonic expression pattern and stimulation of the differentiation of VEGFR2-expressing endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Cetartioda
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InterPro; IPR002400; -.
Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                          PROSITE; PS00249; PDGF_1; PROSITE; PS50278; PDGF_2;
                                                                                                                                                                                                                                                                                                                       InterPro; IPR000072; -
Pfam; PF00341; PDGF; 1
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                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00141; PDGF; 1.
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                                                                                                                                                                                                                                                        SM00141; PDGF;
                                                                  61;
                                                                                    Similarity
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                                                                  Conservative
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                                                                                                                                                                        46681 MW;
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                                                                                  61.7%;
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                                                              16;
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VASCULAR ENDOTHELIAL GROWTH FACTOR
; 58BA84317A3C8E2D CRC64;
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VASCULAR ENDOTHELIAL GROWTH
; 099BFCC79151BF2B CRC64;
                                                                Pred. No. 1.405; Mismatches
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Pred. No. 1e-33;
                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata;
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                                                                                    369;
No. 1.
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                                                   DB 6;
1.4e-33;
22;
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   Query Match
Best Local S
Matches 32
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HSSP; P15692; 2ve...
InterPro; IPR000072; -.
Pfam; PF00341; PDGF; 1.
PROSITE; PS50278; PDGF_2; 1
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O35757; CTEMBLEEL 05, CTEMBLEEL 05, LTEMBLEEL 05, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LTEMBLEEL 16, LT
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NON_TER 1 1
NON_TER 126 126
SEQUENCE 126 AA; 139
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Q9GLX1;
Q1-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                               TISSUE=LUNG;
Mandriota S.J., Pepper M.S.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ
EMBL; AF099135; AAG29747.1; -.
NON_TER 1 1
NON_TER 122 122
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Mammalia; Eutheria;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
VASCULAR ENDOTHELIAL GROWTH
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Submitted (JUN-1997) to the
EMBL; AF010302; AAB63248.1;
HSSP; P15692; 2VPF.
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NCBI_TaxID=10116;
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae; Bovinae; Bos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 VNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCL 100
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   Similarity 94.32; Conservative
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                                                                                                                                                                122
122 /
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                                                                                                                                                                    ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126
13977
                                                                                                                                                                    13820 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rodentia;
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                                  29.8%;
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Score 178; DB 6;
Pred. No. 1.4e-12;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
FACTOR-D (FRAGMENT).
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Last annotation update)
FACTOR-C (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 207; DB
Pred. No. 7.6e
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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thi; Muridae; Murinae; Rattus.
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.6e-16;
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                                                                                                                                                                                                                                                                                                  databases
                                                                Length 122;
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      Indels
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Best Local S
Matches 38
Pfam; PF00341; PDGF; 1.
PROSITE; PS00249; PDGF 1.
PROSITE; PS00249; PDGF 1.
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InterPro; IPR00072;
Pfam; PF00341; PDGF; 1.
PROSITE; PS00249; PDGF; 1.
PROSITE; PS00279; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         Q9JKX7;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MR-2001 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ehrenbergi: the role of vascular endothelial growth factor.";
FEBS Lett. 452:133-140(1999).
EMBL; AF186236; AAD56245.1;
InterPro. Trocord.
                                                                                                          Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF222779; AAF25958.1; -.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                          VASCULAR ENDOTHELIAL GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9JКX7
                                                                                                                                                       Al20 in rat masseter muscle.
                                                                                                                                                                      Ishii H., Arakawa T., Okayama M., Oota Developmental expression of vascular (VEGF-A) splicing variants, VEGF-A188,
                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99313148; PubMed=10386577;
Avivi A., Resnick M.B., Nevo E., Jo
"Adaptive hypoxic tolerance in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SESNITMQIMRIK-PHQS-QHIGEMSFLQHNRCECRPKKDR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STSYISKOLFEISVPLTSVPELVPVKVANHTGCKCLPTAPR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence up
(TrEMBLrel. 16, Last annotation
DOTHELIAL GROWTH FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
            PDGF_1; 1.
PDGF_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
FACTOR-A144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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Pred. No. 8.8
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8, VEGF-Al64,
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                                                                                                                                                                        a T., Inomata K.;
l growth factor-A
, VEGF-A144, and V
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Best Local
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                                                                       O9UH58 PRELIMINARY;
O9UH58;
O1-MAY-2000 (TrEMBLrel. 13, C
O1-MAY-2000 (TrEMBLrel. 13, L
O1-MAY-2001 (TrEMBLrel. 16, L
VASCULAR ENDOTHELIAL GROWTH F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9QXG7 PRELIMINARY;
Q9QXG7;
01-MAY-2000 (TrEMBLrel. 13, C:
01-MAY-2000 (TrEMBLrel. 16, L:
01-MAR-2001 (TrEMBLrel. 16, L:
VASCULAR ENDOTHELIAL GROWTH F/
         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                  VEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Ishii H., Arakawa T., Okayama M., Oota I., Takuma
"Developmental expression of vascular endothelial
"Developmental expression of Vascular endothelial
""""" enlicing variants, VEGF-A188, VEGF-A164,
NCBI_TaxID=9606;
                                                              (DJ261G23.6.2).
                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000072; -. Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1999) to the EMBL; AF215725; AAF19211.1; HSSP; P15692; 1VPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (VEGF-A) splicing variants,
masseter muscle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00141; PDGF; 1. SEQUENCE 170 AA; 20018 MW;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00141; PDGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                EVVKFMD-VYQRSYCRPIETLYDIFQEYPDEIEYIFKPSCVPLMRCAGCCNDEALECVPT
                                                                                                                                                                                                  SESNVTMQIMRIK-PHQS-QHIGEMSFLQHSRCECRPKKDR 135
                                                                                                                                                                                                                                                                            ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETLKVIDEEWORTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVVKFMD-VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCAGCCNDEALECVPT
                                                                                                                                                                                                                                                                                                     l Similarity
37; Conser
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                                                                                                                                                                                                                                                                                                                                                                214 AA;
                                                                                                                                                                                                                                                                                                      Conservative
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Rodentia;
       Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                  25239 MW;
                                                                                                                                                                                                                                                                                                               28.7%;
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36.6%;
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Last annotat
FACTOR-A188.
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                                                                        Last sequence update)
Last annotation update)
FACTOR ISOFORM 121 PRECURSOR
                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                   Score 171.5; DB 11;
Pred. No. 1.3e-11;
7; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                  60FBB876F5304946 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Best Local
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Pfam; PF00341; PDGF; 1.
PROSITE; PS00249; PDGF-1; 1
PROSITE; PS50278; PDGF-2; 1
SMART; SM00141; PDGF; 1.
Q9UL23
Q9UL23;
                                                                                                                                                                                                                                                                                                                              01-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
SIGNAL
                                                                                                                                                                                                   Williams S.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL186131; CAC19517.1; -
SEQUENCE 171 AA; 20064 MW; D02ECA735FF6E9F8 CRC64;
                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2000) to the EMBL; AF214570; AAF19659.1; EMBL; AL136131; CAC19515.1;
                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DJ261G23.6.5 (VASCULAR ENDOTHELIAL GROWTH FACTOR).
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            VEGF.
                                                                                                                                                                                                                                                                                                                                                             Q9Н1W8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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                                                               EESNITMQIMRIK----
                                                                                  STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPR 105
                                                                                                                 ETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEESLICMNT 64
                                                                                                                                                                                                                                                                                                                                                                                                                            EESNITMQIMRIK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
37; Conserv
                                                                                                                                                          Similarity
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                                                                                                                                                  Conservative
            PRELIMINARY;
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17219
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35
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                                                              PHQGQHIGEMSFLQHNKCECRPKKDR 136
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the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 169.5;
Pred. No. 1.5e
14; Mismatches
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                                                                                                                                                Pred. No. 1.7
                                                                                                                                                          Score 169.5; DB 4; Pred. No. 1.7e-11;
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                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Catarrhini; Hominidae;
         PRT;
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          174
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; Homo.
                                                                                                                                                                    171;
                                                                                                                                                11;
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RESULT
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Best Local
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                                                                                                                                                                                                    O60720 PRELIMINARY; PRT; 209 AA.
O60720;
O1-AUG-1998 (TYEMBLIFEL 07, Created)
O1-MAY-1999 (TYEMBLIFEL 10, Last sequence update)
O1-MAR-2001 (TYEMBLIFEL 16, Last annotation update)
VEGF183 PROTEIN PRECURSOR (VASCULAR ENDOTHELIAL GROWTH
CDJ261G23.6.6) (VASCULAR ENDOTHELIAL GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and receptor mRNA expression in identification of VEGF148 mRNA, Clin. Sci. 97:303-312(1999).
Submitted (DEC-2000) to the EMBL; AJ010438; CAA09179.1;
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clin. Sci. 97:303-
EMBL; AF091352; AAI
HSSP; P15692; 2VPF
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01-MAY-2000 (TIEMBLIE). 13, Last sequence up
01-MAR-2001 (TIEMBLIE). 16, Last annotation
VASCULAR PERMEABILITY FACTOR 148.
                                             Williams S.
                                                                                                              Submitted
                                                                                                                                   Jingjing L.,
                                                                                                                                                         TISSUE=RETINA;
                                                                                                                                                                             SEQUENCE OF 114-209
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=GLOMERULI;
MEDLINE=99394945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            MEDLINE=99096474; PubMed=9878851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Heterogeneous vascular endothelial growth and receptor mRNA expression in human glome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harper S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EESNITMQIMRIK-----PHQGQHIGEMSFLQHNKCECRPKKDR
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37; Conserv
                                                                                                            (MAY-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 169.5;
Pred. No. 1.8e
14; Mismatches
                        EMBL/GenBank/DDBJ
                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harrison
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae;
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RESULT 15
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Best Local Similarity 35.2
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000072; -.
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; -; 1.
PROSITE; PS00249; PDGF_1; 1
PROSITE; PS50278; PDGF_2; 1
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Williams S.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL136131; CAC19512.1; -
SEQUENCE 232 AA; 27042 MW; FB49F364446F4D01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9H1W9;
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01261G23.6.3 (VASCULAR ENDOTHELIAL GROWTH FACTOR).
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SIGNAL
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EMBL; AL136131; CAC19514.1; -.
HSSP; P15692; 2VPF.
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                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                          98 EESNITMQIMRIK-----PHQGQHIGEMSFLQHNKCECRPKKDR 136
                                                                                                        65 STSYISKQLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPR 105
                                                                                                                                     39 EVVKFMD-VYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 EESNITMQIMRIK-----PHQGQHIGEMSFLQHNKCECRPKKDR 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STSYISKOLFEISVPLTSVP----ELVPVKVANHTGCKCLPTAPR 105
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27
209 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 POTENTIAL.
209 VEGF183 PROTEIN.
24422 MW; F01CCEACD945D6CA CRC64;
                17,
                                                                                                                                                                                                   28.3%; Score 169.5; DB 4; Length 232; 35.2%; Pred. No. 2.3e-11; Live 14; Mismatches 43; Indels 11
              2001, 14:50:57
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